Method	BLASTN
NCBI GI	g170053
BLAST score	80
E value	3.0e-37
Match length	103
% identity	95
NCBI Description	Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.	48148
Seq. ID	leu701151270.h1
Method	BLASTN
NCBI GI	g1277165
BLAST score	48
E value	3.0e-18
Match length	105
% identity	93
NCBI Description	Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No.	48149
Seq. ID	leu701151287.h1
Method	BLASTX
NCBI GI	g1352075
BLAST score	182
E value	3.0e-14
Match length	55
% identity	64
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_1076460_pir__S52393 beta-galactosidase (EC 3.2.1.23) - wild cabbage >gi_669059_emb_CAA59162_ (X84684) beta-galactosidase [Brassica oleracea]

Seq. No.	48150
Seq. ID	leu701151301.h1
Method	BLASTX
NCBI GI	g531389
BLAST score	251
E value	5.0e-22
Match length	72
% identity	60
NCBI Description	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No.	48151
Seq. ID	leu701151332.h1
Method	BLASTN
NCBI GI	g170067
BLAST score	99
E value	1.0e-48
Match length	215
% identity	74
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP3) gene, complete cds

Seq. No.	48152
Seq. ID	leu701151347.h1
Method	BLASTN
NCBI GI	g2961299

BLAST score 36
E value 2.0e-11
Match length 48
% identity 94
NCBI Description Cicer arietinum mRNA for ribosomal protein L24

Seq. No. 48153
Seq. ID leu701151537.h1
Method BLASTX
NCBI GI g1752734
BLAST score 153
E value 1.0e-10
Match length 67
% identity 46
NCBI Description (D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No. 48154
Seq. ID leu701151565.h1
Method BLASTN
NCBI GI g669002
BLAST score 130
E value 3.0e-67
Match length 134
% identity 99
NCBI Description Glycine max calnexin mRNA, complete cds

Seq. No. 48155
Seq. ID leu701151576.h1
Method BLASTX
NCBI GI g3287695
BLAST score 154
E value 9.0e-11
Match length 42
% identity 60
NCBI Description (AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No. 48156
Seq. ID leu701151653.h1
Method BLASTX
NCBI GI g4063760
BLAST score 254
E value 3.0e-22
Match length 80
% identity 59
NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq. No. 48157
Seq. ID leu701151711.h1
Method BLASTX
NCBI GI g4467147
BLAST score 192
E value 3.0e-15
Match length 68
% identity 56
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	48158
Seq. ID	leu701151723.h1
Method	BLASTN
NCBI GI	g479144
BLAST score	186
E value	1.0e-100
Match length	210
% identity	97
NCBI Description	G.max mRNA for ATP synthase subunit

Seq. No.	48159
Seq. ID	leu701151769.h1
Method	BLASTX
NCBI GI	g4097547
BLAST score	190
E value	1.0e-14
Match length	84
% identity	36
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	48160
Seq. ID	leu701151793.h1
Method	BLASTX
NCBI GI	g3482978
BLAST score	255
E value	1.0e-22
Match length	61
% identity	82
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	48161
Seq. ID	leu701151887.h1
Method	BLASTX
NCBI GI	g538502
BLAST score	211
E value	4.0e-17
Match length	62
% identity	61
NCBI Description	(L36231) peroxidase [Stylosanthes humilis]

Seq. No.	48162
Seq. ID	leu701151994.h1
Method	BLASTX
NCBI GI	g4219092
BLAST score	335
E value	9.0e-32
Match length	90
% identity	74
NCBI Description	(AF117707) putative copper/zinc superoxide dismutase copper chaperone precursor [Lycopersicon esculentum]

Seq. No.	48163
Seq. ID	leu701152066.h1
Method	BLASTN
NCBI GI	g169980
BLAST score	85

E value	3.0e-40
Match length	157
% identity	89
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	48164
Seq. ID	leu701152117.h1
Method	BLASTX
NCBI GI	g294668
BLAST score	125
E value	7.0e-13
Match length	43
% identity	83
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	48165
Seq. ID	leu701152165.h1
Method	BLASTN
NCBI GI	g4490734
BLAST score	40
E value	3.0e-13
Match length	52
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	48166
Seq. ID	leu701152204.h1
Method	BLASTX
NCBI GI	g3043656
BLAST score	259
E value	8.0e-23
Match length	80
% identity	61
NCBI Description	(AB011138) KIAA0566 protein [Homo sapiens]

Seq. No.	48167
Seq. ID	leu701152210.h1
Method	BLASTX
NCBI GI	g3548808
BLAST score	282
E value	2.0e-25
Match length	87
% identity	62
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	48168
Seq. ID	leu701152213.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	163
E value	9.0e-87
Match length	183
% identity	98
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	48169

Seq. ID	leu701152302.h1
Method	BLASTX
NCBI GI	g2832661
BLAST score	185
E value	2.0e-14
Match length	73
% identity	60
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	48170
Seq. ID	leu701152315.h1
Method	BLASTX
NCBI GI	g1707007
BLAST score	158
E value	3.0e-11
Match length	66
% identity	9
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48171
Seq. ID	leu701152324.h1
Method	BLASTX
NCBI GI	g126151
BLAST score	154
E value	2.0e-10
Match length	53
% identity	58
NCBI Description	LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi_282898_pir__S27365 lectin precursor - soybean >gi_170006 (K00821) lectin prepeptide [Glycine max]

Seq. No.	48172
Seq. ID	leu701152334.h1
Method	BLASTX
NCBI GI	g2288997
BLAST score	283
E value	1.0e-25
Match length	71
% identity	79
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48173
Seq. ID	leu701152385.h1
Method	BLASTN
NCBI GI	g1565222
BLAST score	97
E value	2.0e-47
Match length	197
% identity	87
NCBI Description	A.thaliana mRNA for MCM2-related protein

Seq. No.	48174
Seq. ID	leu701152523.h1
Method	BLASTX
NCBI GI	g4262148
BLAST score	167

E value	4.0e-12
Match length	77
% identity	37
NCBI Description	(AC005275) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	48175
Seq. ID	leu701152561.h1
Method	BLASTX
NCBI GI	g1236961
BLAST score	215
E value	8.0e-18
Match length	53
% identity	72
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	48176
Seq. ID	leu701152573.h1
Method	BLASTN
NCBI GI	g170053
BLAST score	215
E value	1.0e-118
Match length	243
% identity	97
NCBI Description	Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.	48177
Seq. ID	leu701152604.h1
Method	BLASTX
NCBI GI	g3810592
BLAST score	247
E value	1.0e-21
Match length	63
% identity	79
NCBI Description	(AC005398) unknown protein [Arabidopsis thaliana]

Seq. No.	48178
Seq. ID	leu701152619.h1
Method	BLASTX
NCBI GI	g2760836
BLAST score	179
E value	1.0e-13
Match length	76
% identity	58
NCBI Description	(AC003105) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	48179
Seq. ID	leu701152647.h1
Method	BLASTX
NCBI GI	g417094
BLAST score	174
E value	5.0e-13
Match length	58
% identity	55
NCBI Description	GLUTATHIONE S-TRANSFERASE 2 (CLASS-THETA) >gi_479387_pir__S33629 glutathione transferase (EC

2.5.1.18) 2 - clove pink (fragment) >gi_553063 (L05916) glutathione s-transferase [Dianthus caryophyllus]

Seq. No.	48180
Seq. ID	leu701152656.h1
Method	BLASTX
NCBI GI	g2642431
BLAST score	244
E value	4.0e-21
Match length	79
% identity	57
NCBI Description	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]

Seq. No.	48181
Seq. ID	leu701152705.h1
Method	BLASTX
NCBI GI	g3876465
BLAST score	166
E value	7.0e-12
Match length	41
% identity	76
NCBI Description	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene;

Seq. No.	48182
Seq. ID	leu701152733.h1
Method	BLASTX
NCBI GI	g4185312
BLAST score	133
E value	4.0e-13
Match length	81
% identity	49
NCBI Description	(AF090446) copia protein [Zea mays]

Seq. No.	48183
Seq. ID	leu701152777.h1
Method	BLASTX
NCBI GI	g126404
BLAST score	155
E value	1.0e-10
Match length	78
% identity	56
NCBI Description	SEED LIPOXYGENASE-2 (L-2) >gi_66331_pir__DASYL1 lipoxygenase (EC 1.13.11.12) 2 - soybean >gi_170014 (J03211) lipoxygenase (EC 1.13.11.12) [Glycine max]

Seq. No.	48184
Seq. ID	leu701152913.h1
Method	BLASTX
NCBI GI	g2811029
BLAST score	316
E value	2.0e-29
Match length	82
% identity	76

NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	48185
Seq. ID	leu701152936.h1
Method	BLASTX
NCBI GI	g4102598
BLAST score	254
E value	3.0e-22
Match length	82
% identity	63
NCBI Description	(AF013466) auxin response factor 4 [Arabidopsis thaliana]

Seq. No.	48186
Seq. ID	leu701152946.h1
Method	BLASTX
NCBI GI	g419789
BLAST score	231
E value	1.0e-19
Match length	61
% identity	69
NCBI Description	hypothetical protein - potato

Seq. No.	48187
Seq. ID	leu701152949.h1
Method	BLASTX
NCBI GI	g4415920
BLAST score	143
E value	3.0e-09
Match length	69
% identity	45
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	48188
Seq. ID	leu701153025.h1
Method	BLASTX
NCBI GI	g3980380
BLAST score	289
E value	1.0e-26
Match length	71
% identity	72
NCBI Description	(AC004561) putative enolase [Arabidopsis thaliana]

Seq. No.	48189
Seq. ID	leu701153074.h1
Method	BLASTX
NCBI GI	g4200122
BLAST score	193
E value	2.0e-15
Match length	69
% identity	51
NCBI Description	(AJ009555) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48190

Seq. ID	leu701153084.h1
Method	BLASTX
NCBI GI	g1565223
BLAST score	267
E value	5.0e-24
Match length	54
% identity	93
NCBI Description	(Y08301) MCM2-related protein [Arabidopsis thaliana]

Seq. No.	48191
Seq. ID	leu701153093.h1
Method	BLASTX
NCBI GI	g4263825
BLAST score	202
E value	2.0e-16
Match length	60
% identity	65
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48192
Seq. ID	leu701153105.h1
Method	BLASTX
NCBI GI	g1168568
BLAST score	208
E value	4.0e-17
Match length	62
% identity	74
NCBI Description	ATP SYNTHASE ALPHA CHAIN >gi_1262600_dbj_BAA04319_ (D17510) H+-ATPase alpha subunit [Pinus thunbergii]

Seq. No.	48193
Seq. ID	leu701153138.h1
Method	BLASTX
NCBI GI	g3859116
BLAST score	310
E value	6.0e-29
Match length	73
% identity	79
NCBI Description	(AF031609) unknown [Oryza sativa]

Seq. No.	48194
Seq. ID	leu701153148.h1
Method	BLASTX
NCBI GI	g123601
BLAST score	201
E value	5.0e-16
Match length	62
% identity	58
NCBI Description	HEAT SHOCK 70 KD PROTEIN >gi_99913_pir__S14992 heat shock protein, 70K - soybean >gi_18663_emb_CAA44620_ (X62799) Heat Shock 70kD protein [Glycine max]

Seq. No.	48195
Seq. ID	leu701153158.h1
Method	BLASTN
NCBI GI	g3264758
BLAST score	73

E value	4.0e-33
Match length	129
% identity	89
NCBI Description	Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA, complete cds

Seq. No.	48196
Seq. ID	leu701153166.h1
Method	BLASTN
NCBI GI	g3264758
BLAST score	72
E value	1.0e-32
Match length	128
% identity	89
NCBI Description	Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA, complete cds

Seq. No.	48197
Seq. ID	leu701153167.h1
Method	BLASTN
NCBI GI	g170053
BLAST score	50
E value	2.0e-19
Match length	74
% identity	92
NCBI Description	Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.	48198
Seq. ID	leu701153309.h1
Method	BLASTX
NCBI GI	g3549626
BLAST score	171
E value	1.0e-12
Match length	76
% identity	50
NCBI Description	(AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No.	48199
Seq. ID	leu701153350.h1
Method	BLASTN
NCBI GI	g18559
BLAST score	45
E value	2.0e-16
Match length	88
% identity	89
NCBI Description	G.max gene for catalase

Seq. No.	48200
Seq. ID	leu701153428.h1
Method	BLASTX
NCBI GI	g2618689
BLAST score	174
E value	6.0e-13
Match length	49
% identity	78
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	48201
Seq. ID	leu701153441.h1
Method	BLASTX
NCBI GI	g3777527
BLAST score	141
E value	3.0e-09
Match length	72
% identity	39
NCBI Description	(AF053008) gag-pol polyprotein [Glycine max]

Seq. No.	48202
Seq. ID	leu701153467.h1
Method	BLASTN
NCBI GI	g3341442
BLAST score	47
E value	1.0e-17
Match length	203
% identity	81
NCBI Description	Glycine max mRNA for root nodule acid phosphatase

Seq. No.	48203
Seq. ID	leu701153472.h1
Method	BLASTX
NCBI GI	g1706695
BLAST score	153
E value	2.0e-10
Match length	44
% identity	61
NCBI Description	PHOSPHOMEVALONATE KINASE >gi_1362436_pir__S57588 phosphomevalonate kinase (EC 2.7.4.2) - yeast (Saccharomyces cerevisiae) >gi_887601_emb_CAA90191_ (Z49939) Erg8p [Saccharomyces cerevisiae]

Seq. No.	48204
Seq. ID	leu701153502.h1
Method	BLASTN
NCBI GI	g4115338
BLAST score	137
E value	3.0e-71
Match length	196
% identity	22
NCBI Description	Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

Seq. No.	48205
Seq. ID	leu701153535.h1
Method	BLASTX
NCBI GI	g4510342
BLAST score	245
E value	4.0e-21
Match length	75
% identity	67
NCBI Description	(AC006921) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	48206
Seq. ID	leu701153540.h1
Method	BLASTN

NCBI GI	g1277167
BLAST score	171
E value	1.0e-91
Match length	171
% identity	100
NCBI Description	Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No.	48207
Seq. ID	leu701153591.h1
Method	BLASTX
NCBI GI	g2827709
BLAST score	251
E value	5.0e-22
Match length	77
% identity	58
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	48208
Seq. ID	leu701153706.h1
Method	BLASTX
NCBI GI	g2827992
BLAST score	312
E value	4.0e-29
Match length	80
% identity	68
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No.	48209
Seq. ID	leu701153758.h1
Method	BLASTX
NCBI GI	g2262118
BLAST score	371
E value	5.0e-36
Match length	83
% identity	82
NCBI Description	(AC002343) cell division protein isolog [Arabidopsis thaliana]

Seq. No.	48210
Seq. ID	leu701154006.h1
Method	BLASTN
NCBI GI	g391604
BLAST score	66
E value	7.0e-29
Match length	130
% identity	88
NCBI Description	Arabidopsis thaliana ATPK15D mRNA for casein kinase II catalytic subunit, complete cds

Seq. No.	48211
Seq. ID	leu701154021.h1
Method	BLASTX
NCBI GI	g4314358
BLAST score	142
E value	2.0e-09
Match length	78
% identity	40

NCBI Description	(AC006340) putative kinesin heavy chain protein [Arabidopsis thaliana]

Seq. No.	48212
Seq. ID	leu701154031.h1
Method	BLASTX
NCBI GI	g1617200
BLAST score	418
E value	2.0e-41
Match length	82
% identity	90
NCBI Description	(Y08607) Shaggy-like kinase 6 [Nicotiana tabacum]

Seq. No.	48213
Seq. ID	leu701154036.h1
Method	BLASTN
NCBI GI	g2351072
BLAST score	73
E value	5.0e-33
Match length	153
% identity	43
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYC6, complete sequence [Arabidopsis thaliana]

Seq. No.	48214
Seq. ID	leu701154041.h1
Method	BLASTX
NCBI GI	g731651
BLAST score	161
E value	3.0e-11
Match length	74
% identity	43
NCBI Description	HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN PUT2-SRB2 INTERGENIC REGION >gi_626608_pir__S46746 hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) >gi_488180 (U00062) Yhr039cp [Saccharomyces cerevisiae]

Seq. No.	48215
Seq. ID	leu701154106.h1
Method	BLASTX
NCBI GI	g3805845
BLAST score	346
E value	4.0e-33
Match length	81
% identity	78
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	48216
Seq. ID	leu701154167.h1
Method	BLASTX
NCBI GI	g3355479
BLAST score	194
E value	3.0e-15
Match length	51
% identity	61
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	48217
Seq. ID	leu701154173.h1
Method	BLASTX
NCBI GI	g1514643
BLAST score	196
E value	2.0e-15
Match length	61
% identity	52
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	48218
Seq. ID	leu701154188.h1
Method	BLASTN
NCBI GI	g1480927
BLAST score	48
E value	4.0e-18
Match length	158
% identity	88
NCBI Description	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene

Seq. No.	48219
Seq. ID	leu701154190.h1
Method	BLASTX
NCBI GI	g3953463
BLAST score	127
E value	1.0e-08
Match length	51
% identity	55
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	48220
Seq. ID	leu701154216.h1
Method	BLASTN
NCBI GI	g4127457
BLAST score	33
E value	3.0e-09
Match length	57
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for myb cov1 protein, partial

Seq. No.	48221
Seq. ID	leu701154259.h1
Method	BLASTX
NCBI GI	g1653767
BLAST score	216
E value	8.0e-18
Match length	68
% identity	62
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	48222
Seq. ID	leu701154296.h1
Method	BLASTX
NCBI GI	g3451075
BLAST score	153

E value	2.0e-10
Match length	43
% identity	67
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	48223
Seq. ID	leu701154334.h1
Method	BLASTN
NCBI GI	g1149570
BLAST score	47
E value	7.0e-18
Match length	115
% identity	85
NCBI Description	A.thaliana mRNA for mitochondrial elongation factor Tu

Seq. No.	48224
Seq. ID	leu701154374.h1
Method	BLASTX
NCBI GI	g4263825
BLAST score	201
E value	4.0e-16
Match length	77
% identity	52
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48225
Seq. ID	leu701154426.h1
Method	BLASTX
NCBI GI	g3850576
BLAST score	302
E value	4.0e-28
Match length	76
% identity	86
NCBI Description	(AC005278) Strong similarity to gb_U04968 nucleotide excision repair protein (ERCC2) from Cricetulus grisseus. [Arabidopsis thaliana]

Seq. No.	48226
Seq. ID	leu701154434.h1
Method	BLASTX
NCBI GI	g1935914
BLAST score	220
E value	2.0e-18
Match length	44
% identity	91
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	48227
Seq. ID	leu701154467.h1
Method	BLASTN
NCBI GI	g999189
BLAST score	110
E value	3.0e-55
Match length	170
% identity	91
NCBI Description	dihydrofolate reductase-thymidylate synthase=bifunctional enzyme [Glycine max, seedling, mRNA, 1794 nt]

Seq. No.	48228
Seq. ID	leu701154507.h1
Method	BLASTX
NCBI GI	g4107343
BLAST score	155
E value	1.0e-10
Match length	75
% identity	44
NCBI Description	(AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq. No.	48229
Seq. ID	leu701154511.h1
Method	BLASTX
NCBI GI	g4388829
BLAST score	156
E value	5.0e-11
Match length	51
% identity	63
NCBI Description	(AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [Arabidopsis thaliana]

Seq. No.	48230
Seq. ID	leu701154550.h1
Method	BLASTX
NCBI GI	g4206209
BLAST score	168
E value	3.0e-12
Match length	62
% identity	50
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	48231
Seq. ID	leu701154559.h1
Method	BLASTN
NCBI GI	g3176097
BLAST score	79
E value	1.0e-36
Match length	199
% identity	85
NCBI Description	Medicago truncatula mRNA for annexin

Seq. No.	48232
Seq. ID	leu701154674.h1
Method	BLASTX
NCBI GI	g2098709
BLAST score	142
E value	4.0e-12
Match length	44
% identity	86
NCBI Description	(U82975) pectinesterase [Citrus sinensis]

Seq. No.	48233
Seq. ID	leu701154690.h1

Method	BLASTX
NCBI GI	g2780194
BLAST score	144
E value	2.0e-09
Match length	49
% identity	59
NCBI Description	(AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No.	48234
Seq. ID	leu701154819.h1
Method	BLASTX
NCBI GI	g481812
BLAST score	284
E value	1.0e-25
Match length	88
% identity	35
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	48235
Seq. ID	leu701154823.h1
Method	BLASTX
NCBI GI	g2982266
BLAST score	301
E value	7.0e-28
Match length	74
% identity	74
NCBI Description	(AF051216) probable fibrillarin [Picea mariana]

Seq. No.	48236
Seq. ID	leu701155205.h1
Method	BLASTN
NCBI GI	g436782
BLAST score	56
E value	6.0e-23
Match length	96
% identity	90
NCBI Description	Rice mRNA for cyc07, complete cds

Seq. No.	48237
Seq. ID	leu701155231.h1
Method	BLASTX
NCBI GI	g3695019
BLAST score	161
E value	3.0e-11
Match length	48
% identity	62
NCBI Description	(AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	48238
Seq. ID	leu701155248.h1
Method	BLASTX
NCBI GI	g2392771
BLAST score	183
E value	4.0e-14
Match length	79

% identity	47
NCBI Description	(AC002534) putative kinesin-like protein [Arabidopsis thaliana]

Seq. No.	48239
Seq. ID	leu701155250.h1
Method	BLASTX
NCBI GI	g1915974
BLAST score	346
E value	5.0e-33
Match length	83
% identity	81
NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi_2102693 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No.	48240
Seq. ID	leu701155290.h1
Method	BLASTX
NCBI GI	g2576411
BLAST score	135
E value	4.0e-15
Match length	57
% identity	77
NCBI Description	(AF012833) similar to dynamin-like protein encoded by GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No.	48241
Seq. ID	leu701155308.h1
Method	BLASTX
NCBI GI	g729470
BLAST score	231
E value	2.0e-19
Match length	55
% identity	82
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	48242
Seq. ID	leu701155348.h1
Method	BLASTX
NCBI GI	g4115922
BLAST score	284
E value	8.0e-26
Match length	82
% identity	67
NCBI Description	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis thaliana]

Seq. No.	48243
Seq. ID	leu701155374.h1
Method	BLASTX

NCBI GI	g1769898
BLAST score	153
E value	1.0e-10
Match length	65
% identity	51
NCBI Description	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq. No.	48244
Seq. ID	leu701155410.h1
Method	BLASTX
NCBI GI	g4580575
BLAST score	291
E value	1.0e-26
Match length	79
% identity	66
NCBI Description	(AF082176) auxin response factor 9 [Arabidopsis thaliana]

Seq. No.	48245
Seq. ID	leu701155447.h1
Method	BLASTX
NCBI GI	g3461817
BLAST score	220
E value	2.0e-18
Match length	76
% identity	53
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	48246
Seq. ID	leu701155455.h1
Method	BLASTX
NCBI GI	g3043656
BLAST score	240
E value	7.0e-21
Match length	75
% identity	61
NCBI Description	(AB011138) KIAA0566 protein [Homo sapiens]

Seq. No.	48247
Seq. ID	leu701155457.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	32
E value	1.0e-08
Match length	48
% identity	94
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	48248
Seq. ID	leu701155466.h1
Method	BLASTX
NCBI GI	g4432802
BLAST score	303
E value	4.0e-28
Match length	79
% identity	66
NCBI Description	(AC006437) putative pol polyprotein, 5' partial

[Arabidopsis thaliana]

Seq. No.	48249
Seq. ID	leu701155468.h1
Method	BLASTX
NCBI GI	g1076479
BLAST score	140
E value	7.0e-09
Match length	78
% identity	50
NCBI Description	MalD1 protein - apple tree (fragment)

Seq. No.	48250
Seq. ID	leu701155514.h1
Method	BLASTX
NCBI GI	g4063745
BLAST score	186
E value	3.0e-14
Match length	75
% identity	41
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48251
Seq. ID	leu701155536.h1
Method	BLASTX
NCBI GI	g3924596
BLAST score	350
E value	2.0e-33
Match length	88
% identity	73
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	48252
Seq. ID	leu701155626.h1
Method	BLASTX
NCBI GI	g4455287
BLAST score	184
E value	2.0e-17
Match length	69
% identity	72
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	48253
Seq. ID	leu701155650.h1
Method	BLASTX
NCBI GI	g3309086
BLAST score	341
E value	2.0e-32
Match length	81
% identity	85
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	48254
Seq. ID	leu701155688.h1
Method	BLASTX

NCBI GI	g3549626
BLAST score	224
E value	6.0e-19
Match length	71
% identity	62
NCBI Description	(AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No.	48255
Seq. ID	leu701155710.h1
Method	BLASTX
NCBI GI	g3201680
BLAST score	285
E value	5.0e-26
Match length	77
% identity	70
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	48256
Seq. ID	leu701155730.h1
Method	BLASTX
NCBI GI	g2911085
BLAST score	141
E value	5.0e-09
Match length	79
% identity	35
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	48257
Seq. ID	leu701155787.h1
Method	BLASTX
NCBI GI	g2582971
BLAST score	203
E value	2.0e-16
Match length	78
% identity	53
NCBI Description	(D83711) TKRP125 [Nicotiana tabacum]

Seq. No.	48258
Seq. ID	leu701155794.h1
Method	BLASTX
NCBI GI	g1172829
BLAST score	253
E value	4.0e-22
Match length	87
% identity	60
NCBI Description	POLY(A)+ RNA EXPORT PROTEIN >gi_1362233_pir__A56119 RNA export protein rae1 - fission yeast (Schizosaccharomyces pombe) >gi_625094 (U14951) polyA+ RNA export [Schizosaccharomyces pombe] >gi_2842504_emb_CAA16856_ (AL021748) polya+ rna export protein [Schizosaccharomyces pombe]

Seq. No.	48259
Seq. ID	leu701155796.h1

Method	BLASTN
NCBI GI	g169958
BLAST score	56
E value	6.0e-23
Match length	80
% identity	93
NCBI Description	Glycine max G-box binding factor (GBF2A) mRNA, 3' end

Seq. No.	48260
Seq. ID	leu701155857.h1
Method	BLASTX
NCBI GI	g2244898
BLAST score	291
E value	2.0e-26
Match length	88
% identity	58
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	48261
Seq. ID	leu701155873.h1
Method	BLASTX
NCBI GI	g4127781
BLAST score	230
E value	3.0e-19
Match length	63
% identity	17
NCBI Description	(AJ012588) Notchless protein [Drosophila melanogaster]

Seq. No.	48262
Seq. ID	leu701155888.h1
Method	BLASTX
NCBI GI	g807698
BLAST score	235
E value	5.0e-20
Match length	87
% identity	55
NCBI Description	(D32206) prepro-cucumisin [Cucumis melo]

Seq. No.	48263
Seq. ID	leu701156009.h1
Method	BLASTX
NCBI GI	g1871187
BLAST score	341
E value	1.0e-32
Match length	76
% identity	79
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	48264
Seq. ID	leu701156050.h1
Method	BLASTX
NCBI GI	g4522009
BLAST score	137
E value	1.0e-08
Match length	32
% identity	75

NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]
Seq. No.	48265
Seq. ID	leu701156075.h1
Method	BLASTX
NCBI GI	g3176669
BLAST score	138
E value	8.0e-09
Match length	72
% identity	40
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]
Seq. No.	48266
Seq. ID	leu701156139.h1
Method	BLASTN
NCBI GI	g166379
BLAST score	69
E value	1.0e-30
Match length	188
% identity	73
NCBI Description	Alfalfa glucose-regulated endoplasmic reticular protein mRNA, complete cds
Seq. No.	48267
Seq. ID	leu701156165.h1
Method	BLASTX
NCBI GI	g3176098
BLAST score	144
E value	2.0e-18
Match length	67
% identity	65
NCBI Description	(Y15036) annexin [Medicago truncatula]
Seq. No.	48268
Seq. ID	leu701156191.h1
Method	BLASTX
NCBI GI	g3859944
BLAST score	229
E value	2.0e-19
Match length	73
% identity	63
NCBI Description	(AF084570) FKBP12 interacting protein [Arabidopsis thaliana]
Seq. No.	48269
Seq. ID	leu701156222.h1
Method	BLASTX
NCBI GI	g4539660
BLAST score	303
E value	6.0e-28
Match length	87
% identity	60
NCBI Description	(AF061282) polyprotein [Sorghum bicolor]
Seq. No.	48270
Seq. ID	leu701156274.h1
Method	BLASTN

NCBI GI	g4567090
BLAST score	48
E value	4.0e-18
Match length	52
% identity	98
NCBI Description	Glycine max SNF-1-like serine/threonine protein kinase mRNA, complete cds

Seq. No.	48271
Seq. ID	leu701156338.h1
Method	BLASTX
NCBI GI	g3599489
BLAST score	182
E value	7.0e-14
Match length	40
% identity	88
NCBI Description	(AF085148) 3-oxoacyl-[acyl-carrier-protein] synthase [Capsicum chinense]

Seq. No.	48272
Seq. ID	leu701156344.h1
Method	BLASTN
NCBI GI	g296408
BLAST score	168
E value	9.0e-90
Match length	208
% identity	95
NCBI Description	G.max ADR12 mRNA

Seq. No.	48273
Seq. ID	leu701156388.h1
Method	BLASTN
NCBI GI	g170053
BLAST score	187
E value	1.0e-101
Match length	215
% identity	97
NCBI Description	Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.	48274
Seq. ID	leu701156413.h1
Method	BLASTX
NCBI GI	g4454051
BLAST score	333
E value	2.0e-31
Match length	72
% identity	78
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	48275
Seq. ID	leu701156442.h1
Method	BLASTN
NCBI GI	g860887
BLAST score	103
E value	5.0e-51
Match length	198

% identity	88
NCBI Description	B.vulgaris chloroplast petG gene, ycf7 gene, psbE gene, psbF gene & ORF32 (fertile pollen)

Seq. No.	48276
Seq. ID	leu701156460.h1
Method	BLASTX
NCBI GI	g3695388
BLAST score	144
E value	2.0e-09
Match length	43
% identity	63
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	48277
Seq. ID	leu701156474.h1
Method	BLASTN
NCBI GI	g3128141
BLAST score	35
E value	2.0e-10
Match length	59
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	48278
Seq. ID	leu701156506.h1
Method	BLASTX
NCBI GI	g3080398
BLAST score	308
E value	2.0e-28
Match length	71
% identity	40
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	48279
Seq. ID	leu701156532.h1
Method	BLASTX
NCBI GI	g3023751
BLAST score	166
E value	6.0e-12
Match length	72
% identity	47
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	48280
Seq. ID	leu701156556.h1
Method	BLASTX
NCBI GI	g3169182
BLAST score	155
E value	9.0e-11
Match length	53
% identity	55

NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]
Seq. No.	48281
Seq. ID	leu701156570.h1
Method	BLASTX
NCBI GI	g2129597
BLAST score	406
E value	5.0e-40
Match length	87
% identity	85
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]
Seq. No.	48282
Seq. ID	leu701156606.h1
Method	BLASTN
NCBI GI	g3341442
BLAST score	108
E value	6.0e-54
Match length	243
% identity	87
NCBI Description	Glycine max mRNA for root nodule acid phosphatase
Seq. No.	48283
Seq. ID	leu701156624.h1
Method	BLASTN
NCBI GI	g498039
BLAST score	49
E value	1.0e-18
Match length	81
% identity	90
NCBI Description	Senecio odorus mRNA, complete ORF
Seq. No.	48284
Seq. ID	leu701156689.h1
Method	BLASTX
NCBI GI	g4038037
BLAST score	151
E value	1.0e-16
Match length	76
% identity	14
NCBI Description	(AC005936) hypothetical protein [Arabidopsis thaliana]
Seq. No.	48285
Seq. ID	leu701156711.h1
Method	BLASTN
NCBI GI	g20834
BLAST score	78
E value	4.0e-36
Match length	186
% identity	85
NCBI Description	P.sativum PHSP1 mRNA for HSP70
Seq. No.	48286
Seq. ID	leu701156739.h1

Method	BLASTX
NCBI GI	g4049353
BLAST score	172
E value	1.0e-12
Match length	43
% identity	67
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	48287
Seq. ID	leu701157093.h1
Method	BLASTN
NCBI GI	g473987
BLAST score	93
E value	5.0e-45
Match length	177
% identity	88
NCBI Description	Rice mRNA, partial homologous to histone H3 gene

Seq. No.	48288
Seq. ID	leu701157157.h1
Method	BLASTX
NCBI GI	g1777312
BLAST score	211
E value	3.0e-17
Match length	71
% identity	56
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	48289
Seq. ID	leu701157213.h1
Method	BLASTN
NCBI GI	g3947720
BLAST score	38
E value	3.0e-12
Match length	78
% identity	87
NCBI Description	Prunus persica mRNA for ribosomal protein S28 (rps28.2)

Seq. No.	48290
Seq. ID	leu701157235.h1
Method	BLASTX
NCBI GI	g3914472
BLAST score	183
E value	4.0e-14
Match length	45
% identity	78
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	48291
Seq. ID	leu701157253.h1
Method	BLASTX
NCBI GI	g2462760
BLAST score	260

E value	4.0e-23
Match length	67
% identity	67
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	48292
Seq. ID	leu701157620.h1
Method	BLASTX
NCBI GI	g3914818
BLAST score	142
E value	3.0e-09
Match length	35
% identity	71
NCBI Description	DNA-DIRECTED RNA POLYMERASE I LARGEST SUBUNIT >gi_1865779_emb_CAA70321_ (Y09103) largest subunit of RNA polymerase I (A) [Drosophila melanogaster]

Seq. No.	48293
Seq. ID	leu701157767.h1
Method	BLASTN
NCBI GI	g871507
BLAST score	48
E value	4.0e-18
Match length	80
% identity	90
NCBI Description	P.sativum mRNA for small GTP-binding protein (clone pGTP13)

Seq. No.	48294
Seq. ID	leu701157769.h1
Method	BLASTX
NCBI GI	g4455371
BLAST score	339
E value	2.0e-32
Match length	77
% identity	79
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	48295
Seq. ID	leu701157773.h1
Method	BLASTX
NCBI GI	g4006913
BLAST score	141
E value	4.0e-09
Match length	67
% identity	48
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48296
Seq. ID	leu701157781.h1
Method	BLASTN
NCBI GI	g296408
BLAST score	184
E value	2.0e-99
Match length	204
% identity	98
NCBI Description	G.max ADR12 mRNA

Seq. No.	48297
Seq. ID	leu701157804.h1
Method	BLASTN
NCBI GI	g886099
BLAST score	216
E value	1.0e-118
Match length	227
% identity	99
NCBI Description	Glycine max putative water channel protein (Pip1) mRNA, complete cds

Seq. No.	48298
Seq. ID	leu701157832.h1
Method	BLASTN
NCBI GI	g3132697
BLAST score	45
E value	1.0e-16
Match length	105
% identity	87
NCBI Description	Pisum sativum SAR DNA-binding protein (SARBP-2) mRNA, complete cds

Seq. No.	48299
Seq. ID	leu701157889.h1
Method	BLASTX
NCBI GI	g3367536
BLAST score	226
E value	4.0e-19
Match length	55
% identity	85
NCBI Description	(AC004392) Contains similarity to symbiosis-related like protein F1N20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene. [Arabidopsis thaliana]

Seq. No.	48300
Seq. ID	lus701015739.h1
Method	BLASTX
NCBI GI	g3064039
BLAST score	151
E value	3.0e-10
Match length	55
% identity	42
NCBI Description	(AF054445) major latex protein homolog [Mesembryanthemum crystallinum]

Seq. No.	48301
Seq. ID	lus701015834.h1
Method	BLASTX
NCBI GI	g2661840
BLAST score	141
E value	4.0e-09
Match length	68
% identity	47
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	48302

Seq. ID	lus701015850.h1
Method	BLASTX
NCBI GI	g3334405
BLAST score	155
E value	1.0e-10
Match length	75
% identity	51
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	48303
Seq. ID	lus701015860.h1
Method	BLASTX
NCBI GI	g1688072
BLAST score	403
E value	1.0e-39
Match length	86
% identity	83
NCBI Description	(U41369) biotin holocarboxylase synthetase [Arabidopsis thaliana]

Seq. No.	48304
Seq. ID	ncj700975101.h1
Method	BLASTN
NCBI GI	g4519183
BLAST score	54
E value	1.0e-21
Match length	126
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	48305
Seq. ID	ncj700975148.h1
Method	BLASTX
NCBI GI	g2462762
BLAST score	351
E value	1.0e-33
Match length	86
% identity	73
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	48306
Seq. ID	ncj700975194.h1
Method	BLASTN
NCBI GI	g886099
BLAST score	132
E value	3.0e-68
Match length	176
% identity	94
NCBI Description	Glycine max putative water channel protein (Pip1) mRNA, complete cds

Seq. No.	48307
Seq. ID	ncj700975211.h1

Method	BLASTX
NCBI GI	g2224892
BLAST score	215
E value	1.0e-17
Match length	69
% identity	62
NCBI Description	(U61386) gibberellin 7-oxidase [Cucurbita maxima]

Seq. No.	48308
Seq. ID	ncj700975241.h1
Method	BLASTX
NCBI GI	g3482924
BLAST score	230
E value	2.0e-19
Match length	78
% identity	58
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	48309
Seq. ID	ncj700975263.h1
Method	BLASTX
NCBI GI	g1709976
BLAST score	221
E value	1.0e-18
Match length	54
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L10A >gi_1078395_pir__S53893 ribosomal protein SSM1 - yeast (Saccharomyces cerevisiae) >gi_732949_emb_CAA50314_ (X70985) SSM1a [Saccharomyces cerevisiae] >gi_732951_emb_CAA50315_ (X70986) SSM1b [Saccharomyces cerevisiae] >gi_1246843_emb_CAA63361_ (X92670) see also X70986 [Saccharomyces cerevisiae] >gi_1322706_emb_CAA96846_ (Z72657) ORF YGL135w [Saccharomyces cerevisiae] >gi_1370456_emb_CAA97935_ (Z73576) ORF YPL220w [Saccharomyces cerevisiae]

Seq. No.	48310
Seq. ID	ncj700975295.h1
Method	BLASTX
NCBI GI	g3892058
BLAST score	156
E value	1.0e-10
Match length	65
% identity	57
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No.	48311
Seq. ID	ncj700975323.h1
Method	BLASTX
NCBI GI	g3560231
BLAST score	165
E value	8.0e-12
Match length	52
% identity	60
NCBI Description	(AL031530) putative edoplasmic reticulum associated protein

[Schizosaccharomyces pombe]

Seq. No.	48312
Seq. ID	ncj700975428.h1
Method	BLASTX
NCBI GI	g4138343
BLAST score	180
E value	1.0e-13
Match length	74
% identity	54
NCBI Description	(AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]

Seq. No.	48313
Seq. ID	ncj700975502.h1
Method	BLASTX
NCBI GI	g4234955
BLAST score	224
E value	1.0e-18
Match length	69
% identity	64
NCBI Description	(AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]

Seq. No.	48314
Seq. ID	ncj700975581.h1
Method	BLASTX
NCBI GI	g2832677
BLAST score	141
E value	5.0e-09
Match length	67
% identity	40
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48315
Seq. ID	ncj700975624.h1
Method	BLASTX
NCBI GI	g3850568
BLAST score	184
E value	5.0e-17
Match length	84
% identity	57
NCBI Description	(AC005278) Similar to hypothetical protein SPAC2F7.14c gi_1052797 from Schizosaccharomyces pombe cosmid gb_Z50142. [Arabidopsis thaliana]

Seq. No.	48316
Seq. ID	ncj700975649.h1
Method	BLASTX
NCBI GI	g1495251
BLAST score	287
E value	5.0e-26
Match length	94
% identity	55
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	48317
Seq. ID	ncj700975650.h1
Method	BLASTX

NCBI GI	g2569938
BLAST score	294
E value	7.0e-27
Match length	86
% identity	62
NCBI Description	(Y15193) GAI [Arabidopsis thaliana]

Seq. No.	48318
Seq. ID	ncj700975741.h1
Method	BLASTX
NCBI GI	g2558664
BLAST score	157
E value	6.0e-11
Match length	78
% identity	42
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48319
Seq. ID	ncj700975771.h1
Method	BLASTX
NCBI GI	g4539383
BLAST score	111
E value	9.0e-13
Match length	76
% identity	53
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	48320
Seq. ID	ncj700975791.h1
Method	BLASTX
NCBI GI	g4454484
BLAST score	147
E value	7.0e-10
Match length	63
% identity	40
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	48321
Seq. ID	ncj700975831.h1
Method	BLASTX
NCBI GI	g2335097
BLAST score	220
E value	2.0e-18
Match length	76
% identity	10
NCBI Description	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	48322
Seq. ID	ncj700975860.h1
Method	BLASTN
NCBI GI	g532289
BLAST score	53
E value	4.0e-21
Match length	73

% identity	93
NCBI Description	Soybean mRNA for late nodulin, complete cds

Seq. No.	48323
Seq. ID	ncj700975862.h1
Method	BLASTX
NCBI GI	g2809241
BLAST score	285
E value	8.0e-26
Match length	92
% identity	66
NCBI Description	(AC002560) F21B7.10 [Arabidopsis thaliana]

Seq. No.	48324
Seq. ID	ncj700976061.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	79
E value	5.0e-37
Match length	123
% identity	91
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	48325
Seq. ID	ncj700976083.h1
Method	BLASTX
NCBI GI	g1652084
BLAST score	147
E value	1.0e-09
Match length	81
% identity	37
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	48326
Seq. ID	ncj700976486.h1
Method	BLASTX
NCBI GI	g2961390
BLAST score	287
E value	2.0e-26
Match length	65
% identity	82
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	48327
Seq. ID	ncj700976509.h1
Method	BLASTX
NCBI GI	g3157952
BLAST score	196
E value	2.0e-15
Match length	73
% identity	49
NCBI Description	(AC002131) F12F1.11 [Arabidopsis thaliana]

Seq. No.	48328
Seq. ID	ncj700976552.h1

Method	BLASTN
NCBI GI	g1053215
BLAST score	172
E value	4.0e-92
Match length	208
% identity	97
NCBI Description	Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	48329
Seq. ID	ncj700976574.h1
Method	BLASTX
NCBI GI	g4160300
BLAST score	257
E value	1.0e-22
Match length	86
% identity	62
NCBI Description	(AJ011893) cyclin D3.1 protein [Nicotiana tabacum]

Seq. No.	48330
Seq. ID	ncj700976575.h1
Method	BLASTX
NCBI GI	g1709758
BLAST score	271
E value	3.0e-24
Match length	52
% identity	94
NCBI Description	PROTEASOME COMPONENT C2 (MACROPAIN SUBUNIT C2) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2) >gi_1066151_dbj_BAA07128_ (D37886) proteasome C2 subunit [Oryza sativa]

Seq. No.	48331
Seq. ID	ncj700976588.h1
Method	BLASTX
NCBI GI	g4490743
BLAST score	189
E value	1.0e-14
Match length	90
% identity	51
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	48332
Seq. ID	ncj700976789.h1
Method	BLASTX
NCBI GI	g2262159
BLAST score	203
E value	3.0e-16
Match length	56
% identity	64
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]

Seq. No.	48333
Seq. ID	ncj700976896.h1
Method	BLASTN
NCBI GI	g4056429

BLAST score	66
E value	7.0e-29
Match length	118
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	48334
Seq. ID	ncj700976983.h1
Method	BLASTX
NCBI GI	g2245020
BLAST score	242
E value	5.0e-21
Match length	53
% identity	91
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	48335
Seq. ID	ncj700977107.h1
Method	BLASTN
NCBI GI	g2204063
BLAST score	37
E value	2.0e-11
Match length	95
% identity	92
NCBI Description	Pisum sativum mRNA for F1 ATPase, complete cds

Seq. No.	48336
Seq. ID	ncj700977203.h1
Method	BLASTN
NCBI GI	g3290208
BLAST score	37
E value	2.0e-11
Match length	49
% identity	94
NCBI Description	Malus domestica MADS-box protein 1 mRNA, complete cds

Seq. No.	48337
Seq. ID	ncj700977231.h1
Method	BLASTX
NCBI GI	g1707657
BLAST score	173
E value	1.0e-12
Match length	78
% identity	51
NCBI Description	(Z71640) DnaJ homologue [Pisum sativum]

Seq. No.	48338
Seq. ID	ncj700977302.h1
Method	BLASTX
NCBI GI	g731651
BLAST score	182
E value	9.0e-14
Match length	79
% identity	43
NCBI Description	HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN PUT2-SRB2 INTERGENIC REGION >gi_626608_pir__S46746

	hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) >gi_488180 (U00062) Yhr039cp [Saccharomyces cerevisiae]
Seq. No.	48339
Seq. ID	ncj700977368.h1
Method	BLASTN
NCBI GI	g18646
BLAST score	69
E value	1.0e-30
Match length	69
% identity	100
NCBI Description	Soybean mRNA for HMG-Y related protein, variant A
Seq. No.	48340
Seq. ID	ncj700977370.h1
Method	BLASTX
NCBI GI	g1711617
BLAST score	159
E value	4.0e-11
Match length	72
% identity	65
NCBI Description	HIGH AFFINITY SULPHATE TRANSPORTER 2 >gi_1085848_pir__S51764 high affinity sulphate transporter - Stylosanthes hamata >gi_607186_emb_CAA57711_ (X82256) high affinity sulphate transporter [Stylosanthes hamata]
Seq. No.	48341
Seq. ID	ncj700977408.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	121
E value	1.0e-61
Match length	233
% identity	88
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds
Seq. No.	48342
Seq. ID	ncj700977436.h1
Method	BLASTX
NCBI GI	g3450842
BLAST score	377
E value	1.0e-36
Match length	92
% identity	77
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]
Seq. No.	48343
Seq. ID	ncj700977467.h1
Method	BLASTN
NCBI GI	g1575728
BLAST score	56
E value	4.0e-23
Match length	112
% identity	88

NCBI Description	Glycine max 14-3-3 related protein SGF14C mRNA, complete cds

Seq. No.	48344
Seq. ID	ncj700977487.h1
Method	BLASTX
NCBI GI	g3461839
BLAST score	347
E value	4.0e-33
Match length	91
% identity	71
NCBI Description	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	48345
Seq. ID	ncj700977510.h1
Method	BLASTN
NCBI GI	g3158475
BLAST score	50
E value	3.0e-19
Match length	98
% identity	88
NCBI Description	Samanea saman aquaporin 2 (Aqp2) mRNA, complete cds

Seq. No.	48346
Seq. ID	ncj700977541.h1
Method	BLASTX
NCBI GI	g4220541
BLAST score	251
E value	7.0e-22
Match length	87
% identity	29
NCBI Description	(AL035356) Rab geranylgeranyl transferase like protein [Arabidopsis thaliana]

Seq. No.	48347
Seq. ID	ncj700977546.h1
Method	BLASTN
NCBI GI	g13196
BLAST score	50
E value	3.0e-19
Match length	66
% identity	94
NCBI Description	Oenothera mitochondrial reverse transcriptose-like gene (R5)

Seq. No.	48348
Seq. ID	ncj700977656.h1
Method	BLASTX
NCBI GI	g2464865
BLAST score	193
E value	5.0e-15
Match length	47
% identity	77
NCBI Description	(Z99707) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	48349

Seq. ID	ncj700977657.h1
Method	BLASTX
NCBI GI	g2194119
BLAST score	321
E value	4.0e-30
Match length	81
% identity	68
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	48350
Seq. ID	ncj700977682.h1
Method	BLASTX
NCBI GI	g4468808
BLAST score	224
E value	1.0e-18
Match length	92
% identity	49
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	48351
Seq. ID	ncj700977689.h1
Method	BLASTX
NCBI GI	g4325342
BLAST score	384
E value	2.0e-37
Match length	92
% identity	83
NCBI Description	(AF128393) No definition line found [Arabidopsis thaliana]

Seq. No.	48352
Seq. ID	ncj700977714.h1
Method	BLASTX
NCBI GI	g4455192
BLAST score	247
E value	2.0e-21
Match length	90
% identity	35
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	48353
Seq. ID	ncj700977724.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	90
E value	4.0e-43
Match length	222
% identity	85
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	48354
Seq. ID	ncj700977748.h1
Method	BLASTX
NCBI GI	g4490297
BLAST score	157
E value	6.0e-11
Match length	81

% identity	40
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	48355
Seq. ID	ncj700977779.h1
Method	BLASTX
NCBI GI	g2980759
BLAST score	165
E value	1.0e-17
Match length	76
% identity	46
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	48356
Seq. ID	ncj700977825.h1
Method	BLASTX
NCBI GI	g3548805
BLAST score	239
E value	2.0e-20
Match length	63
% identity	65
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	48357
Seq. ID	ncj700977854.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	90
E value	3.0e-43
Match length	246
% identity	84
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	48358
Seq. ID	ncj700977933.h1
Method	BLASTX
NCBI GI	g3935170
BLAST score	276
E value	5.0e-25
Match length	72
% identity	69
NCBI Description	(AC004557) F17L21.13 [Arabidopsis thaliana]

Seq. No.	48359
Seq. ID	ncj700977949.h1
Method	BLASTX
NCBI GI	g2129753
BLAST score	305
E value	2.0e-28
Match length	60
% identity	95
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	48360

Seq. ID	ncj700977983.h1
Method	BLASTN
NCBI GI	g161354
BLAST score	46
E value	6.0e-17
Match length	86
% identity	88
NCBI Description	P.miliaris histone H2B-2.1 gene, complete cds

Seq. No.	48361
Seq. ID	ncj700978017.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	229
E value	1.0e-126
Match length	253
% identity	98
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	48362
Seq. ID	ncj700978020.h1
Method	BLASTN
NCBI GI	g2815404
BLAST score	37
E value	2.0e-11
Match length	53
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	48363
Seq. ID	ncj700978079.h1
Method	BLASTX
NCBI GI	g2780194
BLAST score	234
E value	6.0e-20
Match length	57
% identity	77
NCBI Description	(AJ003197) adenine nucleotide translocator [Lupinus albus]

Seq. No.	48364
Seq. ID	ncj700978126.h1
Method	BLASTX
NCBI GI	g585973
BLAST score	181
E value	1.0e-13
Match length	86
% identity	50
NCBI Description	FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A fructokinase [Solanum tuberosum]

Seq. No.	48365
Seq. ID	ncj700978144.h1
Method	BLASTX
NCBI GI	g4204263

BLAST score	308
E value	2.0e-28
Match length	70
% identity	77
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	48366
Seq. ID	ncj700978148.h1
Method	BLASTX
NCBI GI	g3023751
BLAST score	151
E value	4.0e-10
Match length	86
% identity	43
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	48367
Seq. ID	ncj700978152.h1
Method	BLASTX
NCBI GI	g2618686
BLAST score	217
E value	8.0e-18
Match length	92
% identity	49
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48368
Seq. ID	ncj700978192.h1
Method	BLASTX
NCBI GI	g4206210
BLAST score	269
E value	6.0e-24
Match length	89
% identity	55
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	48369
Seq. ID	ncj700978205.h1
Method	BLASTN
NCBI GI	g18578
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	Soybean ENOD2B gene for Ngm-75

Seq. No.	48370
Seq. ID	ncj700978222.h1
Method	BLASTX
NCBI GI	g4539397
BLAST score	231

E value	2.0e-19
Match length	94
% identity	51
NCBI Description	(AL035526) cellulose synthase-like protein [Arabidopsis thaliana]

Seq. No.	48371
Seq. ID	ncj700978251.h1
Method	BLASTN
NCBI GI	g710431
BLAST score	192
E value	1.0e-104
Match length	216
% identity	98
NCBI Description	Glycine max low molecular weight heat shock protein Hsp23.9 (Gmhsp23.9) mRNA, complete cds

Seq. No.	48372
Seq. ID	ncj700978252.h1
Method	BLASTX
NCBI GI	g1353239
BLAST score	346
E value	6.0e-33
Match length	94
% identity	69
NCBI Description	(U10245) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	48373
Seq. ID	ncj700978291.h1
Method	BLASTX
NCBI GI	g1280611
BLAST score	176
E value	2.0e-13
Match length	63
% identity	52
NCBI Description	(U53860) steroid reductase DET2 [Arabidopsis thaliana]

Seq. No.	48374
Seq. ID	ncj700978302.h1
Method	BLASTN
NCBI GI	g310560
BLAST score	252
E value	1.0e-140
Match length	259
% identity	100
NCBI Description	Soybean ascorbate peroxidase mRNA, complete cds

Seq. No.	48375
Seq. ID	ncj700978327.h1
Method	BLASTX
NCBI GI	g2668492
BLAST score	144
E value	5.0e-16
Match length	92
% identity	55
NCBI Description	(D89981) metal-transporting P-type ATPase [Arabidopsis thaliana]

Seq. No.	48376
Seq. ID	ncj700978361.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	255
E value	1.0e-141
Match length	270
% identity	99
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	48377
Seq. ID	ncj700978426.h1
Method	BLASTX
NCBI GI	g4206194
BLAST score	378
E value	1.0e-36
Match length	95
% identity	76
NCBI Description	(AF071527) GH3-like protein [Arabidopsis thaliana] >gi_4262168_gb_AAD14468_ (AC005275) putative GH3-like protein [Arabidopsis thaliana]

Seq. No.	48378
Seq. ID	ncj700978433.h1
Method	BLASTX
NCBI GI	g2494174
BLAST score	168
E value	4.0e-12
Match length	71
% identity	51
NCBI Description	GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	48379
Seq. ID	ncj700978454.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	65
E value	2.0e-28
Match length	155
% identity	90
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	48380
Seq. ID	ncj700978466.h1
Method	BLASTX
NCBI GI	g2583119
BLAST score	177
E value	3.0e-13
Match length	65
% identity	14
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48381
Seq. ID	ncj700978472.h1

Method	BLASTX
NCBI GI	g4406780
BLAST score	250
E value	5.0e-22
Match length	56
% identity	82
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	48382
Seq. ID	ncj700978491.h1
Method	BLASTX
NCBI GI	g3560529
BLAST score	202
E value	3.0e-16
Match length	49
% identity	84
NCBI Description	(AF039598) light harvesting chlorophyll A/B binding protein [Prunus persica]

Seq. No.	48383
Seq. ID	ncj700978514.h1
Method	BLASTX
NCBI GI	g2104536
BLAST score	151
E value	2.0e-10
Match length	43
% identity	56
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	48384
Seq. ID	ncj700978537.h1
Method	BLASTX
NCBI GI	g4220472
BLAST score	271
E value	3.0e-24
Match length	61
% identity	89
NCBI Description	(AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]

Seq. No.	48385
Seq. ID	ncj700978639.h1
Method	BLASTX
NCBI GI	g4454012
BLAST score	398
E value	4.0e-39
Match length	90
% identity	80
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	48386
Seq. ID	ncj700978668.h1
Method	BLASTX
NCBI GI	g2245072

BLAST score 204
E value 2.0e-16
Match length 82
% identity 60
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 48387
Seq. ID ncj700978669.h1
Method BLASTX
NCBI GI g3249103
BLAST score 290
E value 2.0e-26
Match length 89
% identity 29
NCBI Description (AC003114) Contains similarity to membrane-associated salt-inducible protein homolog TM021B04.10 gb_2191192 from A. thaliana BAC gb_AF007271. [Arabidopsis thaliana]

Seq. No. 48388
Seq. ID ncj700978677.h1
Method BLASTX
NCBI GI g4539452
BLAST score 320
E value 6.0e-30
Match length 88
% identity 73
NCBI Description (AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No. 48389
Seq. ID ncj700978688.h1
Method BLASTX
NCBI GI g3063453
BLAST score 210
E value 5.0e-17
Match length 90
% identity 53
NCBI Description (AC003981) F22O13.15 [Arabidopsis thaliana]

Seq. No. 48390
Seq. ID ncj700978836.h1
Method BLASTX
NCBI GI g1362162
BLAST score 134
E value 5.0e-13
Match length 72
% identity 38
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 48391
Seq. ID ncj700978979.h1
Method BLASTX
NCBI GI g3319358
BLAST score 259
E value 5.0e-23
Match length 57

% identity	86
NCBI Description	(AF077407) Arabidopsis thaliana CLC-d chloride channel protein (GB:Z71450) [Arabidopsis thaliana]

Seq. No.	48392
Seq. ID	ncj700979179.h1
Method	BLASTN
NCBI GI	g3290208
BLAST score	113
E value	6.0e-57
Match length	160
% identity	93
NCBI Description	Malus domestica MADS-box protein 1 mRNA, complete cds

Seq. No.	48393
Seq. ID	ncj700979192.h1
Method	BLASTX
NCBI GI	g2191136
BLAST score	125
E value	5.0e-15
Match length	72
% identity	60
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	48394
Seq. ID	ncj700979388.h1
Method	BLASTX
NCBI GI	g1617268
BLAST score	169
E value	3.0e-12
Match length	76
% identity	53
NCBI Description	(Z72153) acyl CoA synthetase [Brassica napus]

Seq. No.	48395
Seq. ID	ncj700979473.h1
Method	BLASTX
NCBI GI	g2347188
BLAST score	259
E value	6.0e-23
Match length	76
% identity	67
NCBI Description	(AC002338) laccase isolog [Arabidopsis thaliana] >gi_3150401 (AC004165) putative laccase [Arabidopsis thaliana]

Seq. No.	48396
Seq. ID	ncj700979481.h1
Method	BLASTX
NCBI GI	g126151
BLAST score	173
E value	8.0e-13
Match length	57
% identity	61

NCBI Description	LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi_282898_pir__S27365 lectin precursor - soybean >gi_170006 (K00821) lectin prepeptide [Glycine max]

Seq. No.	48397
Seq. ID	ncj700979508.h2
Method	BLASTN
NCBI GI	g1556445
BLAST score	78
E value	3.0e-36
Match length	158
% identity	87
NCBI Description	Hordeum vulgare alpha tubulin (tubA) mRNA, complete cds

Seq. No.	48398
Seq. ID	ncj700979509.h2
Method	BLASTN
NCBI GI	g170067
BLAST score	113
E value	6.0e-57
Match length	129
% identity	48
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP3) gene, complete cds

Seq. No.	48399
Seq. ID	ncj700979521.h2
Method	BLASTN
NCBI GI	g644492
BLAST score	97
E value	2.0e-47
Match length	169
% identity	90
NCBI Description	Corn elongation factor 1alpha gene, complete cds

Seq. No.	48400
Seq. ID	ncj700979561.h2
Method	BLASTX
NCBI GI	g4539394
BLAST score	162
E value	1.0e-11
Match length	78
% identity	10
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	48401
Seq. ID	ncj700979602.h2
Method	BLASTX
NCBI GI	g4103757
BLAST score	219
E value	4.0e-18
Match length	81
% identity	59
NCBI Description	(AF027376) MADS1 [Corylus avellana]

Seq. No.	48402
Seq. ID	ncj700979623.h2

Method	BLASTX
NCBI GI	g3810596
BLAST score	152
E value	3.0e-10
Match length	77
% identity	38
NCBI Description	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq. No.	48403
Seq. ID	ncj700979643.h2
Method	BLASTN
NCBI GI	g2304954
BLAST score	276
E value	1.0e-154
Match length	280
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	48404
Seq. ID	ncj700979651.h2
Method	BLASTN
NCBI GI	g1655579
BLAST score	113
E value	7.0e-57
Match length	269
% identity	86
NCBI Description	C.roseus mRNA for S-adenosyl-L-methionine synthetase

Seq. No.	48405
Seq. ID	ncj700979724.h2
Method	BLASTX
NCBI GI	g4559368
BLAST score	249
E value	1.0e-21
Match length	70
% identity	63
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48406
Seq. ID	ncj700979737.h2
Method	BLASTX
NCBI GI	g3132478
BLAST score	237
E value	3.0e-20
Match length	86
% identity	59
NCBI Description	(AC003096) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	48407
Seq. ID	ncj700979762.h2
Method	BLASTN
NCBI GI	g21016
BLAST score	55
E value	1.0e-22
Match length	103
% identity	88

NCBI Description	P.vulgaris loxA gene for lipoxygenase

Seq. No.	48408
Seq. ID	ncj700979791.h2
Method	BLASTX
NCBI GI	g2911060
BLAST score	151
E value	3.0e-10
Match length	40
% identity	70
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana] >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	48409
Seq. ID	ncj700979916.h1
Method	BLASTX
NCBI GI	g4455209
BLAST score	140
E value	5.0e-09
Match length	35
% identity	69
NCBI Description	(AL035440) putative Proline synthetase associated protein [Arabidopsis thaliana]

Seq. No.	48410
Seq. ID	ncj700980006.h1
Method	BLASTX
NCBI GI	g4063743
BLAST score	297
E value	3.0e-27
Match length	96
% identity	62
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48411
Seq. ID	ncj700980023.h1
Method	BLASTX
NCBI GI	g3046693
BLAST score	138
E value	8.0e-09
Match length	23
% identity	91
NCBI Description	(AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No.	48412
Seq. ID	ncj700980177.h1
Method	BLASTN
NCBI GI	g255576
BLAST score	81
E value	8.0e-38
Match length	153
% identity	88
NCBI Description	small auxin up RNA gene cluster: orf 6B [Glycine max=soybeans, cv. Wayne, Genomic, 665 nt]

Seq. No.	48413
Seq. ID	ncj700980194.h1
Method	BLASTN
NCBI GI	g169360
BLAST score	71
E value	5.0e-32
Match length	142
% identity	88
NCBI Description	P.vulgaris PVPK-1 protein, complete cds

Seq. No.	48414
Seq. ID	ncj700980321.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	231
E value	1.0e-127
Match length	243
% identity	99
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	48415
Seq. ID	ncj700980340.h1
Method	BLASTN
NCBI GI	g886099
BLAST score	131
E value	1.0e-67
Match length	179
% identity	93
NCBI Description	Glycine max putative water channel protein (Pip1) mRNA, complete cds

Seq. No.	48416
Seq. ID	ncj700980390.h1
Method	BLASTX
NCBI GI	g3641252
BLAST score	401
E value	2.0e-39
Match length	83
% identity	94
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	48417
Seq. ID	ncj700980414.h1
Method	BLASTX
NCBI GI	g2731443
BLAST score	145
E value	2.0e-09
Match length	47
% identity	53
NCBI Description	(U96923) [prot= cDNA of the glycoamidase gene [Aspergillus niger]

Seq. No.	48418
Seq. ID	ncj700980420.h1
Method	BLASTX
NCBI GI	g3618316

BLAST score	182
E value	9.0e-14
Match length	42
% identity	40
NCBI Description	(AB001886) zinc finger protein [Oryza sativa]

Seq. No.	48419
Seq. ID	ncj700980439.h1
Method	BLASTX
NCBI GI	g4063743
BLAST score	264
E value	2.0e-23
Match length	80
% identity	64
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48420
Seq. ID	ncj700980524.h1
Method	BLASTX
NCBI GI	g2392772
BLAST score	342
E value	1.0e-32
Match length	85
% identity	78
NCBI Description	(AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	48421
Seq. ID	ncj700980589.h1
Method	BLASTN
NCBI GI	g2695862
BLAST score	106
E value	9.0e-53
Match length	214
% identity	88
NCBI Description	Pisum sativum mRNA for 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase, clone pPS1A

Seq. No.	48422
Seq. ID	ncj700980590.h1
Method	BLASTX
NCBI GI	g2352427
BLAST score	157
E value	7.0e-11
Match length	77
% identity	17
NCBI Description	(AF004161) peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]

Seq. No.	48423
Seq. ID	ncj700980619.h1
Method	BLASTX
NCBI GI	g3876642
BLAST score	239
E value	2.0e-20
Match length	77

% identity	61
NCBI Description	(Z81526) predicted using Genefinder; cDNA EST EMBL:C09939 comes from this gene; cDNA EST EMBL:C12888 comes from this gene; cDNA EST yk265g7.5 comes from this gene; cDNA EST yk412g10.5 comes from this gene; cDNA EST yk224f7.5 co

Seq. No.	48424
Seq. ID	ncj700980626.h1
Method	BLASTX
NCBI GI	g2829862
BLAST score	235
E value	6.0e-20
Match length	93
% identity	46
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	48425
Seq. ID	ncj700980788.h1
Method	BLASTX
NCBI GI	g3915070
BLAST score	381
E value	4.0e-37
Match length	91
% identity	82
NCBI Description	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) >gi_1841704_emb_CAB06653_ (Z85984) histidyl tRNA Synthetase [Oryza sativa]

Seq. No.	48426
Seq. ID	ncj700980831.h1
Method	BLASTX
NCBI GI	g3341694
BLAST score	269
E value	3.0e-24
Match length	57
% identity	91
NCBI Description	(AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No.	48427
Seq. ID	ncj700980835.h1
Method	BLASTX
NCBI GI	g4558672
BLAST score	214
E value	2.0e-17
Match length	88
% identity	55
NCBI Description	(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis thaliana]

Seq. No.	48428
Seq. ID	ncj700980844.h1
Method	BLASTX
NCBI GI	g3522956
BLAST score	349
E value	2.0e-33
Match length	91

% identity	69
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	48429
Seq. ID	ncj700980960.h1
Method	BLASTX
NCBI GI	g1552379
BLAST score	191
E value	6.0e-31
Match length	86
% identity	78
NCBI Description	(Y08155) pectin methylesterase [Silene latifolia ssp. alba]

Seq. No.	48430
Seq. ID	ncj700981037.h1
Method	BLASTN
NCBI GI	g1778375
BLAST score	110
E value	4.0e-55
Match length	138
% identity	95
NCBI Description	Pisum sativum PsRT17-1 mRNA, complete cds

Seq. No.	48431
Seq. ID	ncj700981082.h1
Method	BLASTN
NCBI GI	g4206101
BLAST score	68
E value	5.0e-30
Match length	128
% identity	88
NCBI Description	Glycine max retroelement diaspora gag-pol polyprotein (gag-pol) pseudogene, partial sequence

Seq. No.	48432
Seq. ID	ncj700981106.h1
Method	BLASTX
NCBI GI	g4102598
BLAST score	189
E value	1.0e-14
Match length	87
% identity	45
NCBI Description	(AF013466) auxin response factor 4 [Arabidopsis thaliana]

Seq. No.	48433
Seq. ID	ncj700981119.h1
Method	BLASTN
NCBI GI	g508303
BLAST score	39
E value	1.0e-12
Match length	59
% identity	92
NCBI Description	Alfalfa bimodular protein (corC) mRNA, complete cds

Seq. No.	48434
Seq. ID	ncj700981134.h1

Method	BLASTN
NCBI GI	g2394299
BLAST score	42
E value	2.0e-14
Match length	73
% identity	89
NCBI Description	Oryza sativa cytochrome C mRNA, complete cds

Seq. No.	48435
Seq. ID	ncj700981162.h1
Method	BLASTN
NCBI GI	g2921511
BLAST score	70
E value	3.0e-31
Match length	146
% identity	87
NCBI Description	Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds

Seq. No.	48436
Seq. ID	ncj700981181.h1
Method	BLASTX
NCBI GI	g2708484
BLAST score	201
E value	3.0e-16
Match length	48
% identity	79
NCBI Description	(U79557) IAA24 [Arabidopsis thaliana]

Seq. No.	48437
Seq. ID	ncj700981241.h1
Method	BLASTX
NCBI GI	g2621249
BLAST score	144
E value	3.0e-09
Match length	82
% identity	46
NCBI Description	(AE000807) conserved protein [Methanobacterium thermoautotrophicum]

Seq. No.	48438
Seq. ID	ncj700981275.h1
Method	BLASTX
NCBI GI	g2780996
BLAST score	231
E value	2.0e-19
Match length	53
% identity	79
NCBI Description	Chain A, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution >gi_2780997_pdb_1KSI_B Chain B, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution

Seq. No.	48439
Seq. ID	ncj700981350.h1
Method	BLASTX
NCBI GI	g3135251

BLAST score	246
E value	3.0e-21
Match length	86
% identity	57
NCBI Description	(AC003058) putative receptor protein kinase [Arabidopsis thaliana] >gi_3176719 (AC002392) putative protein kinase [Arabidopsis thaliana]

Seq. No.	48440
Seq. ID	ncj700981426.h1
Method	BLASTX
NCBI GI	g1709618
BLAST score	177
E value	3.0e-13
Match length	55
% identity	46
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_625437_pir__JC2291 protein disulfide-isomerase (EC 5.3.4.1) - Humicola insolens >gi_712823_bbs_157479 (S74296) protein disulfide isomerase, PDI {EC 5.3.4.1} [Humicola insolens, KASI, Peptide, 505 aa] [Humicola insolens] >gi_1089933_prf__2018168A protein disulfide isomerase [Humicola insolens]

Seq. No.	48441
Seq. ID	ncj700981472.h1
Method	BLASTN
NCBI GI	g170091
BLAST score	227
E value	1.0e-125
Match length	262
% identity	97
NCBI Description	Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No.	48442
Seq. ID	ncj700981492.h1
Method	BLASTX
NCBI GI	g4063751
BLAST score	161
E value	2.0e-11
Match length	85
% identity	39
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	48443
Seq. ID	ncj700981519.h1
Method	BLASTX
NCBI GI	g1142621
BLAST score	236
E value	5.0e-20
Match length	72
% identity	65
NCBI Description	(U18349) phaseolin G-box binding protein PG2 [Phaseolus vulgaris]

Seq. No.	48444
Seq. ID	ncj700981620.h1
Method	BLASTX
NCBI GI	g1771160
BLAST score	231
E value	1.0e-19
Match length	84
% identity	51
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	48445
Seq. ID	ncj700981690.h1
Method	BLASTX
NCBI GI	g2052383
BLAST score	349
E value	3.0e-33
Match length	69
% identity	87
NCBI Description	(U66345) calreticulin [Arabidopsis thaliana]

Seq. No.	48446
Seq. ID	ncj700981718.h1
Method	BLASTX
NCBI GI	g1707019
BLAST score	227
E value	5.0e-19
Match length	94
% identity	41
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48447
Seq. ID	ncj700981775.h1
Method	BLASTX
NCBI GI	g2654226
BLAST score	162
E value	1.0e-11
Match length	64
% identity	53
NCBI Description	(AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis thaliana]

Seq. No.	48448
Seq. ID	ncj700981874.h1
Method	BLASTX
NCBI GI	g2827466
BLAST score	168
E value	3.0e-12
Match length	63
% identity	48
NCBI Description	(AF044253) potassium channel beta 2 subunit [Homo sapiens]

Seq. No.	48449
Seq. ID	ncj700981877.h1
Method	BLASTX

NCBI GI	g4510418
BLAST score	217
E value	5.0e-18
Match length	73
% identity	60
NCBI Description	(AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48450
Seq. ID	ncj700981968.h1
Method	BLASTX
NCBI GI	g3790188
BLAST score	159
E value	4.0e-13
Match length	48
% identity	85
NCBI Description	(Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum]

Seq. No.	48451
Seq. ID	ncj700982047.h1
Method	BLASTX
NCBI GI	g4512018
BLAST score	213
E value	8.0e-28
Match length	77
% identity	82
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	48452
Seq. ID	ncj700982078.h1
Method	BLASTX
NCBI GI	g3785972
BLAST score	210
E value	4.0e-17
Match length	57
% identity	77
NCBI Description	(AC005560) putative auxin transport protein [Arabidopsis thaliana] >gi_4262249_gb_AAD14542_ (AC006200) putative auxin transport protein [Arabidopsis thaliana]

Seq. No.	48453
Seq. ID	ncj700982151.h1
Method	BLASTX
NCBI GI	g3080390
BLAST score	351
E value	1.0e-33
Match length	91
% identity	65
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	48454
Seq. ID	ncj700982187.h1
Method	BLASTX
NCBI GI	g2833380
BLAST score	419
E value	1.0e-41

Match length	86
% identity	97
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2) (PRS II) >gi_2146772_pir__S71262 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) II - Arabidopsis thaliana (fragment) >gi_1064885_emb_CAA63552_ (X92974) phosphoribosyl pyrophosphate synthetase II [Arabidopsis thaliana]

Seq. No.	48455
Seq. ID	ncj700982222.h1
Method	BLASTN
NCBI GI	g169974
BLAST score	93
E value	6.0e-45
Match length	93
% identity	100
NCBI Description	Glycine max vspA gene, complete cds

Seq. No.	48456
Seq. ID	ncj700982240.h1
Method	BLASTN
NCBI GI	g258159
BLAST score	34
E value	1.0e-09
Match length	73
% identity	87
NCBI Description	psbD=reaction center protein D2 {5'region} [tobacco, Chloroplast, 90 nt]

Seq. No.	48457
Seq. ID	ncj700982260.h1
Method	BLASTN
NCBI GI	g21000
BLAST score	39
E value	9.0e-13
Match length	63
% identity	90
NCBI Description	Bean DNA for glycine-rich cell wall protein GRP 1.0

Seq. No.	48458
Seq. ID	ncj700982486.h1
Method	BLASTX
NCBI GI	g1352463
BLAST score	189
E value	8.0e-15
Match length	41
% identity	88
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	48459
Seq. ID	ncj700982494.h1
Method	BLASTX
NCBI GI	g548771
BLAST score	220

E value	1.0e-23
Match length	64
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L3-2 >gi_101073_pir__S25592 ribosomal protein L3 - fission yeast (Schizosaccharomyces pombe) >gi_5059_emb_CAA40901_ (X57734) ribosomal protein L3 [Schizosaccharomyces pombe]

Seq. No.	48460
Seq. ID	ncj700982530.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	208
E value	9.0e-17
Match length	50
% identity	84
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	48461
Seq. ID	ncj700982553.h1
Method	BLASTN
NCBI GI	g452360
BLAST score	110
E value	4.0e-55
Match length	206
% identity	88
NCBI Description	V.faba mRNA for guanine nucleotide regulatory protein (807bp)

Seq. No.	48462
Seq. ID	ncj700982593.h1
Method	BLASTX
NCBI GI	g2780996
BLAST score	313
E value	4.0e-29
Match length	92
% identity	61
NCBI Description	Chain A, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution >gi_2780997_pdb_1KSI_B Chain B, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution

Seq. No.	48463
Seq. ID	ncj700982633.h1
Method	BLASTN
NCBI GI	g3599418
BLAST score	93
E value	5.0e-45
Match length	206
% identity	94
NCBI Description	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	48464
Seq. ID	ncj700982670.h1
Method	BLASTX

NCBI GI	g2244833
BLAST score	227
E value	5.0e-19
Match length	76
% identity	62
NCBI Description	(Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No.	48465
Seq. ID	ncj700982676.h1
Method	BLASTX
NCBI GI	g2505869
BLAST score	326
E value	1.0e-30
Match length	91
% identity	18
NCBI Description	(Y12227) polyA binding protein PAB3 [Arabidopsis thaliana]

Seq. No.	48466
Seq. ID	ncj700982686.h1
Method	BLASTN
NCBI GI	g3241923
BLAST score	39
E value	1.0e-12
Match length	47
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	48467
Seq. ID	ncj700982729.h1
Method	BLASTX
NCBI GI	g4538624
BLAST score	202
E value	4.0e-16
Match length	86
% identity	47
NCBI Description	(AJ133502) hypothetical protein [Nicotiana tabacum]

Seq. No.	48468
Seq. ID	ncj700982737.h1
Method	BLASTN
NCBI GI	g2055227
BLAST score	35
E value	2.0e-10
Match length	121
% identity	87
NCBI Description	Glycine max mRNA for SRC1, complete cds

Seq. No.	48469
Seq. ID	ncj700982814.h1
Method	BLASTX
NCBI GI	g461736
BLAST score	162
E value	1.0e-11
Match length	69
% identity	54
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR

>gi_478786_pir__S29316 chaperonin 60 - cucurbit
>gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita sp.]

Seq. No.	48470
Seq. ID	ncj700982855.h1
Method	BLASTX
NCBI GI	g4102600
BLAST score	230
E value	2.0e-19
Match length	77
% identity	68
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	48471
Seq. ID	ncj700982861.h1
Method	BLASTX
NCBI GI	g4567301
BLAST score	183
E value	7.0e-14
Match length	60
% identity	62
NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No.	48472
Seq. ID	ncj700982867.h1
Method	BLASTX
NCBI GI	g1346521
BLAST score	317
E value	1.0e-29
Match length	88
% identity	69
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2133316_pir__S65800 methionine adenosyltransferase (EC 2.5.1.6) - Neurospora crassa >gi_882335 (U21547) S-adenosylmethionine synthetase [Neurospora crassa] >gi_1589103_prf__2210293A Met(S-adenosyl) synthetase [Neurospora crassa]

Seq. No.	48473
Seq. ID	ncj700982894.h1
Method	BLASTX
NCBI GI	g2239236
BLAST score	144
E value	2.0e-09
Match length	61
% identity	44
NCBI Description	(Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]

Seq. No.	48474
Seq. ID	ncj700983018.h1
Method	BLASTX
NCBI GI	g2129578
BLAST score	399
E value	4.0e-39

Match length	100
% identity	86
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	48475
Seq. ID	ncj700983085.h1
Method	BLASTN
NCBI GI	g2924257
BLAST score	100
E value	4.0e-49
Match length	148
% identity	92
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	48476
Seq. ID	ncj700983158.h1
Method	BLASTX
NCBI GI	g2648032
BLAST score	168
E value	2.0e-12
Match length	43
% identity	84
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	48477
Seq. ID	ncj700983255.h1
Method	BLASTX
NCBI GI	g4539320
BLAST score	412
E value	1.0e-40
Match length	93
% identity	80
NCBI Description	(AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	48478
Seq. ID	ncj700983302.h1
Method	BLASTX
NCBI GI	g2462834
BLAST score	190
E value	1.0e-14
Match length	69
% identity	55
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48479
Seq. ID	ncj700983307.h1
Method	BLASTX
NCBI GI	g3935147
BLAST score	249
E value	1.0e-21
Match length	90
% identity	57

NCBI Description	(AC005106) T25N20.11 [Arabidopsis thaliana]
Seq. No.	48480
Seq. ID	ncj700983330.h1
Method	BLASTX
NCBI GI	g2583120
BLAST score	260
E value	7.0e-23
Match length	81
% identity	62
NCBI Description	(AC002387) putative receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	48481
Seq. ID	ncj700983428.h1
Method	BLASTX
NCBI GI	g3913425
BLAST score	433
E value	3.0e-43
Match length	89
% identity	97
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.	48482
Seq. ID	ncj700983472.h1
Method	BLASTX
NCBI GI	g4454048
BLAST score	163
E value	1.0e-11
Match length	87
% identity	38
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]
Seq. No.	48483
Seq. ID	ncj700983481.h1
Method	BLASTN
NCBI GI	g407474
BLAST score	118
E value	7.0e-60
Match length	174
% identity	92
NCBI Description	P.sativum, mRNA for T-protein of glycine decarboxylase complex
Seq. No.	48484
Seq. ID	ncj700983527.h1
Method	BLASTX
NCBI GI	g2462828
BLAST score	174
E value	7.0e-13
Match length	44
% identity	70
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.	48485

Seq. ID	ncj700983543.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	98
E value	6.0e-48
Match length	248
% identity	86
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	48486
Seq. ID	ncj700983605.h1
Method	BLASTX
NCBI GI	g113391
BLAST score	203
E value	2.0e-16
Match length	78
% identity	50
NCBI Description	ALCOHOL DEHYDROGENASE A CHAIN >gi_65891_pir__DEMSAA alcohol dehydrogenase (EC 1.1.1.1) A - mouse >gi_309094 (M11307) alcohol dehydrogenase [Mus caroli] >gi_387092 (M18480) alcohol dehydrogenase [Mus musculus] >gi_387093 (M22679) alcohol dehydrogenase [Mus musculus] >gi_225879_prf__1402250A alcohol dehydrogenase [Mus musculus]

Seq. No.	48487
Seq. ID	ncj700983756.h1
Method	BLASTN
NCBI GI	g2564051
BLAST score	34
E value	1.0e-09
Match length	42
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	48488
Seq. ID	ncj700983879.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	159
E value	2.0e-84
Match length	278
% identity	92
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	48489
Seq. ID	ncj700983984.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	71
E value	8.0e-32
Match length	255
% identity	82
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	48490
Seq. ID	ncj700984028.h1
Method	BLASTN
NCBI GI	g20728
BLAST score	77
E value	2.0e-35
Match length	237
% identity	86
NCBI Description	Pea chloroplast GAPA mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13)

Seq. No.	48491
Seq. ID	ncj700984075.h1
Method	BLASTX
NCBI GI	g556409
BLAST score	124
E value	6.0e-10
Match length	82
% identity	49
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	48492
Seq. ID	ncj700984078.h1
Method	BLASTX
NCBI GI	g3786007
BLAST score	140
E value	4.0e-09
Match length	59
% identity	49
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48493
Seq. ID	ncj700984144.h1
Method	BLASTN
NCBI GI	g3142328
BLAST score	140
E value	6.0e-73
Match length	292
% identity	95
NCBI Description	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq. No.	48494
Seq. ID	ncj700984164.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	240
E value	1.0e-132
Match length	244
% identity	100
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	48495

Seq. ID	ncj700984170.h1
Method	BLASTN
NCBI GI	g1236948
BLAST score	102
E value	9.0e-51
Match length	114
% identity	97
NCBI Description	Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No.	48496
Seq. ID	ncj700984171.h1
Method	BLASTX
NCBI GI	g2826900
BLAST score	410
E value	2.0e-40
Match length	99
% identity	78
NCBI Description	(AB004461) DNA polymerase alpha catalytic subunit [Oryza sativa]

Seq. No.	48497
Seq. ID	ncj700984230.h1
Method	BLASTX
NCBI GI	g4539460
BLAST score	204
E value	3.0e-16
Match length	91
% identity	4
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	48498
Seq. ID	ncj700984238.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	198
E value	1.0e-107
Match length	262
% identity	94
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	48499
Seq. ID	ncj700984248.h1
Method	BLASTX
NCBI GI	g2244818
BLAST score	173
E value	6.0e-13
Match length	60
% identity	55
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48500
Seq. ID	ncj700984309.h1
Method	BLASTX
NCBI GI	g2961383
BLAST score	155
E value	1.0e-10
Match length	70

% identity	54
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	48501
Seq. ID	ncj700984325.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	92
E value	2.0e-44
Match length	227
% identity	86
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	48502
Seq. ID	ncj700984335.h1
Method	BLASTX
NCBI GI	g2129953
BLAST score	154
E value	1.0e-10
Match length	39
% identity	67
NCBI Description	laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542) diphenol oxidase [Nicotiana tabacum]

Seq. No.	48503
Seq. ID	ncj700984466.h1
Method	BLASTX
NCBI GI	g2583108
BLAST score	157
E value	5.0e-11
Match length	59
% identity	63
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	48504
Seq. ID	ncj700984468.h1
Method	BLASTX
NCBI GI	g3249105
BLAST score	195
E value	3.0e-15
Match length	87
% identity	49
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	48505
Seq. ID	ncj700984474.h1
Method	BLASTN
NCBI GI	g167293
BLAST score	84
E value	1.0e-39
Match length	160
% identity	88
NCBI Description	Colletotrichum gloeosporioides glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds

Seq. No.	48506
Seq. ID	ncj700984615.h1
Method	BLASTX
NCBI GI	g1176658
BLAST score	168
E value	4.0e-12
Match length	75
% identity	47
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	48507
Seq. ID	ncj700984620.h1
Method	BLASTX
NCBI GI	g3176691
BLAST score	150
E value	5.0e-10
Match length	70
% identity	50
NCBI Description	(AC003671) Contains homology to serine/threonine protein kinase gb_X99618 from Mycobacterium tuberculosis. ESTs gb_F14403, gb_F14404, and gb_N96730 come from this gene. [Arabidopsis thaliana]

Seq. No.	48508
Seq. ID	ncj700984648.h1
Method	BLASTN
NCBI GI	g166935
BLAST score	112
E value	3.0e-56
Match length	212
% identity	88
NCBI Description	A.thaliana ubiquitin extension protein (UBQ6) gene, complete cds

Seq. No.	48509
Seq. ID	ncj700984735.h1
Method	BLASTX
NCBI GI	g3121829
BLAST score	197
E value	2.0e-15
Match length	88
% identity	23
NCBI Description	CHROMATIN ASSEMBLY FACTOR I P60 SUBUNIT (CAF-I 60 KD SUBUNIT) >gi_2134915_pir__B56731 chromatin assembly factor I p60 chain - human >gi_882260 (U20980) chromatin assembly factor-I p60 subunit [Homo sapiens]

Seq. No.	48510
Seq. ID	ncj700984765.h1
Method	BLASTN
NCBI GI	g1262439
BLAST score	280
E value	1.0e-156
Match length	280
% identity	100

NCBI Description	Glycine max lipoxygenase (vlxC) mRNA, complete cds
Seq. No.	48511
Seq. ID	ncj700984769.h1
Method	BLASTX
NCBI GI	g2492792
BLAST score	323
E value	3.0e-30
Match length	89
% identity	73
NCBI Description	LATE NODULIN 56 (N-56) >gi_532290_dbj_BAA07212_ (D38015) soybean late nodulin [Glycine max]
Seq. No.	48512
Seq. ID	ncj700984781.h1
Method	BLASTX
NCBI GI	g132944
BLAST score	334
E value	1.0e-31
Match length	74
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.	48513
Seq. ID	ncj700984793.h1
Method	BLASTX
NCBI GI	g4262140
BLAST score	151
E value	4.0e-10
Match length	25
% identity	100
NCBI Description	(AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
Seq. No.	48514
Seq. ID	ncj700984853.h1
Method	BLASTN
NCBI GI	g4567193
BLAST score	40
E value	2.0e-13
Match length	140
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence
Seq. No.	48515
Seq. ID	ncj700984871.h1
Method	BLASTX
NCBI GI	g4559331
BLAST score	212
E value	3.0e-17
Match length	65
% identity	71
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.	48516

Seq. ID	ncj700984950.h1
Method	BLASTX
NCBI GI	g3152613
BLAST score	142
E value	3.0e-09
Match length	68
% identity	41
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48517
Seq. ID	ncj700984979.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	98
E value	6.0e-48
Match length	142
% identity	92
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	48518
Seq. ID	ncj700985002.h1
Method	BLASTX
NCBI GI	g3080420
BLAST score	173
E value	9.0e-13
Match length	59
% identity	58
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	48519
Seq. ID	ncj700985015.h1
Method	BLASTX
NCBI GI	g3695389
BLAST score	434
E value	3.0e-43
Match length	94
% identity	44
NCBI Description	(AF096371) contains similarity to D-isomer specific 2-hydroxyacid dehydrogenases (Pfam: 2-Hacid_DH.hmm, score: 19.11) [Arabidopsis thaliana]

Seq. No.	48520
Seq. ID	ncj700985022.h1
Method	BLASTN
NCBI GI	g11576
BLAST score	118
E value	4.0e-60
Match length	146
% identity	96
NCBI Description	Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NADH dehydrogenase and ORF

Seq. No.	48521
Seq. ID	ncj700985045.h1

Method	BLASTN
NCBI GI	g1196896
BLAST score	170
E value	7.0e-91
Match length	272
% identity	99
NCBI Description	Glycine max acidic ribosomal protein P0 mRNA, complete cds

Seq. No.	48522
Seq. ID	ncj700985105.h1
Method	BLASTX
NCBI GI	g2398829
BLAST score	146
E value	9.0e-10
Match length	42
% identity	69
NCBI Description	(Y11220) mitochondrial uncoupling protein [Solanum tuberosum]

Seq. No.	48523
Seq. ID	ncj700985160.h1
Method	BLASTX
NCBI GI	g2262178
BLAST score	324
E value	2.0e-30
Match length	90
% identity	72
NCBI Description	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]

Seq. No.	48524
Seq. ID	ncj700985190.h1
Method	BLASTX
NCBI GI	g3242708
BLAST score	196
E value	2.0e-15
Match length	79
% identity	48
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	48525
Seq. ID	ncj700985245.h1
Method	BLASTX
NCBI GI	g3522933
BLAST score	329
E value	5.0e-31
Match length	71
% identity	83
NCBI Description	(AC004411) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	48526
Seq. ID	ncj700985247.h1
Method	BLASTX
NCBI GI	g3914472
BLAST score	274
E value	1.0e-24

Match length	66
% identity	80
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	48527
Seq. ID	ncj700985325.h1
Method	BLASTX
NCBI GI	g2655008
BLAST score	184
E value	3.0e-14
Match length	69
% identity	48
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	48528
Seq. ID	ncj700985381.h1
Method	BLASTX
NCBI GI	g2642153
BLAST score	146
E value	1.0e-09
Match length	76
% identity	45
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	48529
Seq. ID	ncj700985401.h1
Method	BLASTX
NCBI GI	g4063751
BLAST score	160
E value	3.0e-11
Match length	44
% identity	75
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	48530
Seq. ID	ncj700985404.h1
Method	BLASTN
NCBI GI	g1276966
BLAST score	47
E value	1.0e-17
Match length	55
% identity	96
NCBI Description	Daucus carota putative ribosomal protein mRNA, somatic embryo clone Gea42, partial cds

Seq. No.	48531
Seq. ID	ncj700985535.h1
Method	BLASTX
NCBI GI	g4467139

BLAST score	303
E value	5.0e-28
Match length	86
% identity	63
NCBI Description	(AL035540) putative protein phosphatase-2c [Arabidopsis thaliana]

Seq. No.	48532
Seq. ID	ncj700985570.h1
Method	BLASTN
NCBI GI	g2618605
BLAST score	39
E value	9.0e-13
Match length	142
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	48533
Seq. ID	ncj700985623.h1
Method	BLASTN
NCBI GI	g3869068
BLAST score	52
E value	2.0e-20
Match length	88
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	48534
Seq. ID	ncj700985644.h1
Method	BLASTX
NCBI GI	g4262233
BLAST score	141
E value	6.0e-09
Match length	49
% identity	53
NCBI Description	(AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48535
Seq. ID	ncj700985686.h1
Method	BLASTX
NCBI GI	g3445200
BLAST score	151
E value	2.0e-10
Match length	35
% identity	71
NCBI Description	(AC004786) putative squalene epoxidase [Arabidopsis thaliana]

Seq. No.	48536
Seq. ID	ncj700985723.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	122
E value	2.0e-62
Match length	218

% identity	93
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	48537
Seq. ID	ncj700985724.h1
Method	BLASTX
NCBI GI	g3202038
BLAST score	126
E value	1.0e-11
Match length	57
% identity	67
NCBI Description	(AF069322) permease 1 [Mesembryanthemum crystallinum]

Seq. No.	48538
Seq. ID	ncj700985727.h1
Method	BLASTX
NCBI GI	g1362019
BLAST score	197
E value	2.0e-15
Match length	60
% identity	72
NCBI Description	zinc finger protein 6 - Arabidopsis thaliana >gi_790683 (L39649) zinc finger protein [Arabidopsis thaliana]

Seq. No.	48539
Seq. ID	ncj700985735.h1
Method	BLASTX
NCBI GI	g2129742
BLAST score	153
E value	3.0e-10
Match length	47
% identity	60
NCBI Description	stress-induced protein OZI1 precursor - Arabidopsis thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	48540
Seq. ID	ncj700985760.h1
Method	BLASTX
NCBI GI	g4104561
BLAST score	212
E value	3.0e-17
Match length	84
% identity	54
NCBI Description	(AF036960) subtilisin-like protease [Glycine max]

Seq. No.	48541
Seq. ID	ncj700985828.h1
Method	BLASTX
NCBI GI	g3047104
BLAST score	437
E value	1.0e-43
Match length	91
% identity	86

NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	48542
Seq. ID	ncj700985835.h1
Method	BLASTX
NCBI GI	g4091008
BLAST score	175
E value	6.0e-13
Match length	87
% identity	51
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]
Seq. No.	48543
Seq. ID	ncj700985862.h1
Method	BLASTX
NCBI GI	g3646450
BLAST score	146
E value	1.0e-09
Match length	89
% identity	42
NCBI Description	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]
Seq. No.	48544
Seq. ID	ncj700985884.h1
Method	BLASTX
NCBI GI	g1172555
BLAST score	172
E value	1.0e-12
Match length	63
% identity	57
NCBI Description	34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) >gi_629720_pir__S46936 34K porin - potato >gi_1076682_pir__A55364 porin (clone pPOM-34) - potato mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA porin [Solanum tuberosum]
Seq. No.	48545
Seq. ID	ncj700985908.h1
Method	BLASTN
NCBI GI	g2218149
BLAST score	127
E value	3.0e-65
Match length	250
% identity	88
NCBI Description	Vigna unguiculata type IIIa membrane protein cp-wap11 mRNA, complete cds
Seq. No.	48546
Seq. ID	ncj700985954.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	237
E value	1.0e-131
Match length	248
% identity	99

NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	48547
Seq. ID	ncj700986017.h1
Method	BLASTX
NCBI GI	g2245133
BLAST score	294
E value	5.0e-27
Match length	80
% identity	71
NCBI Description	(Z97344) PSII D1 protein processing enzyme [Arabidopsis thaliana]

Seq. No.	48548
Seq. ID	ncj700986037.h1
Method	BLASTX
NCBI GI	g3152620
BLAST score	211
E value	3.0e-17
Match length	69
% identity	61
NCBI Description	(AC004482) putative C2H2 zinc finger protein [Arabidopsis thaliana]

Seq. No.	48549
Seq. ID	ncj700986053.h1
Method	BLASTX
NCBI GI	g2497538
BLAST score	294
E value	5.0e-27
Match length	79
% identity	76
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	48550
Seq. ID	ncj700986059.h1
Method	BLASTX
NCBI GI	g2980759
BLAST score	229
E value	2.0e-19
Match length	82
% identity	14
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	48551
Seq. ID	ncj700986079.h1
Method	BLASTX
NCBI GI	g2970051
BLAST score	237
E value	3.0e-20
Match length	69
% identity	54
NCBI Description	(AB012110) ARG10 [Vigna radiata]

Seq. No.	48552
Seq. ID	ncj700986154.h1

Method	BLASTX
NCBI GI	g1149595
BLAST score	177
E value	2.0e-13
Match length	70
% identity	50
NCBI Description	(Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase [Brassica napus]

Seq. No.	48553
Seq. ID	ncj700986228.h1
Method	BLASTX
NCBI GI	g1839188
BLAST score	159
E value	8.0e-21
Match length	62
% identity	76
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	48554
Seq. ID	ncj700986282.h1
Method	BLASTX
NCBI GI	g3096947
BLAST score	156
E value	8.0e-11
Match length	44
% identity	66
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	48555
Seq. ID	ncj700986292.h1
Method	BLASTX
NCBI GI	g1946355
BLAST score	245
E value	2.0e-21
Match length	77
% identity	57
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	48556
Seq. ID	ncj700986348.h1
Method	BLASTX
NCBI GI	g2501337
BLAST score	391
E value	3.0e-38
Match length	97
% identity	73
NCBI Description	AMINE OXIDASE PRECURSOR [COPPER-CONTAINING] >gi_2129875_pir__C44239 amine oxidase (copper-containing) (EC 1.4.3.6) precursor - garden pea >gi_685198 (L39931) copper amine oxidase [Pisum sativum]

Seq. No.	48557
Seq. ID	ncj700986352.h1

Method	BLASTX
NCBI GI	g2196878
BLAST score	432
E value	5.0e-43
Match length	90
% identity	88
NCBI Description	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	48558
Seq. ID	ncj700986526.h1
Method	BLASTX
NCBI GI	g1314711
BLAST score	206
E value	4.0e-28
Match length	69
% identity	83
NCBI Description	(U54615) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_3068712 (AF049236) calcium dependent protein kinase [Arabidopsis thaliana]

Seq. No.	48559
Seq. ID	ncj700986613.h1
Method	BLASTX
NCBI GI	g3044214
BLAST score	370
E value	7.0e-36
Match length	85
% identity	82
NCBI Description	(AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	48560
Seq. ID	ncj700986621.h1
Method	BLASTN
NCBI GI	g886099
BLAST score	186
E value	1.0e-100
Match length	226
% identity	96
NCBI Description	Glycine max putative water channel protein (Pip1) mRNA, complete cds

Seq. No.	48561
Seq. ID	ncj700986642.h1
Method	BLASTX
NCBI GI	g4510395
BLAST score	278
E value	4.0e-25
Match length	79
% identity	66
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	48562
Seq. ID	ncj700986653.h1
Method	BLASTN
NCBI GI	g1408470

BLAST score	64
E value	1.0e-27
Match length	120
% identity	88
NCBI Description	Arabidopsis thaliana actin depolymerizing factor 1 (AtADF1) mRNA, complete cds

Seq. No.	48563
Seq. ID	ncj700986694.h1
Method	BLASTX
NCBI GI	g2832629
BLAST score	147
E value	9.0e-10
Match length	78
% identity	45
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	48564
Seq. ID	ncj700986722.h1
Method	BLASTX
NCBI GI	g1709918
BLAST score	445
E value	1.0e-44
Match length	92
% identity	90
NCBI Description	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) >gi_438899 (L23833) glutamine phosphoribosylpyrophosphate amidotransferase [Glycine max]

Seq. No.	48565
Seq. ID	ncj700986809.h1
Method	BLASTX
NCBI GI	g3164126
BLAST score	184
E value	5.0e-14
Match length	87
% identity	37
NCBI Description	(D78598) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	48566
Seq. ID	ncj700986814.h1
Method	BLASTX
NCBI GI	g3834307
BLAST score	168
E value	2.0e-12
Match length	35
% identity	86
NCBI Description	(AC005679) Strong similarity to gene T10I14.120 gi_2832679 putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs gb_N65887 and gb_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No.	48567
Seq. ID	ncj700986820.h1

Method	BLASTX
NCBI GI	g3337361
BLAST score	146
E value	1.0e-09
Match length	55
% identity	47
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	48568
Seq. ID	ncj700986825.h1
Method	BLASTN
NCBI GI	g1946221
BLAST score	80
E value	3.0e-37
Match length	119
% identity	93
NCBI Description	M.domestica mRNA for knotted1-like homeobox protein

Seq. No.	48569
Seq. ID	ncj700986861.h1
Method	BLASTX
NCBI GI	g3894157
BLAST score	147
E value	6.0e-10
Match length	70
% identity	11
NCBI Description	(AC005312) putative protein kinase, 3' partial [Arabidopsis thaliana]

Seq. No.	48570
Seq. ID	ncj700986879.h1
Method	BLASTX
NCBI GI	g3885336
BLAST score	232
E value	7.0e-20
Match length	69
% identity	37
NCBI Description	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	48571
Seq. ID	ncj700986934.h1
Method	BLASTX
NCBI GI	g4204793
BLAST score	314
E value	2.0e-29
Match length	73
% identity	41
NCBI Description	(U52079) P-glycoprotein [Solanum tuberosum]

Seq. No.	48572
Seq. ID	ncj700987001.h1
Method	BLASTX
NCBI GI	g4558558
BLAST score	336
E value	9.0e-32
Match length	94

% identity	67
NCBI Description	(AC007138) putative polygalacturonidase [Arabidopsis thaliana]

Seq. No.	48573
Seq. ID	ncj700987036.h1
Method	BLASTN
NCBI GI	g169980
BLAST score	68
E value	5.0e-30
Match length	120
% identity	89
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	48574
Seq. ID	ncj700987105.h1
Method	BLASTX
NCBI GI	g3687230
BLAST score	176
E value	2.0e-19
Match length	81
% identity	65
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48575
Seq. ID	ncj700987125.h1
Method	BLASTX
NCBI GI	g3157941
BLAST score	172
E value	1.0e-12
Match length	52
% identity	60
NCBI Description	(AC002131) Contains similarity to hypothetical protein gb_U95973 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	48576
Seq. ID	ncj700987134.h1
Method	BLASTX
NCBI GI	g2494111
BLAST score	191
E value	6.0e-15
Match length	52
% identity	60
NCBI Description	(AC002376) Contains similarity to Glycine protein kinase 6 (gb_M67449). [Arabidopsis thaliana]

Seq. No.	48577
Seq. ID	ncj700987155.h1
Method	BLASTX
NCBI GI	g1518540
BLAST score	148
E value	8.0e-10
Match length	44
% identity	70
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	48578

Seq. ID	ncj700987224.h1
Method	BLASTX
NCBI GI	g3128190
BLAST score	179
E value	2.0e-13
Match length	56
% identity	66
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	48579
Seq. ID	ncj700987226.h1
Method	BLASTN
NCBI GI	g410285
BLAST score	148
E value	9.0e-78
Match length	232
% identity	91
NCBI Description	Pisum sativum rho (ras-related) GTP-binding protein mRNA, complete cds

Seq. No.	48580
Seq. ID	ncj700987230.h1
Method	BLASTX
NCBI GI	g3641838
BLAST score	170
E value	3.0e-18
Match length	63
% identity	76
NCBI Description	(AL023094) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	48581
Seq. ID	ncj700987267.h1
Method	BLASTX
NCBI GI	g3337361
BLAST score	429
E value	1.0e-42
Match length	90
% identity	86
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	48582
Seq. ID	ncj700987273.h1
Method	BLASTX
NCBI GI	g3482924
BLAST score	234
E value	7.0e-20
Match length	80
% identity	59
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	48583
Seq. ID	ncj700987322.h1
Method	BLASTN
NCBI GI	g4165487
BLAST score	89

E value	1.0e-42
Match length	145
% identity	90
NCBI Description	Hordeum vulgare mRNA for alpha-tubulin

Seq. No.	48584
Seq. ID	ncj700987369.h1
Method	BLASTN
NCBI GI	g3449321
BLAST score	32
E value	1.0e-08
Match length	56
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	48585
Seq. ID	ncj700987371.h1
Method	BLASTX
NCBI GI	g3402686
BLAST score	187
E value	2.0e-14
Match length	80
% identity	26
NCBI Description	(AC004697) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	48586
Seq. ID	ncj700987416.h1
Method	BLASTX
NCBI GI	g1209756
BLAST score	184
E value	5.0e-14
Match length	87
% identity	45
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	48587
Seq. ID	ncj700987461.h1
Method	BLASTN
NCBI GI	g2444419
BLAST score	165
E value	6.0e-88
Match length	196
% identity	95
NCBI Description	Glycine max ribosome-associated protein p40 mRNA, complete cds

Seq. No.	48588
Seq. ID	ncj700987504.h1
Method	BLASTX
NCBI GI	g2459442
BLAST score	210
E value	5.0e-17
Match length	89
% identity	52
NCBI Description	(AC002332) putative DNA-binding protein PD1 [Arabidopsis

thaliana]

Seq. No.	48589
Seq. ID	ncj700987547.h1
Method	BLASTX
NCBI GI	g1173638
BLAST score	190
E value	6.0e-15
Match length	48
% identity	69
NCBI Description	(U35779) 1-aminocyclopropane-1-carboxylate synthase [Triticum aestivum]

Seq. No.	48590
Seq. ID	ncj700987553.h1
Method	BLASTX
NCBI GI	g4337196
BLAST score	371
E value	5.0e-36
Match length	82
% identity	85
NCBI Description	(AC006403) putative serine/threonine receptor kinase [Arabidopsis thaliana]

Seq. No.	48591
Seq. ID	ncj700987560.h1
Method	BLASTX
NCBI GI	g3482932
BLAST score	142
E value	4.0e-09
Match length	57
% identity	54
NCBI Description	(AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	48592
Seq. ID	ncj700987625.h1
Method	BLASTN
NCBI GI	g2149954
BLAST score	99
E value	1.0e-48
Match length	186
% identity	89
NCBI Description	Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA, complete cds

Seq. No.	48593
Seq. ID	ncj700987638.h1
Method	BLASTX
NCBI GI	g2129651
BLAST score	197
E value	2.0e-19
Match length	86
% identity	53
NCBI Description	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana]

Seq. No.	48594
Seq. ID	ncj700987685.h1
Method	BLASTN
NCBI GI	g2924257
BLAST score	73
E value	4.0e-33
Match length	140
% identity	89
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	48595
Seq. ID	ncj700987714.h1
Method	BLASTX
NCBI GI	g3461833
BLAST score	137
E value	3.0e-17
Match length	86
% identity	55
NCBI Description	(AC004138) putative expansin [Arabidopsis thaliana]

Seq. No.	48596
Seq. ID	ncj700987716.h1
Method	BLASTX
NCBI GI	g2149640
BLAST score	176
E value	4.0e-13
Match length	40
% identity	75
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	48597
Seq. ID	ncj700987784.h1
Method	BLASTN
NCBI GI	g3204102
BLAST score	38
E value	2.0e-12
Match length	85
% identity	87
NCBI Description	Cicer arietinum mRNA for hypothetical protein, clone Can35, partial

Seq. No.	48598
Seq. ID	ncj700987791.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	177
E value	3.0e-95
Match length	184
% identity	99
NCBI Description	G.max ADR6 mRNA

Seq. No.	48599
Seq. ID	ncj700987816.h1
Method	BLASTX
NCBI GI	g1352243
BLAST score	265
E value	2.0e-23

Match length	91
% identity	60
NCBI Description	LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1 >gi_625972_pir__A54841 DET1 protein - Arabidopsis thaliana >gi_510275 (L33695) DET1 [Arabidopsis thaliana] >gi_3695414 (AF096373) Arabidopsis thaliana light-mediated development protein DET1 (SP:P48732) [Arabidopsis thaliana] >gi_4538982_emb_CAB39770.1_ (AL049487) Deetiolated1 (DET1) light signal transduction protein [Arabidopsis thaliana]

Seq. No.	48600
Seq. ID	ncj700987852.h1
Method	BLASTX
NCBI GI	g2832679
BLAST score	281
E value	2.0e-25
Match length	89
% identity	61
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	48601
Seq. ID	ncj700987948.h1
Method	BLASTN
NCBI GI	g2852444
BLAST score	43
E value	4.0e-15
Match length	103
% identity	85
NCBI Description	Salix bakko mRNA for SUI1 homolog, complete cds

Seq. No.	48602
Seq. ID	ncj700987978.h1
Method	BLASTX
NCBI GI	g309673
BLAST score	211
E value	4.0e-17
Match length	65
% identity	77
NCBI Description	(L19651) light harvesting protein [Pisum sativum]

Seq. No.	48603
Seq. ID	ncj700988108.h1
Method	BLASTN
NCBI GI	g2502084
BLAST score	52
E value	2.0e-20
Match length	64
% identity	95
NCBI Description	Vigna radiata adenosine triphosphatase mRNA, partial cds

Seq. No.	48604
Seq. ID	ncj700988134.h1
Method	BLASTX
NCBI GI	g4574740
BLAST score	154
E value	2.0e-15
Match length	60

% identity 55
NCBI Description (AF134402) Tat-binding protein-1 [Drosophila melanogaster]

Seq. No. 48605
Seq. ID ncj700988148.h1
Method BLASTN
NCBI GI g402635
BLAST score 119
E value 2.0e-60
Match length 241
% identity 91
NCBI Description L.albus gene for beta-tubulin

Seq. No. 48606
Seq. ID ncj700988164.h1
Method BLASTX
NCBI GI g1706956
BLAST score 210
E value 3.0e-17
Match length 42
% identity 90
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 48607
Seq. ID ncj700988195.h1
Method BLASTX
NCBI GI g3068713
BLAST score 255
E value 2.0e-22
Match length 84
% identity 65
NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 48608
Seq. ID ncj700988310.h1
Method BLASTX
NCBI GI g4432822
BLAST score 150
E value 3.0e-10
Match length 57
% identity 51
NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No. 48609
Seq. ID ncj700988387.h1
Method BLASTX
NCBI GI g3212848
BLAST score 171
E value 1.0e-12
Match length 45
% identity 71
NCBI Description (AC004005) putative inositol polyphosphate-5-phosphatase [Arabidopsis thaliana]

Seq. No. 48610
Seq. ID ncj700988425.h1
Method BLASTN

NCBI GI	g407474
BLAST score	76
E value	5.0e-35
Match length	160
% identity	87
NCBI Description	P.sativum, mRNA for T-protein of glycine decarboxylase complex

Seq. No.	48611
Seq. ID	ncj700988507.h1
Method	BLASTX
NCBI GI	g3176691
BLAST score	250
E value	5.0e-22
Match length	72
% identity	43
NCBI Description	(AC003671) Contains homology to serine/threonine protein kinase gb_X99618 from Mycobacterium tuberculosis. ESTs gb_F14403, gb_F14404, and gb_N96730 come from this gene. [Arabidopsis thaliana]

Seq. No.	48612
Seq. ID	ncj700988521.h1
Method	BLASTX
NCBI GI	g542157
BLAST score	362
E value	8.0e-35
Match length	82
% identity	82
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	48613
Seq. ID	ncj700988605.h1
Method	BLASTX
NCBI GI	g2947063
BLAST score	228
E value	4.0e-19
Match length	95
% identity	30
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	48614
Seq. ID	ncj700988625.h1
Method	BLASTX
NCBI GI	g4006827
BLAST score	345
E value	7.0e-33
Match length	88
% identity	74
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	48615
Seq. ID	ncj700988643.h1
Method	BLASTN
NCBI GI	g2370311
BLAST score	80

E value	3.0e-37
Match length	232
% identity	84
NCBI Description	Medicago sativa mRNA for DnaJ-like protein

Seq. No.	48616
Seq. ID	ncj700988679.h1
Method	BLASTX
NCBI GI	g3859114
BLAST score	366
E value	3.0e-35
Match length	77
% identity	90
NCBI Description	(AF031608) MS5-like protein [Arabidopsis thaliana]

Seq. No.	48617
Seq. ID	nsy700645504.h1
Method	BLASTX
NCBI GI	g3122288
BLAST score	425
E value	3.0e-42
Match length	93
% identity	35
NCBI Description	IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) (KAP ALPHA) >gi_1568635 (U69533) AtKAP alpha [Arabidopsis thaliana]

Seq. No.	48618
Seq. ID	nsy700645508.h1
Method	BLASTX
NCBI GI	g4158232
BLAST score	239
E value	2.0e-20
Match length	59
% identity	78
NCBI Description	(Y18626) reversibly glycosylated polypeptide [Triticum aestivum]

Seq. No.	48619
Seq. ID	nsy700645524.h1
Method	BLASTX
NCBI GI	g3834323
BLAST score	173
E value	1.0e-12
Match length	49
% identity	65
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	48620
Seq. ID	nsy700645525.h1
Method	BLASTX
NCBI GI	g3641252
BLAST score	200
E value	8.0e-16
Match length	94
% identity	15
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No.	48621
Seq. ID	nsy700645539.h1
Method	BLASTX
NCBI GI	g4220529
BLAST score	330
E value	4.0e-31
Match length	93
% identity	59
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	48622
Seq. ID	nsy700645547.h1
Method	BLASTN
NCBI GI	g508303
BLAST score	39
E value	1.0e-12
Match length	59
% identity	92
NCBI Description	Alfalfa bimodular protein (corC) mRNA, complete cds

Seq. No.	48623
Seq. ID	nsy700645605.h1
Method	BLASTX
NCBI GI	g3355474
BLAST score	191
E value	9.0e-15
Match length	73
% identity	53
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	48624
Seq. ID	nsy700645661.h1
Method	BLASTX
NCBI GI	g3004556
BLAST score	165
E value	1.0e-11
Match length	56
% identity	52
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48625
Seq. ID	nsy700645693.h1
Method	BLASTX
NCBI GI	g3142294
BLAST score	336
E value	8.0e-32
Match length	75
% identity	85
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	48626
Seq. ID	pcp700988705.h1
Method	BLASTX

NCBI GI	g3122858
BLAST score	257
E value	8.0e-23
Match length	58
% identity	88
NCBI Description	D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate dehydrogenase [Arabidopsis thaliana] >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]

Seq. No.	48627
Seq. ID	pcp700988708.h1
Method	BLASTX
NCBI GI	g4210712
BLAST score	243
E value	6.0e-21
Match length	84
% identity	58
NCBI Description	(AJ006870) purple acid phosphatase [Ipomoea batatas]

Seq. No.	48628
Seq. ID	pcp700988809.h1
Method	BLASTX
NCBI GI	g4559388
BLAST score	321
E value	5.0e-30
Match length	90
% identity	68
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48629
Seq. ID	pcp700988818.h1
Method	BLASTX
NCBI GI	g4454019
BLAST score	248
E value	2.0e-21
Match length	84
% identity	54
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	48630
Seq. ID	pcp700988914.h1
Method	BLASTN
NCBI GI	g170027
BLAST score	32
E value	9.0e-09
Match length	36
% identity	97
NCBI Description	Soybean peribacteroid membrane protein (nod24) gene, complete cds

Seq. No.	48631
Seq. ID	pcp700989095.h1
Method	BLASTN
NCBI GI	g3033512
BLAST score	163

E value	9.0e-87
Match length	218
% identity	94
NCBI Description	Phaseolus vulgaris rubisco activase (Rca1) mRNA, complete cds

Seq. No.	48632
Seq. ID	pcp700989139.h1
Method	BLASTX
NCBI GI	g2961384
BLAST score	198
E value	1.0e-15
Match length	57
% identity	63
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	48633
Seq. ID	pcp700989152.h1
Method	BLASTN
NCBI GI	g602358
BLAST score	60
E value	2.0e-25
Match length	132
% identity	87
NCBI Description	P.sativum mRNA for type II chlorophyll a/b binding protein

Seq. No.	48634
Seq. ID	pcp700989171.h1
Method	BLASTN
NCBI GI	g310562
BLAST score	117
E value	2.0e-59
Match length	175
% identity	94
NCBI Description	Glycine max calmodulin (SCaM-5) mRNA, complete cds

Seq. No.	48635
Seq. ID	pcp700989212.h1
Method	BLASTX
NCBI GI	g3702332
BLAST score	178
E value	3.0e-13
Match length	84
% identity	40
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	48636
Seq. ID	pcp700989257.h1
Method	BLASTX
NCBI GI	g3643611
BLAST score	293
E value	6.0e-27
Match length	68
% identity	76
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

09560744.000

Seq. No.	48637
Seq. ID	pcp700989382.h1
Method	BLASTX
NCBI GI	g2760844
BLAST score	243
E value	3.0e-21
Match length	53
% identity	81
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48638
Seq. ID	pcp700989412.h1
Method	BLASTX
NCBI GI	g3540207
BLAST score	142
E value	2.0e-18
Match length	92
% identity	54
NCBI Description	(AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	48639
Seq. ID	pcp700989491.h1
Method	BLASTN
NCBI GI	g3158473
BLAST score	39
E value	8.0e-13
Match length	59
% identity	92
NCBI Description	Samanea saman aquaporin 1 (Aqp1) mRNA, complete cds

Seq. No.	48640
Seq. ID	pcp700989557.h1
Method	BLASTX
NCBI GI	g1532135
BLAST score	243
E value	5.0e-21
Match length	79
% identity	76
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]

Seq. No.	48641
Seq. ID	pcp700989578.h1
Method	BLASTX
NCBI GI	g3402697
BLAST score	353
E value	7.0e-34
Match length	81
% identity	74
NCBI Description	(AC004261) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	48642
Seq. ID	pcp700989586.h1
Method	BLASTN
NCBI GI	g4165487
BLAST score	70

E value	3.0e-31
Match length	110
% identity	91
NCBI Description	Hordeum vulgare mRNA for alpha-tubulin

Seq. No.	48643
Seq. ID	pcp700989626.h1
Method	BLASTX
NCBI GI	g116359
BLAST score	201
E value	5.0e-16
Match length	54
% identity	63
NCBI Description	HEVAMINE A (CHITINASE / LYSOZYME >gi_82026_pir__S17205 chitinase (EC 3.2.1.14) hevamine - Para rubber tree >gi_234388_bbs_52808 hevamine [Hevea brasiliensis, Peptide Partial, 273 aa] >gi_1311006_pdb_1HVQ_ Glycosidase, Chitin Degradation, Multifunctional Enzyme Mol_id: 1; Molecule: Hevamine A; Chain: Null; Ec: 3.2.1.14, 3.2.1.17; Heterogen: N-,N'-,N''-Triacetyl-Chitotriose; Other_details: Plant EndochitinaseLYSOZYME >gi_1421554_pdb_1LLO_ Hevamine A (A Plant EndochitinaseLYSOZYME) COMPLEXED WITH Allosamidin >gi_1942537_pdb_2HVM_ Hevamine A At 1.8 Angstrom Resolution

Seq. No.	48644
Seq. ID	pcp700989634.h1
Method	BLASTN
NCBI GI	g1277163
BLAST score	250
E value	1.0e-138
Match length	254
% identity	100
NCBI Description	Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No.	48645
Seq. ID	pcp700989638.h1
Method	BLASTX
NCBI GI	g3885340
BLAST score	142
E value	4.0e-09
Match length	31
% identity	84
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	48646
Seq. ID	pcp700989639.h1
Method	BLASTX
NCBI GI	g2894606
BLAST score	254
E value	2.0e-22
Match length	59
% identity	80
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	48647
Seq. ID	pcp700989702.h1

Method	BLASTN
NCBI GI	g4406529
BLAST score	101
E value	1.0e-49
Match length	113
% identity	97
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	48648
Seq. ID	pcp700989812.h1
Method	BLASTN
NCBI GI	g18755
BLAST score	53
E value	2.0e-21
Match length	81
% identity	91
NCBI Description	Soybean SRS4 mRNA for ribulose-1,5-bisphosphate carboxylase (Rubisco) small subunit, partial cds

Seq. No.	48649
Seq. ID	pcp700989868.h1
Method	BLASTN
NCBI GI	g20740
BLAST score	108
E value	6.0e-54
Match length	248
% identity	86
NCBI Description	Pisum sativum mRNA for P protein, a part of glycine cleavage complex

Seq. No.	48650
Seq. ID	pcp700989873.h1
Method	BLASTX
NCBI GI	g3608128
BLAST score	257
E value	9.0e-23
Match length	63
% identity	76
NCBI Description	(AC005314) hypothetical protein [Arabidopsis thaliana] >gi_4263794_gb_AAD15454_ (AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48651
Seq. ID	pcp700989877.h1
Method	BLASTX
NCBI GI	g309673
BLAST score	202
E value	3.0e-16
Match length	63
% identity	76
NCBI Description	(L19651) light harvesting protein [Pisum sativum]

Seq. No.	48652
Seq. ID	pcp700989881.h1
Method	BLASTX
NCBI GI	g2129626

BLAST score	277
E value	6.0e-25
Match length	82
% identity	67
NCBI Description	J-domain protein - Arabidopsis thaliana >gi_928936_emb_CAA89204_ (Z49238) J-domain protein [Arabidopsis thaliana] >gi_1585434_prf__2124427A diamide resistance gene [Arabidopsis thaliana]

Seq. No.	48653
Seq. ID	pcp700989887.h1
Method	BLASTX
NCBI GI	g3548802
BLAST score	147
E value	6.0e-10
Match length	46
% identity	61
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	48654
Seq. ID	pcp700990029.h1
Method	BLASTX
NCBI GI	g3236254
BLAST score	312
E value	4.0e-29
Match length	81
% identity	73
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	48655
Seq. ID	pcp700990076.h1
Method	BLASTX
NCBI GI	g471329
BLAST score	150
E value	3.0e-11
Match length	75
% identity	41
NCBI Description	(X75451) translation initiation factor eIF-2B-delta [Oryctolagus cuniculus]

Seq. No.	48656
Seq. ID	pcp700990106.h1
Method	BLASTN
NCBI GI	g16495
BLAST score	36
E value	4.0e-11
Match length	44
% identity	95
NCBI Description	A.thaliana mRNA for plastid ribosomal protein CL15

Seq. No.	48657
Seq. ID	pcp700990120.h1
Method	BLASTX
NCBI GI	g3377517
BLAST score	270

E value	4.0e-24
Match length	71
% identity	75
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	48658
Seq. ID	pcp700990121.h1
Method	BLASTN
NCBI GI	g2055227
BLAST score	183
E value	1.0e-98
Match length	251
% identity	93
NCBI Description	Glycine max mRNA for SRC1, complete cds

Seq. No.	48659
Seq. ID	pcp700990167.h1
Method	BLASTX
NCBI GI	g4539344
BLAST score	323
E value	2.0e-30
Match length	84
% identity	69
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	48660
Seq. ID	pcp700990215.h1
Method	BLASTX
NCBI GI	g3135251
BLAST score	136
E value	1.0e-08
Match length	72
% identity	40
NCBI Description	(AC003058) putative receptor protein kinase [Arabidopsis thaliana] >gi_3176719 (AC002392) putative protein kinase [Arabidopsis thaliana]

Seq. No.	48661
Seq. ID	pcp700990218.h1
Method	BLASTX
NCBI GI	g4455350
BLAST score	209
E value	5.0e-17
Match length	53
% identity	70
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	48662
Seq. ID	pcp700990243.h1
Method	BLASTX
NCBI GI	g2827141
BLAST score	276
E value	6.0e-25
Match length	74
% identity	69
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	48663
Seq. ID	pcp700990268.h1
Method	BLASTN
NCBI GI	g602358
BLAST score	35
E value	2.0e-10
Match length	51
% identity	92
NCBI Description	P.sativum mRNA for type II chlorophyll a/b binding protein

Seq. No.	48664
Seq. ID	pcp700990275.h1
Method	BLASTX
NCBI GI	g3953458
BLAST score	157
E value	7.0e-11
Match length	46
% identity	63
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	48665
Seq. ID	pcp700990289.h1
Method	BLASTX
NCBI GI	g3046815
BLAST score	251
E value	4.0e-22
Match length	64
% identity	77
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	48666
Seq. ID	pcp700990303.h1
Method	BLASTX
NCBI GI	g4580472
BLAST score	260
E value	2.0e-29
Match length	82
% identity	75
NCBI Description	(AC006081) DNA binding protein;similar to CDC27 and nuclear scaffold proteins [Arabidopsis thaliana]

Seq. No.	48667
Seq. ID	pcp700990312.h1
Method	BLASTN
NCBI GI	g18556
BLAST score	244
E value	1.0e-135
Match length	263
% identity	99
NCBI Description	G.max DNA for Cab5

Seq. No.	48668
Seq. ID	pcp700990368.h1
Method	BLASTX
NCBI GI	g1076632
BLAST score	353

E value	8.0e-34
Match length	76
% identity	80
NCBI Description	protein kinase - common tobacco >gi_506534_emb_CAA50374_ (X71057) protein kinase [Nicotiana tabacum]

Seq. No.	48669
Seq. ID	pcp700990412.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	56
E value	8.0e-23
Match length	96
% identity	90
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	48670
Seq. ID	pcp700990418.h1
Method	BLASTX
NCBI GI	g4508081
BLAST score	253
E value	5.0e-22
Match length	87
% identity	59
NCBI Description	(AC005882) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	48671
Seq. ID	pcp700990425.h1
Method	BLASTX
NCBI GI	g266989
BLAST score	337
E value	7.0e-32
Match length	64
% identity	100
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_322517_pir__S28603 GTP-binding protein - Arabidopsis thaliana >gi_166734 (M95795) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	48672
Seq. ID	pcp700990474.h1
Method	BLASTX
NCBI GI	g2765821
BLAST score	168
E value	4.0e-12
Match length	83
% identity	45
NCBI Description	(Z95496) Mlo-h1 protein [Hordeum vulgare]

Seq. No.	48673
Seq. ID	pcp700990501.h1
Method	BLASTN
NCBI GI	g2564050
BLAST score	34
E value	7.0e-10
Match length	98
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	48674
Seq. ID	pcp700990567.h1
Method	BLASTX
NCBI GI	g3892057
BLAST score	174
E value	4.0e-13
Match length	49
% identity	38
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48675
Seq. ID	pcp700990646.h1
Method	BLASTN
NCBI GI	g20829
BLAST score	44
E value	3.0e-16
Match length	72
% identity	90
NCBI Description	P.sativum pcr gene for protochlorophyllide reductase

Seq. No.	48676
Seq. ID	pcp700990662.h1
Method	BLASTN
NCBI GI	g3378649
BLAST score	43
E value	1.0e-15
Match length	83
% identity	88
NCBI Description	M.sativa mRNA translated from abscisic activated gene

Seq. No.	48677
Seq. ID	pcp700990737.h1
Method	BLASTN
NCBI GI	g340697
BLAST score	77
E value	1.0e-35
Match length	135
% identity	92
NCBI Description	Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA

Seq. No.	48678
Seq. ID	pcp700990802.h1
Method	BLASTX
NCBI GI	g3550985
BLAST score	201
E value	3.0e-16
Match length	38
% identity	97
NCBI Description	(AB010740) OsS5a [Oryza sativa]

Seq. No.	48679
Seq. ID	pcp700990809.h1
Method	BLASTX
NCBI GI	g3892057
BLAST score	387

E value	8.0e-38
Match length	87
% identity	51
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48680
Seq. ID	pcp700990926.h1
Method	BLASTX
NCBI GI	g2827631
BLAST score	241
E value	6.0e-21
Match length	57
% identity	79
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	48681
Seq. ID	pcp700991095.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	165
E value	6.0e-88
Match length	217
% identity	94
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	48682
Seq. ID	pcp700991110.h1
Method	BLASTX
NCBI GI	g1082359
BLAST score	142
E value	4.0e-09
Match length	86
% identity	40
NCBI Description	excision repair protein ERCC5 - human >gi_306742 (L20046) excision repair protein [Homo sapiens]

Seq. No.	48683
Seq. ID	pcp700991122.h1
Method	BLASTX
NCBI GI	g4262226
BLAST score	182
E value	9.0e-14
Match length	45
% identity	73
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	48684
Seq. ID	pcp700991130.h1
Method	BLASTX
NCBI GI	g1685005
BLAST score	197
E value	1.0e-15
Match length	86
% identity	48
NCBI Description	(U32644) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No.	48685
Seq. ID	pcp700991138.h1
Method	BLASTX
NCBI GI	g2980641
BLAST score	359
E value	2.0e-34
Match length	88
% identity	77
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	48686
Seq. ID	pcp700991171.h1
Method	BLASTX
NCBI GI	g2529686
BLAST score	205
E value	9.0e-17
Match length	66
% identity	58
NCBI Description	(AC002535) putative G-beta-repeat containing protein, 5' partial [Arabidopsis thaliana]

Seq. No.	48687
Seq. ID	pcp700991190.h1
Method	BLASTX
NCBI GI	g2289003
BLAST score	283
E value	1.0e-25
Match length	70
% identity	77
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	48688
Seq. ID	pcp700991248.h1
Method	BLASTX
NCBI GI	g3242702
BLAST score	188
E value	1.0e-14
Match length	60
% identity	60
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48689
Seq. ID	pcp700991255.h1
Method	BLASTX
NCBI GI	g2959767
BLAST score	241
E value	6.0e-21
Match length	57
% identity	81
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	48690
Seq. ID	pcp700991287.h1

Method	BLASTN
NCBI GI	g2773269
BLAST score	176
E value	1.0e-94
Match length	212
% identity	96
NCBI Description	Glycine max ferredoxin-dependent glutamate synthase (glu) mRNA, partial cds

Seq. No.	48691
Seq. ID	pcp700991308.h1
Method	BLASTX
NCBI GI	g2245113
BLAST score	182
E value	9.0e-14
Match length	63
% identity	52
NCBI Description	(Z97343) glycerol-3-phosphate permease homolog [Arabidopsis thaliana]

Seq. No.	48692
Seq. ID	pcp700991313.h1
Method	BLASTX
NCBI GI	g3776567
BLAST score	303
E value	5.0e-28
Match length	81
% identity	65
NCBI Description	(AC005388) Strong similarity to F21B7.33 gi_2809264 from A. thaliana BAC gb_AC002560. EST gb_N65119 comes from this gene. [Arabidopsis thaliana]

Seq. No.	48693
Seq. ID	pcp700991337.h1
Method	BLASTX
NCBI GI	g3482974
BLAST score	307
E value	2.0e-28
Match length	80
% identity	78
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	48694
Seq. ID	pcp700991361.h1
Method	BLASTX
NCBI GI	g3927835
BLAST score	319
E value	6.0e-30
Match length	82
% identity	73
NCBI Description	(AC005727) similar to Streptomyces PapA [Arabidopsis thaliana]

Seq. No.	48695
Seq. ID	pcp700991379.h1
Method	BLASTN

NCBI GI	g1139584
BLAST score	76
E value	8.0e-35
Match length	136
% identity	89
NCBI Description	Lupinus albus tRNA nucleotidyltransferase (CCA1) mRNA, complete cds

Seq. No.	48696
Seq. ID	pcp700991408.h1
Method	BLASTN
NCBI GI	g829118
BLAST score	92
E value	1.0e-44
Match length	140
% identity	91
NCBI Description	P.vulgaris gene for cyclophilin

Seq. No.	48697
Seq. ID	pcp700991418.h1
Method	BLASTX
NCBI GI	g136057
BLAST score	157
E value	6.0e-11
Match length	63
% identity	51
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	48698
Seq. ID	pcp700991427.h1
Method	BLASTX
NCBI GI	g3281853
BLAST score	253
E value	3.0e-22
Match length	77
% identity	61
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	48699
Seq. ID	pcp700991430.h1
Method	BLASTX
NCBI GI	g2252827
BLAST score	246
E value	2.0e-21
Match length	62
% identity	69
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	48700
Seq. ID	pcp700991446.h1
Method	BLASTX
NCBI GI	g4522003
BLAST score	140
E value	6.0e-09

Match length	56
% identity	52
NCBI Description	(AC007069) putative protein kinase [Arabidopsis thaliana]

Seq. No.	48701
Seq. ID	pcp700992006.h1
Method	BLASTX
NCBI GI	g4539010
BLAST score	179
E value	1.0e-13
Match length	56
% identity	66
NCBI Description	(AL049481) putative DNA-directed RNA polymerase [Arabidopsis thaliana]

Seq. No.	48702
Seq. ID	pcp700992049.h1
Method	BLASTX
NCBI GI	g2781351
BLAST score	218
E value	3.0e-18
Match length	51
% identity	80
NCBI Description	(AC003113) F24O1.7 [Arabidopsis thaliana]

Seq. No.	48703
Seq. ID	pcp700992203.h1
Method	BLASTX
NCBI GI	g1345132
BLAST score	269
E value	3.0e-24
Match length	65
% identity	9
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	48704
Seq. ID	pcp700992205.h1
Method	BLASTX
NCBI GI	g2564958
BLAST score	143
E value	4.0e-09
Match length	89
% identity	4
NCBI Description	(AF030001) tenascin X [Mus musculus]

Seq. No.	48705
Seq. ID	pcp700992235.h1
Method	BLASTN
NCBI GI	g217908
BLAST score	54
E value	8.0e-22
Match length	82
% identity	91
NCBI Description	Pumpkin mRNA for glycolate oxidase, complete cds

Seq. No.	48706
Seq. ID	pcp700992271.h1
Method	BLASTN
NCBI GI	g3241923
BLAST score	35
E value	2.0e-10
Match length	73
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	48707
Seq. ID	pcp700992272.h1
Method	BLASTX
NCBI GI	g4335731
BLAST score	241
E value	1.0e-20
Match length	89
% identity	47
NCBI Description	(AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No.	48708
Seq. ID	pcp700992290.h1
Method	BLASTX
NCBI GI	g3292816
BLAST score	347
E value	4.0e-33
Match length	89
% identity	67
NCBI Description	(AL031018) putative fizzy-related protein [Arabidopsis thaliana]

Seq. No.	48709
Seq. ID	pcp700992314.h1
Method	BLASTX
NCBI GI	g2827561
BLAST score	326
E value	1.0e-30
Match length	87
% identity	70
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292809_emb_CAA19799_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	48710
Seq. ID	pcp700992328.h1
Method	BLASTN
NCBI GI	g1732468
BLAST score	135
E value	5.0e-70
Match length	254
% identity	89
NCBI Description	Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No.	48711
Seq. ID	pcp700992363.h1

Method	BLASTN
NCBI GI	g4406529
BLAST score	76
E value	8.0e-35
Match length	235
% identity	83
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	48712
Seq. ID	pcp700992482.h1
Method	BLASTX
NCBI GI	g508304
BLAST score	154
E value	9.0e-11
Match length	35
% identity	77
NCBI Description	(L22305) corC [Medicago sativa]

Seq. No.	48713
Seq. ID	pcp700992491.h1
Method	BLASTX
NCBI GI	g3451074
BLAST score	245
E value	2.0e-21
Match length	61
% identity	72
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	48714
Seq. ID	pcp700992668.h1
Method	BLASTX
NCBI GI	g3264757
BLAST score	161
E value	2.0e-23
Match length	75
% identity	77
NCBI Description	(AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No.	48715
Seq. ID	pcp700992681.h1
Method	BLASTX
NCBI GI	g3184498
BLAST score	151
E value	1.0e-12
Match length	83
% identity	26
NCBI Description	(AC004798) R31546_1 [Homo sapiens]

Seq. No.	48716
Seq. ID	pcp700992706.h1
Method	BLASTX
NCBI GI	g3399777
BLAST score	205
E value	2.0e-16
Match length	71
% identity	55

NCBI Description	(AF069738) symbiotic ammonium transporter; nodulin [Glycine max]

Seq. No.	48717
Seq. ID	pcp700992722.h1
Method	BLASTN
NCBI GI	g3158475
BLAST score	63
E value	5.0e-27
Match length	178
% identity	84
NCBI Description	Samanea saman aquaporin 2 (Aqp2) mRNA, complete cds

Seq. No.	48718
Seq. ID	pcp700992760.h1
Method	BLASTX
NCBI GI	g4205113
BLAST score	149
E value	4.0e-10
Match length	52
% identity	44
NCBI Description	(AF000520) cell wall invertase [Fragaria x ananassa]

Seq. No.	48719
Seq. ID	pcp700993034.h1
Method	BLASTN
NCBI GI	g169820
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	Oryza sativa triosephosphate isomerase (Rictpi) mRNA, complete cds

Seq. No.	48720
Seq. ID	pcp700993084.h1
Method	BLASTX
NCBI GI	g3142289
BLAST score	177
E value	2.0e-13
Match length	68
% identity	47
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	48721
Seq. ID	pcp700993225.h1
Method	BLASTX
NCBI GI	g3643611
BLAST score	316
E value	1.0e-29
Match length	60
% identity	88
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	48722
Seq. ID	pcp700993235.h1

Method	BLASTN
NCBI GI	g169141
BLAST score	49
E value	7.0e-19
Match length	109
% identity	86
NCBI Description	Pea putative protein serine/threonine kinase (PsPK4) mRNA, partial cds

Seq. No.	48723
Seq. ID	pcp700993278.h1
Method	BLASTX
NCBI GI	g2245004
BLAST score	192
E value	3.0e-15
Match length	56
% identity	62
NCBI Description	(Z97341) similarity to membrane transport protein [Arabidopsis thaliana]

Seq. No.	48724
Seq. ID	pcp700993285.h1
Method	BLASTX
NCBI GI	g4539383
BLAST score	251
E value	4.0e-22
Match length	59
% identity	69
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	48725
Seq. ID	pcp700993317.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	50
E value	3.0e-19
Match length	145
% identity	87
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	48726
Seq. ID	pcp700993318.h1
Method	BLASTX
NCBI GI	g2980764
BLAST score	325
E value	1.0e-30
Match length	71
% identity	80
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	48727
Seq. ID	pcp700993353.h1
Method	BLASTX
NCBI GI	g1652704
BLAST score	154

E value	1.0e-10
Match length	60
% identity	48
NCBI Description	(D90907) hypothetical protein [Synechocystis sp.]

Seq. No.	48728
Seq. ID	pcp700993367.h1
Method	BLASTX
NCBI GI	g3738306
BLAST score	339
E value	3.0e-32
Match length	84
% identity	77
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	48729
Seq. ID	pcp700993436.h1
Method	BLASTX
NCBI GI	g3738300
BLAST score	173
E value	8.0e-13
Match length	45
% identity	71
NCBI Description	(AC005309) putative glutaredoxin [Arabidopsis thaliana] >gi_4249396 (AC006072) putative glutaredoxin [Arabidopsis thaliana]

Seq. No.	48730
Seq. ID	pcp700993487.h1
Method	BLASTN
NCBI GI	g19747
BLAST score	38
E value	4.0e-12
Match length	74
% identity	88
NCBI Description	N.sylvestris psaDa gene for PSI-D2

Seq. No.	48731
Seq. ID	pcp700993513.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	246
E value	1.0e-136
Match length	258
% identity	99
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	48732
Seq. ID	pcp700993575.h1
Method	BLASTX
NCBI GI	g131754
BLAST score	212
E value	2.0e-17
Match length	58
% identity	66
NCBI Description	PPLZ02 PROTEIN >gi_99973_pir__S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_

(X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]

Seq. No.	48733
Seq. ID	pcp700993667.h1
Method	BLASTX
NCBI GI	g2674203
BLAST score	249
E value	1.0e-21
Match length	83
% identity	64
NCBI Description	(AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No.	48734
Seq. ID	pcp700993704.h1
Method	BLASTX
NCBI GI	g1839022
BLAST score	142
E value	4.0e-09
Match length	45
% identity	56
NCBI Description	(Y11121) amino acid carrier [Ricinus communis]

Seq. No.	48735
Seq. ID	pcp700993705.h1
Method	BLASTN
NCBI GI	g1419035
BLAST score	144
E value	2.0e-75
Match length	236
% identity	90
NCBI Description	M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase, P5CS-1

Seq. No.	48736
Seq. ID	pcp700993758.h1
Method	BLASTX
NCBI GI	g417743
BLAST score	147
E value	7.0e-10
Match length	47
% identity	53
NCBI Description	NEUROLYSIN PRECURSOR (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP) >gi_346478_pir__A43411 soluble angiotensin-binding protein - pig >gi_217709_dbj_BAA01949_ (D11336) soluble angiotesin-binding protein [Sus scrofa] >gi_1783122_dbj_BAA19060_ (AB000170) endopeptidase 24.16 type M1 [Sus scrofa] >gi_1871389_dbj_BAA19104_ (AB000425) endopeptidase 24.16 type M1 [Sus scrofa]

Seq. No.	48737
Seq. ID	pcp700993807.h1
Method	BLASTX
NCBI GI	g3063453

BLAST score 161
E value 2.0e-15
Match length 75
% identity 57
NCBI Description (AC003981) F22O13.15 [Arabidopsis thaliana]

Seq. No. 48738
Seq. ID pcp700993854.h1
Method BLASTX
NCBI GI g1199786
BLAST score 139
E value 1.0e-08
Match length 85
% identity 19
NCBI Description (D83379) regulatory subunit of cAMP-dependent histone kinase [Hemicentrotus pulcherrimus]

Seq. No. 48739
Seq. ID pcp700993872.h1
Method BLASTN
NCBI GI g4406529
BLAST score 73
E value 5.0e-33
Match length 181
% identity 85
NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 48740
Seq. ID pcp700993878.h1
Method BLASTX
NCBI GI g2760323
BLAST score 240
E value 1.0e-20
Match length 74
% identity 21
NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No. 48741
Seq. ID pcp700993920.h1
Method BLASTX
NCBI GI g3582344
BLAST score 323
E value 3.0e-30
Match length 92
% identity 65
NCBI Description (AC005496) putative cell division protein [Arabidopsis thaliana]

Seq. No. 48742
Seq. ID pcp700993922.h1
Method BLASTX
NCBI GI g4539351
BLAST score 208
E value 9.0e-17
Match length 92
% identity 49

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 48743
Seq. ID pcp700993968.h1
Method BLASTN
NCBI GI g508303
BLAST score 39
E value 1.0e-12
Match length 59
% identity 92
NCBI Description Alfalfa bimodular protein (corC) mRNA, complete cds

Seq. No. 48744
Seq. ID pcp700994045.h1
Method BLASTX
NCBI GI g2213599
BLAST score 251
E value 6.0e-22
Match length 83
% identity 57
NCBI Description (AC000348) T7N9.19 [Arabidopsis thaliana]

Seq. No. 48745
Seq. ID pcp700994084.h1
Method BLASTX
NCBI GI g1694621
BLAST score 168
E value 3.0e-12
Match length 37
% identity 81
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]

Seq. No. 48746
Seq. ID pcp700994212.h1
Method BLASTN
NCBI GI g1370200
BLAST score 106
E value 9.0e-53
Match length 173
% identity 91
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC2

Seq. No. 48747
Seq. ID pcp700994224.h1
Method BLASTX
NCBI GI g3402694
BLAST score 188
E value 4.0e-19
Match length 73
% identity 68
NCBI Description (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]

Seq. No. 48748
Seq. ID pcp700994276.h1
Method BLASTX
NCBI GI g3329368
BLAST score 171

E value	2.0e-26
Match length	75
% identity	73
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	48749
Seq. ID	pcp700994318.h1
Method	BLASTX
NCBI GI	g1345132
BLAST score	174
E value	8.0e-13
Match length	89
% identity	43
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	48750
Seq. ID	pcp700994323.h1
Method	BLASTX
NCBI GI	g3021270
BLAST score	300
E value	1.0e-27
Match length	88
% identity	67
NCBI Description	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No.	48751
Seq. ID	pcp700994373.h1
Method	BLASTX
NCBI GI	g2735766
BLAST score	259
E value	8.0e-23
Match length	61
% identity	84
NCBI Description	(AF008652) MADS transcriptional factor; STMADS11 [Solanum tuberosum]

Seq. No.	48752
Seq. ID	pcp700994379.h1
Method	BLASTX
NCBI GI	g3894166
BLAST score	165
E value	9.0e-12
Match length	71
% identity	46
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	48753
Seq. ID	pcp700994415.h1
Method	BLASTN
NCBI GI	g493019
BLAST score	71
E value	8.0e-32

Match length	75
% identity	99
NCBI Description	Glycine max delta-aminolevulinic acid dehydratase (Alad) mRNA, complete cds

Seq. No.	48754
Seq. ID	pcp700994508.h2
Method	BLASTX
NCBI GI	g1076580
BLAST score	188
E value	5.0e-20
Match length	84
% identity	62
NCBI Description	alcohol dehydrogenase homolog ADH3b - tomato >gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 390 aa] [Lycopersicon esculentum]

Seq. No.	48755
Seq. ID	pcp700994583.h2
Method	BLASTN
NCBI GI	g4406529
BLAST score	139
E value	2.0e-72
Match length	203
% identity	92
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	48756
Seq. ID	pcp700994633.h1
Method	BLASTX
NCBI GI	g2651310
BLAST score	179
E value	2.0e-13
Match length	53
% identity	64
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	48757
Seq. ID	pcp700994639.h1
Method	BLASTX
NCBI GI	g3402718
BLAST score	135
E value	1.0e-11
Match length	64
% identity	54
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48758
Seq. ID	pcp700994688.h1
Method	BLASTX
NCBI GI	g4558564
BLAST score	292
E value	8.0e-27
Match length	77

% identity	73
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	48759
Seq. ID	pcp700994709.h1
Method	BLASTN
NCBI GI	g1053044
BLAST score	114
E value	2.0e-57
Match length	264
% identity	100
NCBI Description	Glycine max histone H3 gene, partial cds, clone S1

Seq. No.	48760
Seq. ID	pcp700994727.h1
Method	BLASTX
NCBI GI	g4510363
BLAST score	171
E value	2.0e-12
Match length	42
% identity	79
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	48761
Seq. ID	pcp700994740.h1
Method	BLASTX
NCBI GI	g4263792
BLAST score	320
E value	5.0e-30
Match length	86
% identity	73
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	48762
Seq. ID	pcp700994747.h1
Method	BLASTX
NCBI GI	g2213884
BLAST score	198
E value	1.0e-15
Match length	74
% identity	57
NCBI Description	(AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	48763
Seq. ID	pcp700994755.h1
Method	BLASTX
NCBI GI	g4204300
BLAST score	240
E value	1.0e-20
Match length	78
% identity	63
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	48764

Seq. ID	pcp700994793.h1
Method	BLASTX
NCBI GI	g4204282
BLAST score	173
E value	8.0e-13
Match length	42
% identity	81
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	48765
Seq. ID	pcp700994824.h1
Method	BLASTN
NCBI GI	g18556
BLAST score	229
E value	1.0e-126
Match length	233
% identity	100
NCBI Description	G.max DNA for Cab5

Seq. No.	48766
Seq. ID	pcp700994834.h1
Method	BLASTX
NCBI GI	g2827555
BLAST score	224
E value	1.0e-18
Match length	87
% identity	59
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	48767
Seq. ID	pcp700994871.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	231
E value	1.0e-127
Match length	250
% identity	99
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	48768
Seq. ID	pcp700994890.h1
Method	BLASTX
NCBI GI	g131384
BLAST score	255
E value	2.0e-22
Match length	69
% identity	81
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	48769
Seq. ID	pcp700994913.h1
Method	BLASTX
NCBI GI	g2245014
BLAST score	189
E value	8.0e-15
Match length	41
% identity	80
NCBI Description	(Z97341) glucosyltransferase homolog [Arabidopsis thaliana]

Seq. No.	48770
Seq. ID	pcp700994996.h1
Method	BLASTX
NCBI GI	g2160692
BLAST score	170
E value	1.0e-12
Match length	48
% identity	67
NCBI Description	(U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	48771
Seq. LD	pcp700995021.h1
Method	BLASTX
NCBI GI	g1710807
BLAST score	197
E value	8.0e-16
Match length	60
% identity	63
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_1185390 (U21105) alphacpn60 [Pisum sativum]

Seq. No.	48772
Seq. ID	pcp700995121.h1
Method	BLASTX
NCBI GI	g2213598
BLAST score	252
E value	5.0e-22
Match length	88
% identity	56
NCBI Description	(AC000348) T7N9.18 [Arabidopsis thaliana]

Seq. No.	48773
Seq. ID	pcp700995147.h1
Method	BLASTX
NCBI GI	g4038594
BLAST score	348
E value	3.0e-33
Match length	87
% identity	77
NCBI Description	(AJ222798) tDET1 protein [Lycopersicon esculentum] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No.	48774

Seq. ID	pcp700995182.h1
Method	BLASTX
NCBI GI	g1255448
BLAST score	348
E value	3.0e-33
Match length	88
% identity	76
NCBI Description	(D50468) mitogen-activated protein kinase [Arabidopsis thaliana]

Seq. No.	48775
Seq. ID	pcp700995192.h1
Method	BLASTX
NCBI GI	g3928543
BLAST score	175
E value	6.0e-13
Match length	68
% identity	50
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	48776
Seq. ID	pcp700995201.h1
Method	BLASTX
NCBI GI	g1076274
BLAST score	215
E value	6.0e-18
Match length	70
% identity	61
NCBI Description	cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No.	48777
Seq. ID	pcp700995232.h1
Method	BLASTN
NCBI GI	g758249
BLAST score	108
E value	5.0e-54
Match length	124
% identity	97
NCBI Description	P.vulgaris mRNA for plasma membrane H+ ATPase

Seq. No.	48778
Seq. ID	pcp700995248.h1
Method	BLASTX
NCBI GI	g4218122
BLAST score	155
E value	7.0e-11
Match length	65
% identity	49
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	48779
Seq. ID	pcp700995324.h1
Method	BLASTX
NCBI GI	g4006924
BLAST score	414
E value	6.0e-41

Match length	90
% identity	81
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	48780
Seq. ID	pcp700995361.h1
Method	BLASTX
NCBI GI	g2342682
BLAST score	260
E value	6.0e-23
Match length	61
% identity	80
NCBI Description	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No.	48781
Seq. ID	pcp700995372.h1
Method	BLASTX
NCBI GI	g4468813
BLAST score	156
E value	1.0e-10
Match length	81
% identity	38
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	48782
Seq. ID	pcp700995386.h1
Method	BLASTN
NCBI GI	g3695062
BLAST score	36
E value	6.0e-11
Match length	137
% identity	82
NCBI Description	Lotus japonicus rac GTPase activating protein 3 mRNA, partial cds

Seq. No.	48783
Seq. ID	pcp700995421.h1
Method	BLASTX
NCBI GI	g2664198
BLAST score	182
E value	8.0e-14
Match length	78
% identity	29
NCBI Description	(AJ003215) GTL1 [Arabidopsis thaliana]

Seq. No.	48784
Seq. ID	pcp700995422.h1
Method	BLASTX
NCBI GI	g3668097
BLAST score	258
E value	1.0e-22
Match length	65
% identity	80
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	48785
Seq. ID	pcp700995427.h1
Method	BLASTN
NCBI GI	g2944388
BLAST score	38
E value	3.0e-12
Match length	42
% identity	98
NCBI Description	Glycine max actin 4 (SAc4) gene, complete cds

Seq. No.	48786
Seq. ID	pcp700995435.h1
Method	BLASTX
NCBI GI	g3885341
BLAST score	169
E value	2.0e-12
Match length	82
% identity	62
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	48787
Seq. ID	pcp700995437.h1
Method	BLASTX
NCBI GI	g4127461
BLAST score	171
E value	1.0e-12
Match length	45
% identity	71
NCBI Description	(AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]

Seq. No.	48788
Seq. ID	pcp700995441.h1
Method	BLASTX
NCBI GI	g2832661
BLAST score	305
E value	3.0e-28
Match length	82
% identity	74
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	48789
Seq. ID	pcp700995527.h1
Method	BLASTX
NCBI GI	g1345132
BLAST score	135
E value	5.0e-18
Match length	105
% identity	29
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 48790

Seq. ID	pcp700995613.h1
Method	BLASTX
NCBI GI	g4006876
BLAST score	150
E value	5.0e-10
Match length	68
% identity	51
NCBI Description	(Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48791
Seq. ID	pcp700995616.h1
Method	BLASTN
NCBI GI	g20740
BLAST score	58
E value	5.0e-24
Match length	175
% identity	89
NCBI Description	Pisum sativum mRNA for P protein, a part of glycine cleavage complex

Seq. No.	48792
Seq. ID	pcp700995621.h1
Method	BLASTX
NCBI GI	g1680686
BLAST score	184
E value	5.0e-14
Match length	86
% identity	43
NCBI Description	(U51330) rust resistance kinase Lr10 [Triticum aestivum]

Seq. No.	48793
Seq. ID	pcp700995681.h1
Method	BLASTN
NCBI GI	g20620
BLAST score	46
E value	4.0e-17
Match length	110
% identity	85
NCBI Description	Pea mRNA for the 33kDa polypeptide of the water-oxidizing complex of photosystem II

Seq. No.	48794
Seq. ID	pcp700995741.h1
Method	BLASTN
NCBI GI	g669002
BLAST score	150
E value	3.0e-79
Match length	162
% identity	98
NCBI Description	Glycine max calnexin mRNA, complete cds

Seq. No.	48795
Seq. ID	pcp700995744.h1
Method	BLASTX
NCBI GI	g3142303
BLAST score	394
E value	1.0e-38

Match length	85
% identity	92
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	48796
Seq. ID	pcp700995752.h1
Method	BLASTX
NCBI GI	g629875
BLAST score	218
E value	3.0e-18
Match length	64
% identity	66
NCBI Description	hypothetical 71.9K protein, LIM18 - Trumpet lily

Seq. No.	48797
Seq. ID	pcp700995857.h1
Method	BLASTX
NCBI GI	g3395439
BLAST score	149
E value	5.0e-10
Match length	38
% identity	79
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48798
Seq. ID	pcp700995881.h1
Method	BLASTX
NCBI GI	g3386596
BLAST score	349
E value	2.0e-33
Match length	79
% identity	86
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana] >gi_3702346 (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	48799
Seq. ID	pmv700888113.h1
Method	BLASTX
NCBI GI	g2947063
BLAST score	231
E value	1.0e-19
Match length	84
% identity	21
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	48800
Seq. ID	pmv700888142.h1
Method	BLASTX
NCBI GI	g4263820
BLAST score	156
E value	8.0e-11
Match length	79

% identity	39
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48801
Seq. ID	pmv700888153.h1
Method	BLASTX
NCBI GI	g1076755
BLAST score	190
E value	9.0e-15
Match length	46
% identity	74
NCBI Description	protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]

Seq. No.	48802
Seq. ID	pmv700888167.h1
Method	BLASTX
NCBI GI	g3941468
BLAST score	373
E value	3.0e-36
Match length	75
% identity	91
NCBI Description	(AF062888) putative transcription factor [Arabidopsis thaliana]

Seq. No.	48803
Seq. ID	pmv700888190.h1
Method	BLASTX
NCBI GI	g584825
BLAST score	324
E value	2.0e-30
Match length	70
% identity	84
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	48804
Seq. ID	pmv700888282.h1
Method	BLASTX
NCBI GI	g1170567
BLAST score	131
E value	1.0e-10
Match length	65
% identity	62
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	48805
Seq. ID	pmv700888294.h1
Method	BLASTX
NCBI GI	g4432841
BLAST score	110
E value	4.0e-10
Match length	80
% identity	42

NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No. 48806
Seq. ID pmv700888346.h1
Method BLASTX
NCBI GI g4006886
BLAST score 340
E value 2.0e-32
Match length 81
% identity 78
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 48807
Seq. ID pmv700888356.h1
Method BLASTX
NCBI GI g2618696
BLAST score 246
E value 2.0e-21
Match length 70
% identity 64
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 48808
Seq. ID pmv700888376.h1
Method BLASTX
NCBI GI g3128168
BLAST score 241
E value 8.0e-21
Match length 62
% identity 69
NCBI Description (AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 48809
Seq. ID pmv700888387.h1
Method BLASTX
NCBI GI g1944575
BLAST score 360
E value 9.0e-35
Match length 80
% identity 82
NCBI Description (Z94058) pectinesterase [Lycopersicon esculentum]

Seq. No. 48810
Seq. ID pmv700888431.h1
Method BLASTX
NCBI GI g4567278
BLAST score 238
E value 2.0e-20
Match length 51
% identity 94
NCBI Description (AC006841) putative anthracycline associated resistance ARX protein [Arabidopsis thaliana]

Seq. No. 48811
Seq. ID pmv700888487.h1
Method BLASTX

NCBI GI	g3702335
BLAST score	256
E value	1.0e-22
Match length	65
% identity	69
NCBI Description	(AC005397) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	48812
Seq. ID	pmv700888516.h1
Method	BLASTN
NCBI GI	g2970446
BLAST score	132
E value	1.0e-68
Match length	132
% identity	100
NCBI Description	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) mRNA, complete cds

Seq. No.	48813
Seq. ID	pmv700888548.h1
Method	BLASTX
NCBI GI	g1469943
BLAST score	129
E value	1.0e-10
Match length	80
% identity	44
NCBI Description	(U49797) cationic amino acid transporter-1 [Cricetulus griseus]

Seq. No.	48814
Seq. ID	pmv700888563.h1
Method	BLASTX
NCBI GI	g2760321
BLAST score	241
E value	1.0e-20
Match length	84
% identity	62
NCBI Description	(AC002130) F1N21.6 [Arabidopsis thaliana]

Seq. No.	48815
Seq. ID	pmv700888578.h1
Method	BLASTN
NCBI GI	g4098318
BLAST score	139
E value	2.0e-72
Match length	243
% identity	89
NCBI Description	Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds

Seq. No.	48816
Seq. ID	pmv700888583.h1
Method	BLASTX
NCBI GI	g4455340
BLAST score	184
E value	4.0e-14
Match length	45

% identity	76
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	48817
Seq. ID	pmv700888617.h1
Method	BLASTN
NCBI GI	g684941
BLAST score	38
E value	3.0e-12
Match length	98
% identity	85
NCBI Description	Medicago sativa S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase (CCOMT) mRNA, complete cds

Seq. No.	48818
Seq. ID	pmv700888623.h1
Method	BLASTN
NCBI GI	g3021374
BLAST score	132
E value	2.0e-68
Match length	147
% identity	98
NCBI Description	Glycine max mRNA for profilin, PRO1

Seq. No.	48819
Seq. ID	pmv700888629.h1
Method	BLASTX
NCBI GI	g2982434
BLAST score	220
E value	2.0e-18
Match length	59
% identity	71
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	48820
Seq. ID	pmv700888648.h1
Method	BLASTX
NCBI GI	g3367593
BLAST score	139
E value	5.0e-09
Match length	44
% identity	59
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana] >gi_3805841_emb_CAA21461_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	48821
Seq. ID	pmv700888742.h1
Method	BLASTX
NCBI GI	g3688186
BLAST score	137
E value	1.0e-08
Match length	72
% identity	39
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 48822

Seq. ID	pmv700888745.h1
Method	BLASTX
NCBI GI	g3559816
BLAST score	332
E value	2.0e-31
Match length	77
% identity	84
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	48823
Seq. ID	pmv700888749.h1
Method	BLASTX
NCBI GI	g3212869
BLAST score	162
E value	1.0e-11
Match length	34
% identity	88
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	48824
Seq. ID	pmv700888762.h1
Method	BLASTX
NCBI GI	g3341443
BLAST score	172
E value	9.0e-13
Match length	69
% identity	52
NCBI Description	(AJ223074) acid phosphatase [Glycine max]

Seq. No.	48825
Seq. ID	pmv700888773.h1
Method	BLASTN
NCBI GI	g2218151
BLAST score	119
E value	1.0e-60
Match length	215
% identity	89
NCBI Description	Vigna unguiculata type IIIa membrane protein cp-wap13 mRNA, complete cds

Seq. No.	48826
Seq. ID	pmv700888779.h1
Method	BLASTX
NCBI GI	g2506139
BLAST score	277
E value	4.0e-25
Match length	77
% identity	71
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	48827
Seq. ID	pmv700888780.h1
Method	BLASTX
NCBI GI	g4160292
BLAST score	136

E value	4.0e-14
Match length	76
% identity	54
NCBI Description	(Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]

Seq. No.	48828
Seq. ID	pmv700888874.h1
Method	BLASTN
NCBI GI	g984307
BLAST score	47
E value	1.0e-17
Match length	79
% identity	94
NCBI Description	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso

Seq. No.	48829
Seq. ID	pmv700888877.h1
Method	BLASTX
NCBI GI	g2914703
BLAST score	231
E value	1.0e-19
Match length	76
% identity	55
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	48830
Seq. ID	pmv700888886.h1
Method	BLASTX
NCBI GI	g3785995
BLAST score	278
E value	3.0e-25
Match length	77
% identity	75
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	48831
Seq. ID	pmv700888893.h1
Method	BLASTX
NCBI GI	g2388689
BLAST score	136
E value	6.0e-19
Match length	58
% identity	84
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	48832
Seq. ID	pmv700888904.h1
Method	BLASTX
NCBI GI	g3608479
BLAST score	216
E value	9.0e-18
Match length	44
% identity	93

NCBI Description	(AF088912) ribosomal protein L15 [Petunia x hybrida]

Seq. No.	48833
Seq. ID	pmv700888959.h1
Method	BLASTX
NCBI GI	g1170603
BLAST score	141
E value	5.0e-09
Match length	78
% identity	40
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN C2F7.03C >gi_2130372_pir__S58147 hypothetical protein SPAC2F7.03c - fission yeast (Schizosaccharomyces pombe) >gi_1052786_emb_CAA90490_ (Z50142) protein kinase [Schizosaccharomyces pombe]

Seq. No.	48834
Seq. ID	pmv700889002.h1
Method	BLASTX
NCBI GI	g2304971
BLAST score	239
E value	1.0e-20
Match length	78
% identity	59
NCBI Description	(U82828) ATM [Homo sapiens]

Seq. No.	48835
Seq. ID	pmv700889004.h1
Method	BLASTN
NCBI GI	g3493646
BLAST score	36
E value	5.0e-11
Match length	56
% identity	91
NCBI Description	Pimpinella brachycarpa transcription activator (MADS1) mRNA, complete cds

Seq. No.	48836
Seq. ID	pmv700889069.h1
Method	BLASTX
NCBI GI	g4218010
BLAST score	164
E value	8.0e-12
Match length	42
% identity	74
NCBI Description	(AC006135) putative sugar transporter [Arabidopsis thaliana] >gi_4309720_gb_AAD15490_ (AC006439) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	48837
Seq. ID	pmv700889120.h1
Method	BLASTX
NCBI GI	g3176726
BLAST score	427
E value	2.0e-42
Match length	89
% identity	82

NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	48838
Seq. ID	pmv700889141.h1
Method	BLASTX
NCBI GI	g3482924
BLAST score	223
E value	1.0e-18
Match length	76
% identity	59
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	48839
Seq. ID	pmv700889153.h1
Method	BLASTX
NCBI GI	g4572671
BLAST score	206
E value	1.0e-16
Match length	90
% identity	52
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	48840
Seq. ID	pmv700889173.h1
Method	BLASTX
NCBI GI	g3367537
BLAST score	367
E value	2.0e-35
Match length	87
% identity	78
NCBI Description	(AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375. [Arabid

Seq. No.	48841
Seq. ID	pmv700889238.h1
Method	BLASTX
NCBI GI	g2864625
BLAST score	346
E value	4.0e-33
Match length	77
% identity	79
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	48842
Seq. ID	pmv700889249.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	111
E value	9.0e-56
Match length	183
% identity	91

NCBI Description	G.max tefS1 gene for elongation factor EF-1a
Seq. No.	48843
Seq. ID	pmv700889271.h1
Method	BLASTN
NCBI GI	g20412
BLAST score	81
E value	7.0e-38
Match length	161
% identity	88
NCBI Description	P.amygdalus mRNA for alpha-tubulin
Seq. No.	48844
Seq. ID	pmv700889272.h1
Method	BLASTX
NCBI GI	g3924615
BLAST score	212
E value	2.0e-17
Match length	62
% identity	61
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]
Seq. No.	48845
Seq. ID	pmv700889279.h1
Method	BLASTX
NCBI GI	g1354510
BLAST score	221
E value	1.0e-18
Match length	70
% identity	59
NCBI Description	(U55205) HAL2-like protein [Arabidopsis thaliana]
Seq. No.	48846
Seq. ID	pmv700889289.h1
Method	BLASTN
NCBI GI	g3869065
BLAST score	43
E value	3.0e-15
Match length	95
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
Seq. No.	48847
Seq. ID	pmv700889335.h1
Method	BLASTX
NCBI GI	g4567316
BLAST score	177
E value	2.0e-13
Match length	47
% identity	70
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]
Seq. No.	48848
Seq. ID	pmv700889362.h1
Method	BLASTX
NCBI GI	g4572674

BLAST score	191
E value	7.0e-20
Match length	54
% identity	87
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	48849
Seq. ID	pmv700889365.h1
Method	BLASTX
NCBI GI	g1076402
BLAST score	269
E value	5.0e-24
Match length	64
% identity	70
NCBI Description	S-like ribonuclease RNS2 - Arabidopsis thaliana

Seq. No.	48850
Seq. ID	pmv700889422.h1
Method	BLASTX
NCBI GI	g4539009
BLAST score	168
E value	3.0e-12
Match length	81
% identity	49
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	48851
Seq. ID	pmv700889495.h1
Method	BLASTX
NCBI GI	g2702277
BLAST score	210
E value	3.0e-17
Match length	62
% identity	56
NCBI Description	(AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] >gi_2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]

Seq. No.	48852
Seq. ID	pmv700889518.h1
Method	BLASTX
NCBI GI	g3107931
BLAST score	229
E value	2.0e-19
Match length	84
% identity	55
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	48853
Seq. ID	pmv700889528.h1
Method	BLASTN
NCBI GI	g1638836
BLAST score	102
E value	2.0e-50
Match length	198
% identity	88
NCBI Description	H.vulgare mRNA for alpha-tubulin

Seq. No.	48854
Seq. ID	pmv700889549.h1
Method	BLASTX
NCBI GI	g2558654
BLAST score	310
E value	6.0e-29
Match length	74
% identity	76
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	48855
Seq. ID	pmv700889571.h1
Method	BLASTN
NCBI GI	g2921511
BLAST score	53
E value	4.0e-21
Match length	69
% identity	94
NCBI Description	Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds

Seq. No.	48856
Seq. ID	pmv700889580.h1
Method	BLASTX
NCBI GI	g3668097
BLAST score	178
E value	2.0e-13
Match length	44
% identity	73
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	48857
Seq. ID	pmv700889688.h1
Method	BLASTX
NCBI GI	g2129473
BLAST score	173
E value	8.0e-13
Match length	69
% identity	48
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	48858
Seq. ID	pmv700889724.h1
Method	BLASTN
NCBI GI	g2961297
BLAST score	38
E value	3.0e-12
Match length	148
% identity	82
NCBI Description	Cicer arietinum mRNA for unidentified protein

Seq. No.	48859
Seq. ID	pmv700889759.h1
Method	BLASTX
NCBI GI	g4206789

BLAST score	310
E value	5.0e-29
Match length	71
% identity	85
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	48860
Seq. ID	pmv700889784.h1
Method	BLASTX
NCBI GI	g2673906
BLAST score	230
E value	1.0e-19
Match length	68
% identity	71
NCBI Description	(AC002561) putative DNA polymerase delta small subunit [Arabidopsis thaliana]

Seq. No.	48861
Seq. ID	pmv700889788.h1
Method	BLASTX
NCBI GI	g3395440
BLAST score	155
E value	7.0e-11
Match length	68
% identity	43
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48862
Seq. ID	pmv700889792.h1
Method	BLASTN
NCBI GI	g170050
BLAST score	111
E value	8.0e-56
Match length	191
% identity	90
NCBI Description	Soybean pyruvate kinase mRNA, complete cds

Seq. No.	48863
Seq. ID	pmv700889810.h1
Method	BLASTX
NCBI GI	g4567289
BLAST score	172
E value	9.0e-13
Match length	77
% identity	57
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48864
Seq. ID	pmv700889819.h1
Method	BLASTX
NCBI GI	g3176874
BLAST score	199
E value	6.0e-16
Match length	76
% identity	46
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis

thaliana]

Seq. No.	48865
Seq. ID	pmv700889934.h1
Method	BLASTN
NCBI GI	g558542
BLAST score	85
E value	3.0e-40
Match length	235
% identity	88
NCBI Description	G.max (Evans) mRNA for zinc-finger protein (C-terminal)

Seq. No.	48866
Seq. ID	pmv700889944.h1
Method	BLASTX
NCBI GI	g4467124
BLAST score	156
E value	7.0e-11
Match length	61
% identity	54
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48867
Seq. ID	pmv700889956.h1
Method	BLASTX
NCBI GI	g2213602
BLAST score	177
E value	2.0e-13
Match length	62
% identity	61
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No.	48868
Seq. ID	pmv700889982.h1
Method	BLASTX
NCBI GI	g2978452
BLAST score	253
E value	2.0e-22
Match length	72
% identity	65
NCBI Description	(AE001274) MCAK; L549.3 [Leishmania major]

Seq. No.	48869
Seq. ID	pmv700890029.h1
Method	BLASTX
NCBI GI	g2129953
BLAST score	264
E value	2.0e-23
Match length	78
% identity	82
NCBI Description	laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542) diphenol oxidase [Nicotiana tabacum]

Seq. No.	48870
Seq. ID	pmv700890033.h1
Method	BLASTX
NCBI GI	g4512624

BLAST score	393
E value	1.0e-38
Match length	80
% identity	91
NCBI Description	(AC004793) Strong similarity to gi_3033401 F19I3.29 putative potassium transporter from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	48871
Seq. ID	pmv700890057.h1
Method	BLASTX
NCBI GI	g2244988
BLAST score	205
E value	1.0e-16
Match length	69
% identity	61
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48872
Seq. ID	pmv700890079.h1
Method	BLASTN
NCBI GI	g1143510
BLAST score	39
E value	4.0e-13
Match length	59
% identity	93
NCBI Description	M.domestica Borkh mRNA for serine/threonine protein phosphatase (PPX)

Seq. No.	48873
Seq. ID	pmv700890165.h1
Method	BLASTX
NCBI GI	g4325282
BLAST score	157
E value	6.0e-11
Match length	62
% identity	50
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	48874
Seq. ID	pmv700890167.h1
Method	BLASTX
NCBI GI	g1871577
BLAST score	227
E value	4.0e-19
Match length	55
% identity	78
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	48875
Seq. ID	pmv700890182.h1
Method	BLASTX
NCBI GI	g3688123
BLAST score	149
E value	5.0e-10

Match length	40
% identity	70
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	48876
Seq. ID	pmv700890204.h1
Method	BLASTX
NCBI GI	g2280530
BLAST score	255
E value	1.0e-31
Match length	78
% identity	82
NCBI Description	(AB005889) ATMYB4 [Arabidopsis thaliana]

Seq. No.	48877
Seq. ID	pmv700890222.h1
Method	BLASTX
NCBI GI	g3176098
BLAST score	274
E value	1.0e-24
Match length	67
% identity	81
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	48878
Seq. ID	pmv700890244.h1
Method	BLASTX
NCBI GI	g126932
BLAST score	139
E value	7.0e-09
Match length	47
% identity	24
NCBI Description	MULTIDRUG RESISTANCE PROTEIN 3 (P-GLYCOPROTEIN 3) >gi_72473_pir__DVHU3 multidrug resistance protein 3 - human >gi_307181 (M23234) P-glycoprotein [Homo sapiens] >gi_4505771_ref_NP_000434.1_pPGY3_ P glycoprotein 3/multiple drug resistance

Seq. No.	48879
Seq. ID	pmv700890294.h1
Method	BLASTX
NCBI GI	g3176098
BLAST score	216
E value	6.0e-18
Match length	54
% identity	76
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	48880
Seq. ID	pmv700890304.h1
Method	BLASTX
NCBI GI	g4263795
BLAST score	320
E value	5.0e-30
Match length	86
% identity	71

NCBI Description	(AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	48881
Seq. ID	pmv700890371.h1
Method	BLASTN
NCBI GI	g1326160
BLAST score	48
E value	4.0e-18
Match length	116
% identity	94
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	48882
Seq. ID	pmv700890393.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	53
E value	4.0e-21
Match length	117
% identity	91
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	48883
Seq. ID	pmv700890404.h1
Method	BLASTX
NCBI GI	g2213594
BLAST score	184
E value	6.0e-24
Match length	68
% identity	75
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	48884
Seq. ID	pmv700890416.h1
Method	BLASTN
NCBI GI	g3297806
BLAST score	34
E value	9.0e-10
Match length	60
% identity	45
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSAII project)

Seq. No.	48885
Seq. ID	pmv700890474.h1
Method	BLASTN
NCBI GI	g3702738
BLAST score	36
E value	5.0e-11
Match length	84
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	48886
Seq. ID	pmv700890485.h1

Method	BLASTX
NCBI GI	g2827143
BLAST score	189
E value	2.0e-15
Match length	48
% identity	92
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	48887
Seq. ID	pmv700890518.h1
Method	BLASTX
NCBI GI	g2104535
BLAST score	336
E value	6.0e-32
Match length	79
% identity	80
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	48888
Seq. ID	pmv700890520.h1
Method	BLASTX
NCBI GI	g3249111
BLAST score	164
E value	9.0e-12
Match length	78
% identity	18
NCBI Description	(AC003114) T12M4.7 [Arabidopsis thaliana]

Seq. No.	48889
Seq. ID	pmv700890566.h1
Method	BLASTX
NCBI GI	g1706958
BLAST score	145
E value	1.0e-09
Match length	42
% identity	71
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	48890
Seq. ID	pmv700890610.h1
Method	BLASTX
NCBI GI	g1369852
BLAST score	357
E value	2.0e-34
Match length	80
% identity	90
NCBI Description	(L46702) kinesin heavy chain-like protein [Solanum tuberosum]

Seq. No.	48891
Seq. ID	pmv700890635.h1
Method	BLASTN
NCBI GI	g1638836
BLAST score	103
E value	6.0e-51
Match length	203

% identity	88
NCBI Description	H.vulgare mRNA for alpha-tubulin

Seq. No.	48892
Seq. ID	pmv700890670.h1
Method	BLASTN
NCBI GI	g207024
BLAST score	117
E value	1.0e-59
Match length	129
% identity	98
NCBI Description	Rat preprosomatostatin complete gene and 5' flank

Seq. No.	48893
Seq. ID	pmv700890722.h1
Method	BLASTX
NCBI GI	g419760
BLAST score	367
E value	1.0e-35
Match length	80
% identity	84
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	48894
Seq. ID	pmv700890728.h1
Method	BLASTN
NCBI GI	g1143510
BLAST score	81
E value	8.0e-38
Match length	145
% identity	89
NCBI Description	M.domestica Borkh mRNA for serine/threonine protein phosphatase (PPX)

Seq. No.	48895
Seq. ID	pmv700890731.h1
Method	BLASTX
NCBI GI	g3834317
BLAST score	390
E value	3.0e-38
Match length	82
% identity	91
NCBI Description	(AC005679) Similar to CDC16 protein gb_U18291 (CDC16Hs) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	48896
Seq. ID	pmv700890788.h1
Method	BLASTX
NCBI GI	g4006867
BLAST score	148
E value	6.0e-10
Match length	59
% identity	46
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	48897
Seq. ID	pmv700890867.h1
Method	BLASTX
NCBI GI	g2129953
BLAST score	310
E value	6.0e-29
Match length	75
% identity	76
NCBI Description	laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542) diphenol oxidase [Nicotiana tabacum]

Seq. No.	48898
Seq. ID	pmv700890873.h1
Method	BLASTX
NCBI GI	g3559805
BLAST score	298
E value	1.0e-27
Match length	69
% identity	68
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	48899
Seq. ID	pmv700890908.h1
Method	BLASTN
NCBI GI	g871505
BLAST score	58
E value	4.0e-24
Match length	86
% identity	92
NCBI Description	P.sativum mRNA for small GTP-binding protein (clone pGTP11)

Seq. No.	48900
Seq. ID	pmv700890922.h1
Method	BLASTX
NCBI GI	g2598575
BLAST score	274
E value	1.0e-24
Match length	78
% identity	73
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	48901
Seq. ID	pmv700890930.h1
Method	BLASTX
NCBI GI	g2244949
BLAST score	271
E value	3.0e-24
Match length	72
% identity	75
NCBI Description	(Z97339) similarity to ORF - Lilium longiflorum [Arabidopsis thaliana]

Seq. No.	48902
Seq. ID	pmv700891007.h1
Method	BLASTX
NCBI GI	g4263522

BLAST score 139
E value 9.0e-09
Match length 87
% identity 24
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 48903
Seq. ID pmv700891015.h1
Method BLASTX
NCBI GI g3080412
BLAST score 166
E value 7.0e-12
Match length 71
% identity 39
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 48904
Seq. ID pmv700891057.h1
Method BLASTX
NCBI GI g132944
BLAST score 163
E value 1.0e-11
Match length 55
% identity 58
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 48905
Seq. ID pmv700891091.h1
Method BLASTX
NCBI GI g2275210
BLAST score 150
E value 5.0e-10
Match length 78
% identity 47
NCBI Description (AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No. 48906
Seq. ID pmv700891119.h1
Method BLASTX
NCBI GI g2062421
BLAST score 434
E value 2.0e-43
Match length 81
% identity 91
NCBI Description (U82123) expansin [Lycopersicon esculentum]

Seq. No. 48907
Seq. ID pmv700891141.h1
Method BLASTN
NCBI GI g1946328
BLAST score 59
E value 1.0e-24
Match length 170
% identity 84

NCBI Description	Nicotiana tabacum prohibitin mRNA, complete cds
Seq. No.	48908
Seq. ID	pmv700891167.h1
Method	BLASTN
NCBI GI	g4324966
BLAST score	174
E value	2.0e-93
Match length	174
% identity	100
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds
Seq. No.	48909
Seq. ID	pmv700891172.h1
Method	BLASTN
NCBI GI	g255576
BLAST score	46
E value	5.0e-17
Match length	130
% identity	84
NCBI Description	small auxin up RNA gene cluster: orf 6B [Glycine max=soybeans, cv. Wayne, Genomic, 665 nt]
Seq. No.	48910
Seq. ID	pmv700891179.h1
Method	BLASTX
NCBI GI	g3885334
BLAST score	239
E value	1.0e-20
Match length	75
% identity	61
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]
Seq. No.	48911
Seq. ID	pmv700891275.h1
Method	BLASTN
NCBI GI	g3212102
BLAST score	61
E value	7.0e-26
Match length	209
% identity	82
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	48912
Seq. ID	pmv700891291.h1
Method	BLASTX
NCBI GI	g4314370
BLAST score	278
E value	2.0e-28
Match length	83
% identity	73
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.	48913
Seq. ID	pmv700891350.h1

Method	BLASTX
NCBI GI	g1522681
BLAST score	187
E value	2.0e-14
Match length	68
% identity	49
NCBI Description	(U49240) symplekin [Homo sapiens] >gi_2143262_emb_CAA71861_ (Y10931) symplekin [Homo sapiens]

Seq. No.	48914
Seq. ID	pmv700891363.h1
Method	BLASTN
NCBI GI	g1326160
BLAST score	36
E value	5.0e-11
Match length	36
% identity	100
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	48915
Seq. ID	pmv700891386.h1
Method	BLASTX
NCBI GI	g3560529
BLAST score	271
E value	2.0e-24
Match length	62
% identity	84
NCBI Description	(AF039598) light harvesting chlorophyll A/B binding protein [Prunus persica]

Seq. No.	48916
Seq. ID	pmv700891389.h1
Method	BLASTX
NCBI GI	g2789660
BLAST score	274
E value	1.0e-24
Match length	74
% identity	72
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	48917
Seq. ID	pmv700891392.h1
Method	BLASTN
NCBI GI	g2687432
BLAST score	41
E value	5.0e-14
Match length	41
% identity	100
NCBI Description	Plumbago auriculata large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	48918
Seq. ID	pmv700891411.h1
Method	BLASTX
NCBI GI	g2245012
BLAST score	225
E value	6.0e-27

Match length	79
% identity	76
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48919
Seq. ID	pmv700891438.h1
Method	BLASTX
NCBI GI	g3075390
BLAST score	323
E value	2.0e-30
Match length	83
% identity	73
NCBI Description	(AC004484) protein kinase ARSK1 [Arabidopsis thaliana]

Seq. No.	48920
Seq. ID	pmv700891439.h1
Method	BLASTX
NCBI GI	g4559353
BLAST score	256
E value	1.0e-22
Match length	77
% identity	66
NCBI Description	(AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]

Seq. No.	48921
Seq. ID	pmv700891464.h1
Method	BLASTX
NCBI GI	g3096947
BLAST score	223
E value	8.0e-19
Match length	52
% identity	77
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	48922
Seq. ID	pmv700891485.h1
Method	BLASTX
NCBI GI	g3831463
BLAST score	156
E value	8.0e-11
Match length	62
% identity	53
NCBI Description	(AC005700) unknown protein [Arabidopsis thaliana]

Seq. No.	48923
Seq. ID	pmv700891492.h1
Method	BLASTN
NCBI GI	g1399304
BLAST score	44
E value	1.0e-15
Match length	132
% identity	84
NCBI Description	Glycine max phosphoinositide-specific phospholipase C P13 mRNA, complete cds

Seq. No.	48924
Seq. ID	pmv700891516.h1
Method	BLASTX
NCBI GI	g1723801
BLAST score	145
E value	1.0e-09
Match length	57
% identity	18
NCBI Description	HYPOTHETICAL REGULATORY PROTEIN IN PDR6-PDR1 INTERGENIC REGION >gi_2133049_pir__S64016 probable regulatory protein YGL014w - yeast (Saccharomyces cerevisiae) >gi_1322473_emb_CAA96714_ (Z72536) ORF YGL014w [Saccharomyces cerevisiae]

Seq. No.	48925
Seq. ID	pmv700891595.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	251
E value	5.0e-22
Match length	73
% identity	67
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	48926
Seq. ID	pmv700891610.h1
Method	BLASTN
NCBI GI	g20061
BLAST score	56
E value	6.0e-23
Match length	112
% identity	88
NCBI Description	Oenothera elata subsp. hookeri mRNA for protein kinase C inhibitor homologue

Seq. No.	48927
Seq. ID	pmv700891629.h1
Method	BLASTX
NCBI GI	g4567305
BLAST score	244
E value	3.0e-21
Match length	77
% identity	55
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48928
Seq. ID	pmv700891638.h1
Method	BLASTN
NCBI GI	g496493
BLAST score	78
E value	4.0e-36
Match length	214
% identity	84
NCBI Description	P.sativum (Rosakrone) mRNA for nonphosphorylating, NADP-specific, glyceraldehyde-3-phosphate dehydrogenase

Seq. No.	48929

Seq. ID	pmv700891640.h1
Method	BLASTX
NCBI GI	g3785977
BLAST score	289
E value	2.0e-26
Match length	73
% identity	71
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	48930
Seq. ID	pmv700891669.h1
Method	BLASTX
NCBI GI	g3287695
BLAST score	249
E value	8.0e-22
Match length	50
% identity	94
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	48931
Seq. ID	pmv700891729.h1
Method	BLASTX
NCBI GI	g3121917
BLAST score	183
E value	5.0e-14
Match length	73
% identity	44
NCBI Description	COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA >gi_1362773_pir__A57090 CSA protein - human >gi_975302 (U28413) CSA protein [Homo sapiens] >gi_4557467_ref_NP_000073.1_pCKN1_ Cockayne syndrome 1 protein

Seq. No.	48932
Seq. ID	pmv700891738.h1
Method	BLASTX
NCBI GI	g3746059
BLAST score	137
E value	1.0e-08
Match length	50
% identity	54
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	48933
Seq. ID	pmv700891793.h1
Method	BLASTX
NCBI GI	g4335773
BLAST score	171
E value	1.0e-12
Match length	66
% identity	61
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	48934
Seq. ID	pmv700891795.h1
Method	BLASTX
NCBI GI	g3269298
BLAST score	226
E value	3.0e-19
Match length	72
% identity	57
NCBI Description	(AL030978) myosin heavy chain - like protein [Arabidopsis thaliana]

Seq. No.	48935
Seq. ID	pmv700891807.h1
Method	BLASTN
NCBI GI	g19272
BLAST score	133
E value	8.0e-69
Match length	185
% identity	93
NCBI Description	Tomato LeEF-1 mRNA for elongation factor 1 alpha

Seq. No.	48936
Seq. ID	pmv700891847.h1
Method	BLASTX
NCBI GI	g2213594
BLAST score	186
E value	3.0e-14
Match length	84
% identity	45
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	48937
Seq. ID	pmv700891856.h1
Method	BLASTN
NCBI GI	g2224730
BLAST score	94
E value	1.0e-45
Match length	243
% identity	91
NCBI Description	Vigna radiata mRNA for Aux22d, complete cds

Seq. No.	48938
Seq. ID	pmv700891875.h1
Method	BLASTN
NCBI GI	g4510323
BLAST score	63
E value	4.0e-27
Match length	155
% identity	85
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	48939
Seq. ID	pmv700891892.h1
Method	BLASTX
NCBI GI	g4567245

BLAST score	302
E value	7.0e-28
Match length	84
% identity	69
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	48940
Seq. ID	pmv700891937.h1
Method	BLASTX
NCBI GI	g3395938
BLAST score	173
E value	5.0e-13
Match length	40
% identity	80
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	48941
Seq. ID	pmv700891969.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	233
E value	1.0e-128
Match length	240
% identity	100
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	48942
Seq. ID	pmv700891971.h1
Method	BLASTX
NCBI GI	g1498120
BLAST score	163
E value	2.0e-16
Match length	65
% identity	75
NCBI Description	(D85416) sulfate transporter [Arabidopsis thaliana]

Seq. No.	48943
Seq. ID	pmv700892119.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	239
E value	1.0e-132
Match length	246
% identity	100
NCBI Description	G.max ADR6 mRNA

Seq. No.	48944
Seq. ID	pmv700892145.h1
Method	BLASTX
NCBI GI	g2633047
BLAST score	165
E value	7.0e-12
Match length	69
% identity	45
NCBI Description	(Z99107) similar to metabolite transporter [Bacillus subtilis] >gi_2633058_emb_CAB12563_ (Z99108) similar to

metabolite transporter [Bacillus subtilis]

Seq. No.	48945
Seq. ID	pmv700892242.h1
Method	BLASTX
NCBI GI	g4512685
BLAST score	341
E value	2.0e-32
Match length	80
% identity	80
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48946
Seq. ID	pmv700892295.h1
Method	BLASTX
NCBI GI	g2462485
BLAST score	183
E value	6.0e-14
Match length	78
% identity	45
NCBI Description	(X93209) NRD1 convertase [Homo sapiens]

Seq. No.	48947
Seq. ID	pmv700892334.h1
Method	BLASTX
NCBI GI	g3242708
BLAST score	342
E value	1.0e-32
Match length	85
% identity	74
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	48948
Seq. ID	pmv700892402.h1
Method	BLASTN
NCBI GI	g170071
BLAST score	159
E value	2.0e-84
Match length	167
% identity	99
NCBI Description	Soybean calmodulin (SCaM-2) mRNA, complete cds

Seq. No.	48949
Seq. ID	pmv700892459.h1
Method	BLASTX
NCBI GI	g2827143
BLAST score	205
E value	1.0e-16
Match length	47
% identity	81
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 48950

Seq. ID	pmv700892480.h1
Method	BLASTN
NCBI GI	g257814
BLAST score	73
E value	4.0e-33
Match length	181
% identity	85
NCBI Description	phenylalanine ammonia-lyase [soybeans, mRNA, 1427 nt]

Seq. No.	48951
Seq. ID	pmv700892536.h1
Method	BLASTX
NCBI GI	g3080428
BLAST score	199
E value	8.0e-16
Match length	58
% identity	60
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	48952
Seq. ID	pmv700892550.h1
Method	BLASTX
NCBI GI	g3183088
BLAST score	146
E value	1.0e-09
Match length	58
% identity	53
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	48953
Seq. ID	pmv700892556.h1
Method	BLASTX
NCBI GI	g3286691
BLAST score	139
E value	8.0e-09
Match length	41
% identity	61
NCBI Description	(AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	48954
Seq. ID	pmv700892647.h1
Method	BLASTN
NCBI GI	g975887
BLAST score	46
E value	5.0e-17
Match length	82
% identity	89
NCBI Description	Mesembryanthemum crystallinum myo-inositol-1-phosphate synthase mRNA, complete cds

Seq. No.	48955
Seq. ID	pmv700892686.h1
Method	BLASTX
NCBI GI	g4490737

BLAST score	154
E value	9.0e-11
Match length	47
% identity	64
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	48956
Seq. ID	pmv700892690.h1
Method	BLASTX
NCBI GI	g3193320
BLAST score	240
E value	8.0e-21
Match length	67
% identity	66
NCBI Description	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No.	48957
Seq. ID	pmv700892694.h1
Method	BLASTN
NCBI GI	g20740
BLAST score	44
E value	8.0e-16
Match length	88
% identity	88
NCBI Description	Pisum sativum mRNA for P protein, a part of glycine cleavage complex

Seq. No.	48958
Seq. ID	pmv700892712.h1
Method	BLASTX
NCBI GI	g2673917
BLAST score	230
E value	2.0e-19
Match length	85
% identity	56
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	48959
Seq. ID	pmv700892744.h1
Method	BLASTN
NCBI GI	g4324966
BLAST score	188
E value	1.0e-101
Match length	188
% identity	100
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No.	48960
Seq. ID	pmv700892840.h1
Method	BLASTN
NCBI GI	g2961297
BLAST score	35
E value	2.0e-10

Match length	71
% identity	87
NCBI Description	Cicer arietinum mRNA for unidentified protein

Seq. No.	48961
Seq. ID	pmv700892909.h1
Method	BLASTN
NCBI GI	g3462613
BLAST score	53
E value	4.0e-21
Match length	117
% identity	86
NCBI Description	Pisum sativum knotted I class homeodomain protein (Kn284) mRNA, partial cds

Seq. No.	48962
Seq. ID	pmv700893014.h1
Method	BLASTX
NCBI GI	g2316016
BLAST score	229
E value	2.0e-19
Match length	79
% identity	68
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	48963
Seq. ID	pmv700893036.h1
Method	BLASTX
NCBI GI	g4572669
BLAST score	386
E value	9.0e-38
Match length	85
% identity	85
NCBI Description	(AC006954) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	48964
Seq. ID	pmv700893040.h1
Method	BLASTX
NCBI GI	g4544399
BLAST score	314
E value	3.0e-29
Match length	83
% identity	70
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	48965
Seq. ID	pmv700893073.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	297
E value	2.0e-27
Match length	70
% identity	84
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	48966
Seq. ID	pmv700893159.h1
Method	BLASTN
NCBI GI	g2935415
BLAST score	55
E value	2.0e-22
Match length	207
% identity	85
NCBI Description	Betula pendula isoflavone reductase homolog mRNA, complete cds

Seq. No.	48967
Seq. ID	pmv700893220.h1
Method	BLASTX
NCBI GI	g2130080
BLAST score	238
E value	2.0e-20
Match length	59
% identity	85
NCBI Description	Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

Seq. No.	48968
Seq. ID	pmv700893389.h1
Method	BLASTX
NCBI GI	g3786009
BLAST score	222
E value	1.0e-18
Match length	52
% identity	85
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	48969
Seq. ID	pmv700893402.h1
Method	BLASTX
NCBI GI	g4249412
BLAST score	130
E value	4.0e-11
Match length	75
% identity	51
NCBI Description	(AC006072) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48970
Seq. ID	pmv700893437.h1
Method	BLASTX
NCBI GI	g4097561
BLAST score	208
E value	5.0e-17
Match length	43
% identity	84
NCBI Description	(U64918) ATGP1 [Arabidopsis thaliana]

Seq. No.	48971
Seq. ID	pmv700893496.h1

Method	BLASTX
NCBI GI	g3892059
BLAST score	197
E value	4.0e-29
Match length	75
% identity	81
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	48972
Seq. ID	pmv700893503.h1
Method	BLASTX
NCBI GI	g1076802
BLAST score	175
E value	4.0e-13
Match length	77
% identity	26
NCBI Description	extensin-like protein - maize >gi_600118_emb_CAA84230_ (Z34465) extensin-like protein [Zea mays] >gi_1096557_prf__2111476A extensin-like domain [Zea mays]

Seq. No.	48973
Seq. ID	pmv700893513.h1
Method	BLASTN
NCBI GI	g1480346
BLAST score	51
E value	6.0e-20
Match length	75
% identity	92
NCBI Description	P.sativum mRNA for ferrodoxin NADP oxidoreductase

Seq. No.	48974
Seq. ID	pmv700893527.h1
Method	BLASTX
NCBI GI	g4539324
BLAST score	163
E value	1.0e-11
Match length	35
% identity	91
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	48975
Seq. ID	pmv700893541.h1
Method	BLASTX
NCBI GI	g4510400
BLAST score	284
E value	6.0e-26
Match length	75
% identity	76
NCBI Description	(AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis thaliana]

Seq. No.	48976
Seq. ID	pmv700893581.h1
Method	BLASTX
NCBI GI	g2832625
BLAST score	270

E value	3.0e-24
Match length	73
% identity	66
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	48977
Seq. ID	pmv700893702.h1
Method	BLASTX
NCBI GI	g2369714
BLAST score	243
E value	5.0e-21
Match length	59
% identity	73
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	48978
Seq. ID	pmv700893707.h1
Method	BLASTN
NCBI GI	g3985958
BLAST score	41
E value	5.0e-14
Match length	137
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	48979
Seq. ID	pmv700893729.h1
Method	BLASTX
NCBI GI	g2500354
BLAST score	356
E value	2.0e-34
Match length	65
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No.	48980
Seq. ID	pmv700893735.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	227
E value	1.0e-125
Match length	235
% identity	99
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	48981
Seq. ID	pmv700893747.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	149
E value	2.0e-78
Match length	229
% identity	96
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	48982
Seq. ID	pmv700893758.h1
Method	BLASTX
NCBI GI	g3128234
BLAST score	327
E value	6.0e-31
Match length	76
% identity	78
NCBI Description	(AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48983
Seq. ID	pmv700893826.h1
Method	BLASTX
NCBI GI	g4218011
BLAST score	332
E value	2.0e-31
Match length	79
% identity	78
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	48984
Seq. ID	pmv700893841.h1
Method	BLASTX
NCBI GI	g4512673
BLAST score	320
E value	4.0e-30
Match length	79
% identity	75
NCBI Description	(AC006931) putative phosphoprotein phosphatase [Arabidopsis thaliana]

Seq. No.	48985
Seq. ID	pmv700893889.h1
Method	BLASTX
NCBI GI	g2660670
BLAST score	146
E value	8.0e-10
Match length	77
% identity	23
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	48986
Seq. ID	pmv700893896.h1
Method	BLASTX
NCBI GI	g531389
BLAST score	212
E value	2.0e-17
Match length	71
% identity	65
NCBI Description	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No.	48987

Seq. ID	pmv700893911.h1
Method	BLASTX
NCBI GI	g2654868
BLAST score	259
E value	5.0e-23
Match length	76
% identity	61
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	48988
Seq. ID	pmv700893966.h1
Method	BLASTN
NCBI GI	g2961299
BLAST score	121
E value	9.0e-62
Match length	201
% identity	90
NCBI Description	Cicer arietinum mRNA for ribosomal protein L24

Seq. No.	48989
Seq. ID	pmv700893968.h1
Method	BLASTX
NCBI GI	g4467135
BLAST score	216
E value	5.0e-18
Match length	71
% identity	68
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	48990
Seq. ID	pmv700893974.h1
Method	BLASTN
NCBI GI	g3869067
BLAST score	35
E value	2.0e-10
Match length	122
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	48991
Seq. ID	pmv700894003.h1
Method	BLASTX
NCBI GI	g2388577
BLAST score	137
E value	1.0e-08
Match length	76
% identity	64
NCBI Description	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No.	48992
Seq. ID	pmv700894016.h1
Method	BLASTX
NCBI GI	g1619300
BLAST score	181
E value	1.0e-13

Match length	87
% identity	46
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	48993
Seq. ID	pmv700894019.h1
Method	BLASTX
NCBI GI	g4063747
BLAST score	327
E value	7.0e-31
Match length	81
% identity	73
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48994
Seq. ID	pmv700894068.h1
Method	BLASTX
NCBI GI	g4567200
BLAST score	284
E value	7.0e-26
Match length	76
% identity	66
NCBI Description	(AC007168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48995
Seq. ID	pmv700894089.h1
Method	BLASTX
NCBI GI	g32709
BLAST score	282
E value	1.0e-25
Match length	79
% identity	68
NCBI Description	(X62570) IFP53 [Homo sapiens]

Seq. No.	48996
Seq. ID	pmv700894095.h1
Method	BLASTX
NCBI GI	g2499488
BLAST score	151
E value	2.0e-10
Match length	52
% identity	65
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	48997
Seq. ID	pmv700894101.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	255
E value	1.0e-141
Match length	259
% identity	100

NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	48998
Seq. ID	pmv700894116.h1
Method	BLASTX
NCBI GI	g3004550
BLAST score	256
E value	2.0e-22
Match length	65
% identity	80
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	48999
Seq. ID	pmv700894129.h1
Method	BLASTX
NCBI GI	g3402684
BLAST score	165
E value	9.0e-13
Match length	54
% identity	72
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49000
Seq. ID	pmv700894150.h1
Method	BLASTX
NCBI GI	g4309738
BLAST score	155
E value	7.0e-11
Match length	29
% identity	97
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	49001
Seq. ID	pmv700894151.h1
Method	BLASTX
NCBI GI	g3738288
BLAST score	315
E value	2.0e-29
Match length	82
% identity	71
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	49002
Seq. ID	pmv700894191.h1
Method	BLASTN
NCBI GI	g18644
BLAST score	76
E value	7.0e-35
Match length	88
% identity	97
NCBI Description	Soybean mRNA for HMG-1 like protein

Seq. No.	49003
Seq. ID	pmv700894196.h1
Method	BLASTN

NCBI GI	g16508
BLAST score	70
E value	3.0e-31
Match length	158
% identity	86
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49004
Seq. ID	pmv700894233.h1
Method	BLASTX
NCBI GI	g4580395
BLAST score	181
E value	9.0e-14
Match length	70
% identity	53
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	49005
Seq. ID	pmv700894234.h1
Method	BLASTX
NCBI GI	g4335773
BLAST score	140
E value	6.0e-09
Match length	27
% identity	96
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	49006
Seq. ID	pmv700894250.h1
Method	BLASTX
NCBI GI	g2262157
BLAST score	154
E value	6.0e-11
Match length	55
% identity	71
NCBI Description	(AC002329) putative ligand-gated ion channel protein [Arabidopsis thaliana]

Seq. No.	49007
Seq. ID	pmv700894279.h1
Method	BLASTX
NCBI GI	g3894169
BLAST score	307
E value	1.0e-28
Match length	66
% identity	79
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49008
Seq. ID	pmv700894314.h1
Method	BLASTX
NCBI GI	g4559333
BLAST score	179
E value	1.0e-13

Match length	48
% identity	75
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	49009
Seq. ID	pmv700894355.h1
Method	BLASTX
NCBI GI	g1825727
BLAST score	213
E value	2.0e-17
Match length	59
% identity	66
NCBI Description	(U88308) C32E8.5 gene product [Caenorhabditis elegans]

Seq. No.	49010
Seq. ID	pmv700894366.h1
Method	BLASTX
NCBI GI	g3559805
BLAST score	330
E value	3.0e-31
Match length	79
% identity	68
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	49011
Seq. ID	pmv700894369.h1
Method	BLASTN
NCBI GI	g4580386
BLAST score	60
E value	2.0e-25
Match length	196
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	49012
Seq. ID	pmv700894372.h1
Method	BLASTX
NCBI GI	g3023947
BLAST score	400
E value	2.0e-39
Match length	77
% identity	95
NCBI Description	PROBABLE HISTONE DEACETYLASE (RPD3 HOMOLOG) >gi_2665840 (AF035815) putative histone deacetylase RPD3 [Zea mays]

Seq. No.	49013
Seq. ID	pmv700894390.h1
Method	BLASTX
NCBI GI	g1669601
BLAST score	176
E value	3.0e-13
Match length	46
% identity	67
NCBI Description	(D88747) AR401 [Arabidopsis thaliana]

Seq. No.	49014
Seq. ID	pmv700894393.h1
Method	BLASTX
NCBI GI	g3668118
BLAST score	232
E value	7.0e-20
Match length	60
% identity	72
NCBI Description	(AJ224078) hypothetical protein [Brassica napus]

Seq. No.	49015
Seq. ID	pmv700894402.h1
Method	BLASTX
NCBI GI	g2252854
BLAST score	207
E value	9.0e-17
Match length	50
% identity	76
NCBI Description	(AF013294) similar to auxin-induced protein [Arabidopsis thaliana]

Seq. No.	49016
Seq. ID	pmv700894404.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	211
E value	1.0e-115
Match length	248
% identity	98
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	49017
Seq. ID	pmv700894425.h1
Method	BLASTX
NCBI GI	g4539452
BLAST score	344
E value	7.0e-33
Match length	82
% identity	72
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	49018
Seq. ID	pmv700894426.h1
Method	BLASTX
NCBI GI	g3462614
BLAST score	259
E value	6.0e-23
Match length	75
% identity	68
NCBI Description	(AF080105) knotted I class homeodomain protein [Pisum sativum]

Seq. No.	49019
Seq. ID	pmv700894562.h1
Method	BLASTN
NCBI GI	g288187

BLAST score	172
E value	4.0e-92
Match length	219
% identity	95
NCBI Description	V.unguiculata cysteine proteinase inhibitor mRNA

Seq. No.	49020
Seq. ID	pmv700894677.h1
Method	BLASTX
NCBI GI	g416688
BLAST score	154
E value	3.0e-14
Match length	55
% identity	68
NCBI Description	AUXIN-INDUCED PROTEIN X10A >gi_81761_pir__JQ1099 auxin-induced protein 10A - soybean >gi_255579_bbs_113701 (S44176) orf X10A [Glycine max=soybeans, cv. Wayne, Peptide, 92 aa] [Glycine max]

Seq. No.	49021
Seq. ID	pmv700894681.h1
Method	BLASTX
NCBI GI	g4309736
BLAST score	119
E value	2.0e-09
Match length	56
% identity	66
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49022
Seq. ID	pmv700894741.h1
Method	BLASTN
NCBI GI	g169664
BLAST score	38
E value	4.0e-12
Match length	46
% identity	96
NCBI Description	Parsley S-adenosylmethionine synthetase (SMS-1) mRNA, 3' end

Seq. No.	49023
Seq. ID	pmv700894756.h1
Method	BLASTX
NCBI GI	g4006915
BLAST score	245
E value	3.0e-21
Match length	80
% identity	60
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49024
Seq. ID	pmv700894759.h1
Method	BLASTX
NCBI GI	g2194131
BLAST score	216
E value	6.0e-18
Match length	72

% identity	61
NCBI Description	(AC002062) Similar to Synechocystis antiviral protein (gb_D90917). [Arabidopsis thaliana]

Seq. No.	49025
Seq. ID	pmv700894796.h1
Method	BLASTX
NCBI GI	g4580462
BLAST score	267
E value	7.0e-24
Match length	78
% identity	42
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49026
Seq. ID	pmv700894844.h1
Method	BLASTX
NCBI GI	g1888557
BLAST score	283
E value	1.0e-25
Match length	81
% identity	59
NCBI Description	(U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

Seq. No.	49027
Seq. ID	pmv700894851.h1
Method	BLASTX
NCBI GI	g1706956
BLAST score	201
E value	1.0e-33
Match length	82
% identity	75
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	49028
Seq. ID	pmv700894905.h1
Method	BLASTX
NCBI GI	g2924509
BLAST score	195
E value	2.0e-15
Match length	85
% identity	52
NCBI Description	(AL022023) subtilisin proteinase - like [Arabidopsis thaliana]

Seq. No.	49029
Seq. ID	pmv700894917.h1
Method	BLASTX
NCBI GI	g3892059
BLAST score	194
E value	3.0e-15
Match length	84
% identity	17
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	49030
Seq. ID	pmv700894930.h1
Method	BLASTX
NCBI GI	g3249085
BLAST score	270
E value	4.0e-24
Match length	87
% identity	64
NCBI Description	(AC004473) T13D8.31 [Arabidopsis thaliana]

Seq. No.	49031
Seq. ID	pmv700894959.h1
Method	BLASTN
NCBI GI	g4204858
BLAST score	72
E value	2.0e-32
Match length	164
% identity	86
NCBI Description	Triticum aestivum heat shock protein 80 mRNA, complete cds

Seq. No.	49032
Seq. ID	pmv700894990.h1
Method	BLASTX
NCBI GI	g1755182
BLAST score	267
E value	8.0e-24
Match length	81
% identity	62
NCBI Description	(U75202) germin-like protein [Arabidopsis thaliana]

Seq. No.	49033
Seq. ID	pmv700895020.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	253
E value	4.0e-22
Match length	84
% identity	57
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	49034
Seq. ID	pmv700895028.h1
Method	BLASTX
NCBI GI	g3980378
BLAST score	189
E value	1.0e-14
Match length	57
% identity	70
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	49035
Seq. ID	pmv700895033.h1
Method	BLASTX
NCBI GI	g3927825
BLAST score	205
E value	2.0e-16

Match length	40
% identity	97
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	49036
Seq. ID	pmv700895047.h1
Method	BLASTX
NCBI GI	g2688830
BLAST score	359
E value	1.0e-34
Match length	83
% identity	82
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	49037
Seq. ID	pmv700895060.h1
Method	BLASTX
NCBI GI	g4490736
BLAST score	293
E value	7.0e-27
Match length	81
% identity	37
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	49038
Seq. ID	pmv700895061.h1
Method	BLASTX
NCBI GI	g2160148
BLAST score	198
E value	1.0e-15
Match length	43
% identity	72
NCBI Description	(AC000375) EST gb_H37044 comes from this gene. [Arabidopsis thaliana]

Seq. No.	49039
Seq. ID	pmv700895068.h1
Method	BLASTN
NCBI GI	g2598656
BLAST score	112
E value	1.0e-56
Match length	140
% identity	95
NCBI Description	Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.	49040
Seq. ID	pmv700895071.h1
Method	BLASTX
NCBI GI	g2244912
BLAST score	217
E value	4.0e-18
Match length	46
% identity	91
NCBI Description	(Z97339) similar to transketolase [Arabidopsis thaliana]

Seq. No.	49041

Seq. ID	pmv700895128.h1
Method	BLASTX
NCBI GI	g3892709
BLAST score	363
E value	5.0e-35
Match length	83
% identity	84
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	49042
Seq. ID	pmv700895130.h1
Method	BLASTX
NCBI GI	g4508078
BLAST score	160
E value	3.0e-11
Match length	36
% identity	78
NCBI Description	(AC005882) 64134 [Arabidopsis thaliana]

Seq. No.	49043
Seq. ID	pmv700895167.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	54
E value	6.0e-22
Match length	106
% identity	89
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	49044
Seq. ID	pmv700895204.h1
Method	BLASTX
NCBI GI	g1136434
BLAST score	274
E value	1.0e-24
Match length	80
% identity	57
NCBI Description	(D80009) KIAA0187 [Homo sapiens]

Seq. No.	49045
Seq. ID	pmv700895244.h1
Method	BLASTX
NCBI GI	g2129539
BLAST score	163
E value	1.0e-11
Match length	76
% identity	45
NCBI Description	AtJ1 protein - Arabidopsis thaliana >gi_564030 (U16246) AtJ1 [Arabidopsis thaliana]

Seq. No.	49046
Seq. ID	pmv700895247.h1
Method	BLASTX
NCBI GI	g2245004
BLAST score	264
E value	2.0e-23
Match length	84

% identity	61
NCBI Description	(Z97341) similarity to membrane transport protein [Arabidopsis thaliana]

Seq. No.	49047
Seq. ID	pmv700895270.h1
Method	BLASTX
NCBI GI	g4512683
BLAST score	283
E value	1.0e-25
Match length	78
% identity	71
NCBI Description	(AC006931) putative lipase [Arabidopsis thaliana] >gi_4559323_gb_AAD22985.1_AC007087_4 (AC007087) putative lipase [Arabidopsis thaliana]

Seq. No.	49048
Seq. ID	pmv700895287.h1
Method	BLASTN
NCBI GI	g2264315
BLAST score	91
E value	8.0e-44
Match length	199
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	49049
Seq. ID	pst700645702.h1
Method	BLASTN
NCBI GI	g4249565
BLAST score	279
E value	1.0e-156
Match length	298
% identity	99
NCBI Description	Glycine max A3B4 glycinin gene, complete cds

Seq. No.	49050
Seq. ID	pst700645711.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	292
E value	1.0e-163
Match length	299
% identity	100
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	49051
Seq. ID	pst700645740.h1
Method	BLASTX
NCBI GI	g3785995
BLAST score	438
E value	1.0e-43
Match length	97
% identity	85
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	49052
Seq. ID	pst700645775.h1
Method	BLASTN
NCBI GI	g806555
BLAST score	269
E value	1.0e-150
Match length	284
% identity	99
NCBI Description	G.soja mRNA for glycinin

Seq. No.	49053
Seq. ID	pst700645785.h1
Method	BLASTN
NCBI GI	g806555
BLAST score	238
E value	1.0e-131
Match length	269
% identity	97
NCBI Description	G.soja mRNA for glycinin

Seq. No.	49054
Seq. ID	pst700645786.h1
Method	BLASTX
NCBI GI	g1220178
BLAST score	190
E value	3.0e-15
Match length	56
% identity	77
NCBI Description	(Z69995) dormancy related protein [Trollius ledebourii]

Seq. No.	49055
Seq. ID	pst700645795.h1
Method	BLASTN
NCBI GI	g1304600
BLAST score	118
E value	6.0e-60
Match length	234
% identity	89
NCBI Description	Human ZNF127-Xq pseudogene

Seq. No.	49056
Seq. ID	pst700645818.h1
Method	BLASTN
NCBI GI	g18638
BLAST score	249
E value	1.0e-138
Match length	275
% identity	98
NCBI Description	Soybean Gy3 gene for glycinin subunit G3

Seq. No.	49057
Seq. ID	pst700645834.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	122
E value	2.0e-62
Match length	221

% identity	89
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	49058
Seq. ID	pst700645854.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	74
E value	1.0e-33
Match length	184
% identity	87
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	49059
Seq. ID	pst700645868.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	141
E value	1.0e-73
Match length	228
% identity	91
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	49060
Seq. ID	pst700645886.h1
Method	BLASTN
NCBI GI	g18634
BLAST score	125
E value	5.0e-64
Match length	275
% identity	87
NCBI Description	Soybean Gy1 gene for glycinin subunit G1

Seq. No.	49061
Seq. ID	pxt700940914.h1
Method	BLASTX
NCBI GI	g2828294
BLAST score	150
E value	5.0e-14
Match length	80
% identity	50
NCBI Description	(AL021687) putatative protein [Arabidopsis thaliana]

Seq. No.	49062
Seq. ID	pxt700940961.h1
Method	BLASTX
NCBI GI	g3668092
BLAST score	313
E value	3.0e-29
Match length	80
% identity	75
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	49063
Seq. ID	pxt700940966.h1

Method	BLASTX
NCBI GI	g3080384
BLAST score	181
E value	1.0e-16
Match length	65
% identity	67
NCBI Description	(AL022603) serine/threonine protein kinase [Arabidopsis thaliana] >gi_3402759_emb_CAA20205.1_ (AL031187) serine/threonine protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	49064
Seq. ID	pxt700941010.h1
Method	BLASTX
NCBI GI	g3786011
BLAST score	297
E value	2.0e-27
Match length	75
% identity	75
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	49065
Seq. ID	pxt700941054.h1
Method	BLASTX
NCBI GI	g2244996
BLAST score	156
E value	8.0e-11
Match length	73
% identity	12
NCBI Description	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]

Seq. No.	49066
Seq. ID	pxt700941062.h1
Method	BLASTX
NCBI GI	g100099
BLAST score	305
E value	3.0e-28
Match length	76
% identity	71
NCBI Description	DNA-binding protein VBP1 - fava bean >gi_1372966 (M81827) CREB-like protein [Vicia faba]

Seq. No.	49067
Seq. ID	pxt700941070.h1
Method	BLASTN
NCBI GI	g3139138
BLAST score	42
E value	1.0e-14
Match length	42
% identity	100
NCBI Description	Lotus japonicus Rac small GTPase (Rac2) gene, promoter region and partial mRNA sequence

Seq. No.	49068
Seq. ID	pxt700941075.h1

Method	BLASTX
NCBI GI	g2943792
BLAST score	160
E value	2.0e-11
Match length	58
% identity	74
NCBI Description	(AB006809) PV72 [Cucurbita sp.]

Seq. No.	49069
Seq. ID	pxt700941087.h1
Method	BLASTX
NCBI GI	g4220522
BLAST score	156
E value	8.0e-11
Match length	78
% identity	46
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	49070
Seq. ID	pxt700941125.h1
Method	BLASTX
NCBI GI	g3805956
BLAST score	274
E value	1.0e-24
Match length	84
% identity	65
NCBI Description	(Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	49071
Seq. ID	pxt700941130.h1
Method	BLASTX
NCBI GI	g4220485
BLAST score	388
E value	6.0e-38
Match length	85
% identity	82
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	49072
Seq. ID	pxt700941144.h1
Method	BLASTX
NCBI GI	g4522009
BLAST score	295
E value	4.0e-27
Match length	71
% identity	72
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	49073
Seq. ID	pxt700941178.h1
Method	BLASTX
NCBI GI	g2865437
BLAST score	190
E value	9.0e-15
Match length	83
% identity	48

NCBI Description (AF039376) polyprotein [Arabidopsis arenosa]

Seq. No. 49074
Seq. ID pxt700941180.h1
Method BLASTX
NCBI GI g3258575
BLAST score 169
E value 1.0e-19
Match length 84
% identity 68
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 49075
Seq. ID pxt700941191.h1
Method BLASTX
NCBI GI g2655098
BLAST score 321
E value 4.0e-30
Match length 83
% identity 75
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 49076
Seq. ID pxt700941195.h1
Method BLASTX
NCBI GI g4006924
BLAST score 229
E value 2.0e-19
Match length 51
% identity 76
NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No. 49077
Seq. ID pxt700941204.h1
Method BLASTX
NCBI GI g2245012
BLAST score 202
E value 4.0e-16
Match length 48
% identity 77
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 49078
Seq. ID pxt700941224.h1
Method BLASTX
NCBI GI g2459435
BLAST score 277
E value 6.0e-25
Match length 72
% identity 72
NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 49079
Seq. ID pxt700941245.h1
Method BLASTX

NCBI GI g4115929
BLAST score 182
E value 8.0e-14
Match length 86
% identity 42
NCBI Description (AF118222) similar to the subtilase family of serine proteases (Pfam: PF00082, Score=48.3, E=2.3e-12, n=4) [Arabidopsis thaliana] >gi_4539412_emb_CAB40045.1_ (AL049524) putative subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 49080
Seq. ID pxt700941258.h1
Method BLASTX
NCBI GI g2842424
BLAST score 279
E value 3.0e-25
Match length 66
% identity 79
NCBI Description (AJ223948) RNA helicase [Homo sapiens]

Seq. No. 49081
Seq. ID pxt700941277.h1
Method BLASTX
NCBI GI g4056506
BLAST score 203
E value 3.0e-16
Match length 64
% identity 61
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 49082
Seq. ID pxt700941304.h1
Method BLASTX
NCBI GI g2769642
BLAST score 372
E value 4.0e-36
Match length 87
% identity 85
NCBI Description (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon esculentum]

Seq. No. 49083
Seq. ID pxt700941346.h1
Method BLASTX
NCBI GI g4107099
BLAST score 138
E value 7.0e-09
Match length 51
% identity 55
NCBI Description (AB015141) AHP1 [Arabidopsis thaliana] >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No. 49084
Seq. ID pxt700941353.h1
Method BLASTX

NCBI GI	g1076414
BLAST score	139
E value	9.0e-09
Match length	69
% identity	42
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	49085
Seq. ID	pxt700941379.h1
Method	BLASTX
NCBI GI	g2244750
BLAST score	195
E value	2.0e-15
Match length	42
% identity	98
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	49086
Seq. ID	pxt700941478.h1
Method	BLASTN
NCBI GI	g806807
BLAST score	82
E value	2.0e-38
Match length	162
% identity	88
NCBI Description	Pisum sativum chaperonin precursor mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	49087
Seq. ID	pxt700941496.h1
Method	BLASTX
NCBI GI	g4512677
BLAST score	168
E value	3.0e-12
Match length	81
% identity	52
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	49088
Seq. ID	pxt700941519.h1
Method	BLASTN
NCBI GI	g3511284
BLAST score	41
E value	4.0e-14
Match length	81
% identity	89
NCBI Description	Populus alba x Populus tremula cellulose synthase (cel1) mRNA, complete cds

Seq. No.	49089
Seq. ID	pxt700941537.h1
Method	BLASTX
NCBI GI	g2497953

BLAST score	235
E value	4.0e-20
Match length	64
% identity	72
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.	49090
Seq. ID	pxt700941584.h1
Method	BLASTX
NCBI GI	g629561
BLAST score	182
E value	6.0e-14
Match length	76
% identity	50
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	49091
Seq. ID	pxt700941664.h1
Method	BLASTX
NCBI GI	g3805851
BLAST score	208
E value	8.0e-17
Match length	88
% identity	44
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	49092
Seq. ID	pxt700941674.h1
Method	BLASTX
NCBI GI	g4510430
BLAST score	148
E value	5.0e-10
Match length	35
% identity	77
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	49093
Seq. ID	pxt700941686.h1
Method	BLASTN
NCBI GI	g497899
BLAST score	65
E value	3.0e-28
Match length	105
% identity	90
NCBI Description	Populus trichocarpa * Populus deltoides (clone sam.Pdx.Pt.2) S-adenosyl methionine synthetase mRNA, complete cds

Seq. No.	49094
Seq. ID	pxt700941690.h1

Method	BLASTX
NCBI GI	g3894191
BLAST score	164
E value	1.0e-11
Match length	42
% identity	64
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	49095
Seq. ID	pxt700941739.h1
Method	BLASTX
NCBI GI	g2244865
BLAST score	178
E value	2.0e-13
Match length	75
% identity	53
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49096
Seq. ID	pxt700941778.h1
Method	BLASTX
NCBI GI	g2950472
BLAST score	179
E value	2.0e-13
Match length	76
% identity	46
NCBI Description	(AL022070) putative autophagocytosis protein [Schizosaccharomyces pombe]

Seq. No.	49097
Seq. ID	pxt700941783.h1
Method	BLASTX
NCBI GI	g4454451
BLAST score	155
E value	3.0e-12
Match length	76
% identity	46
NCBI Description	(AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49098
Seq. ID	pxt700941896.h1
Method	BLASTX
NCBI GI	g1877397
BLAST score	148
E value	5.0e-10
Match length	35
% identity	77
NCBI Description	(Y11591) shaggy-like kinase [Ricinus communis]

Seq. No.	49099
Seq. ID	pxt700941948.h1
Method	BLASTN
NCBI GI	g493621
BLAST score	56
E value	4.0e-23
Match length	148
% identity	84

NCBI Description	A. thaliana mRNA for chloroplast envelope Ca2+-ATPase, complete cds >gi_4176434_emb_X69941_CHATACA1B A.thaliana chloroplast ACA1 mRNA encoding envelope Ca2+-ATPase
Seq. No.	49100
Seq. ID	pxt700942011.h1
Method	BLASTX
NCBI GI	g2749982
BLAST score	184
E value	5.0e-14
Match length	85
% identity	53
NCBI Description	(AF036705) Similar to phytoene desaturase; coded for by C. elegans cDNA CEESX74F; coded for by C. elegans cDNA yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans cDNA yk257d4.5;
Seq. No.	49101
Seq. ID	pxt700942088.h1
Method	BLASTN
NCBI GI	g3983533
BLAST score	50
E value	3.0e-19
Match length	62
% identity	95
NCBI Description	Arabidopsis thaliana BAC T24G3 from chromosome V near 70 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	49102
Seq. ID	pxt700942113.h1
Method	BLASTX
NCBI GI	g3549626
BLAST score	219
E value	3.0e-18
Match length	79
% identity	52
NCBI Description	(AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
Seq. No.	49103
Seq. ID	pxt700942124.h1
Method	BLASTX
NCBI GI	g3219939
BLAST score	147
E value	6.0e-10
Match length	52
% identity	58
NCBI Description	HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I >gi_2094864_emb_CAB08603_ (Z95334) unknown [Schizosaccharomyces pombe]
Seq. No.	49104
Seq. ID	pxt700942145.h1
Method	BLASTX
NCBI GI	g120674
BLAST score	110
E value	8.0e-10

Match length	63
% identity	62
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66015_pir__DENDG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - common buttercup >gi_21066_emb_CAA42903_ (X60345) glyceraldehyde 3-phosphate dehydrogenase [Ranunculus acris]

Seq. No.	49105
Seq. ID	pxt700942164.h1
Method	BLASTN
NCBI GI	g3421412
BLAST score	49
E value	8.0e-19
Match length	65
% identity	94
NCBI Description	Oryza sativa protein phosphatase 2A 55 kDa B regulatory subunit gene, complete cds

Seq. No.	49106
Seq. ID	pxt700942321.h1
Method	BLASTX
NCBI GI	g2370253
BLAST score	208
E value	3.0e-28
Match length	80
% identity	82
NCBI Description	(Y13273) putative protein kinase [Lycopersicon esculentum]

Seq. No.	49107
Seq. ID	pxt700942358.h1
Method	BLASTX
NCBI GI	g3193302
BLAST score	212
E value	2.0e-17
Match length	73
% identity	60
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) [Arabidopsis thaliana]

Seq. No.	49108
Seq. ID	pxt700942505.h1
Method	BLASTX
NCBI GI	g2459412
BLAST score	219
E value	3.0e-18
Match length	80
% identity	56
NCBI Description	(AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No.	49109
Seq. ID	pxt700942511.h1
Method	BLASTX
NCBI GI	g4006825
BLAST score	147

E value	9.0e-10
Match length	47
% identity	57
NCBI Description	(AC005970) G9a-like protein [Arabidopsis thaliana]

Seq. No.	49110
Seq. ID	pxt700942547.h1
Method	BLASTX
NCBI GI	g400350
BLAST score	150
E value	4.0e-10
Match length	77
% identity	40
NCBI Description	NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1) >gi_83347_pir__S23408 prematurely terminated mRNA decay factor NAM7 - yeast (Saccharomyces cerevisiae) >gi_4023_emb_CAA44266_ (X62394) helicase [Saccharomyces cerevisiae] >gi_173142 (M76659) zinc finger protein [Saccharomyces cerevisiae] >gi_807962_emb_CAA89226_ (Z49259) Nam7p [Saccharomyces cerevisiae]

Seq. No.	49111
Seq. ID	pxt700942549.h1
Method	BLASTX
NCBI GI	g1346882
BLAST score	141
E value	5.0e-09
Match length	67
% identity	49
NCBI Description	PHYTOENE SYNTHASE PRECURSOR (MEL5) >gi_2129505_pir__S56668 geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) precursor - muskmelon >gi_870985_emb_CAA85775_ (Z37543) phytoene synthase [Cucumis melo]

Seq. No.	49112
Seq. ID	pxt700942655.h1
Method	BLASTX
NCBI GI	g4249391
BLAST score	141
E value	6.0e-09
Match length	64
% identity	42
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	49113
Seq. ID	pxt700942679.h1
Method	BLASTN
NCBI GI	g11763
BLAST score	145
E value	5.0e-76
Match length	256
% identity	89
NCBI Description	N.rustica chloroplast atpB gene for ATPase subunit beta

Seq. No.	49114
Seq. ID	pxt700942707.h1
Method	BLASTX
NCBI GI	g2258317
BLAST score	108
E value	8.0e-09
Match length	75
% identity	45
NCBI Description	(AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]

Seq. No.	49115
Seq. ID	pxt700942725.h1
Method	BLASTN
NCBI GI	g4138678
BLAST score	123
E value	7.0e-63
Match length	262
% identity	87
NCBI Description	V.faba mRNA for amino acid transporter

Seq. No.	49116
Seq. ID	pxt700942808.h1
Method	BLASTN
NCBI GI	g18517
BLAST score	133
E value	6.0e-69
Match length	221
% identity	90
NCBI Description	Glycine max L. Merr mRNA for 4-coumarate:CoA ligase (clone 4CL14)

Seq. No.	49117
Seq. ID	pxt700942833.h1
Method	BLASTX
NCBI GI	g4544423
BLAST score	184
E value	9.0e-18
Match length	57
% identity	79
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49118
Seq. ID	pxt700942893.h1
Method	BLASTX
NCBI GI	g3367568
BLAST score	181
E value	7.0e-14
Match length	46
% identity	67
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	49119
Seq. ID	pxt700942939.h1
Method	BLASTX
NCBI GI	g4467124

BLAST score	205
E value	2.0e-16
Match length	58
% identity	66
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49120
Seq. ID	pxt700942962.h1
Method	BLASTX
NCBI GI	g1351408
BLAST score	162
E value	2.0e-11
Match length	84
% identity	46
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	49121
Seq. ID	pxt700942976.h1
Method	BLASTX
NCBI GI	g4559339
BLAST score	282
E value	1.0e-25
Match length	75
% identity	76
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	49122
Seq. ID	pxt700943042.h1
Method	BLASTX
NCBI GI	g4432867
BLAST score	254
E value	3.0e-22
Match length	91
% identity	52
NCBI Description	(AC006300) putative dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	49123
Seq. ID	pxt700943068.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	274
E value	1.0e-153
Match length	274
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	49124
Seq. ID	pxt700943089.h1
Method	BLASTX
NCBI GI	g2529675
BLAST score	231

E value	1.0e-19
Match length	48
% identity	88
NCBI Description	(AC002535) putative AP2 domain containing protein [Arabidopsis thaliana]

Seq. No.	49125
Seq. ID	pxt700943103.h1
Method	BLASTX
NCBI GI	g3970652
BLAST score	270
E value	4.0e-31
Match length	82
% identity	75
NCBI Description	(X77499) amino acid permease [Arabidopsis thaliana]

Seq. No.	49126
Seq. ID	pxt700943120.h1
Method	BLASTN
NCBI GI	g3746902
BLAST score	149
E value	2.0e-78
Match length	233
% identity	91
NCBI Description	Pisum sativum signal recognition particle 54 kDa subunit precursor (Ffc) mRNA, nuclear gene encoding chloroplast protein, partial cds

Seq. No.	49127
Seq. ID	pxt700943133.h1
Method	BLASTX
NCBI GI	g3738285
BLAST score	144
E value	2.0e-09
Match length	42
% identity	62
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	49128
Seq. ID	pxt700943175.h1
Method	BLASTX
NCBI GI	g3063457
BLAST score	251
E value	5.0e-22
Match length	62
% identity	69
NCBI Description	(AC003981) F22O13.19 [Arabidopsis thaliana]

Seq. No.	49129
Seq. ID	pxt700943187.h1
Method	BLASTX
NCBI GI	g3157941
BLAST score	153
E value	1.0e-13
Match length	78
% identity	39
NCBI Description	(AC002131) Contains similarity to hypothetical protein

gb_U95973 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	49130
Seq. ID	pxt700943196.h1
Method	BLASTX
NCBI GI	g3243234
BLAST score	167
E value	4.0e-12
Match length	58
% identity	59
NCBI Description	(AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No.	49131
Seq. ID	pxt700943234.h1
Method	BLASTX
NCBI GI	g2739044
BLAST score	199
E value	9.0e-16
Match length	50
% identity	72
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	49132
Seq. ID	pxt700943246.h1
Method	BLASTX
NCBI GI	g4006854
BLAST score	196
E value	8.0e-25
Match length	86
% identity	61
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	49133
Seq. ID	pxt700943249.h1
Method	BLASTN
NCBI GI	g21012
BLAST score	53
E value	4.0e-21
Match length	84
% identity	92
NCBI Description	Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase (GS,EC 6.3.1.2)

Seq. No.	49134
Seq. ID	pxt700943251.h1
Method	BLASTN
NCBI GI	g1928978
BLAST score	92
E value	2.0e-44
Match length	260
% identity	88
NCBI Description	Vigna unguiculata phospholipase D mRNA, complete cds

Seq. No.	49135
Seq. ID	pxt700943277.h1

Method	BLASTN
NCBI GI	g3982595
BLAST score	229
E value	1.0e-126
Match length	256
% identity	98
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	49136
Seq. ID	pxt700943352.h1
Method	BLASTX
NCBI GI	g2244997
BLAST score	146
E value	1.0e-09
Match length	48
% identity	56
NCBI Description	(Z97341) unnamed protein product [Arabidopsis thaliana]

Seq. No.	49137
Seq. ID	pxt700943363.h1
Method	BLASTN
NCBI GI	g310568
BLAST score	73
E value	4.0e-33
Match length	160
% identity	88
NCBI Description	Glycine max homeobox-containing (Sbh1) mRNA, complete cds

Seq. No.	49138
Seq. ID	pxt700943365.h1
Method	BLASTN
NCBI GI	g4234940
BLAST score	38
E value	3.0e-12
Match length	94
% identity	86
NCBI Description	Populus tremula x Populus tremuloides cytosolic phosphoglucomutase (pgm) mRNA, complete cds

Seq. No.	49139
Seq. ID	pxt700943382.h1
Method	BLASTX
NCBI GI	g1781334
BLAST score	153
E value	2.0e-10
Match length	44
% identity	64
NCBI Description	(Y10468) peroxidase [Spinacia oleracea]

Seq. No.	49140
Seq. ID	pxt700943404.h1
Method	BLASTX
NCBI GI	g4512624
BLAST score	200
E value	6.0e-16
Match length	77
% identity	57

NCBI Description	(AC004793) Strong similarity to gi_3033401 F19I3.29 putative potassium transporter from Arabidopsis thaliana BAC gb_AC004238
Seq. No.	49141
Seq. ID	pxt700943432.h1
Method	BLASTN
NCBI GI	g1781039
BLAST score	90
E value	3.0e-43
Match length	189
% identity	90
NCBI Description	M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase, P5CS-2
Seq. No.	49142
Seq. ID	pxt700943440.h1
Method	BLASTX
NCBI GI	g3834317
BLAST score	205
E value	2.0e-16
Match length	84
% identity	55
NCBI Description	(AC005679) Similar to CDC16 protein gb_U18291 (CDC16Hs) from Homo sapiens. [Arabidopsis thaliana]
Seq. No.	49143
Seq. ID	pxt700943447.h1
Method	BLASTX
NCBI GI	g2253010
BLAST score	308
E value	1.0e-28
Match length	79
% identity	71
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]
Seq. No.	49144
Seq. ID	pxt700943522.h1
Method	BLASTX
NCBI GI	g3688528
BLAST score	271
E value	3.0e-24
Match length	76
% identity	62
NCBI Description	(AJ004958) pre-pro-TPE4A protein [Pisum sativum]
Seq. No.	49145
Seq. ID	pxt700943528.h1
Method	BLASTX
NCBI GI	g4263527
BLAST score	283
E value	9.0e-26
Match length	87
% identity	39
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49146
Seq. ID	pxt700943531.h1
Method	BLASTX
NCBI GI	g3080396
BLAST score	340
E value	3.0e-32
Match length	84
% identity	70
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	49147
Seq. ID	pxt700943541.h1
Method	BLASTX
NCBI GI	g2465923
BLAST score	138
E value	1.0e-08
Match length	43
% identity	63
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	49148
Seq. ID	pxt700943602.h1
Method	BLASTX
NCBI GI	g2781362
BLAST score	190
E value	1.0e-14
Match length	86
% identity	47
NCBI Description	(AC003113) F24O1.18 [Arabidopsis thaliana]

Seq. No.	49149
Seq. ID	pxt700943643.h1
Method	BLASTX
NCBI GI	g2827555
BLAST score	341
E value	2.0e-32
Match length	85
% identity	41
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	49150
Seq. ID	pxt700943658.h1
Method	BLASTX
NCBI GI	g2828293
BLAST score	162
E value	2.0e-11
Match length	88
% identity	39
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	49151
Seq. ID	pxt700943671.h1
Method	BLASTN
NCBI GI	g870789
BLAST score	54

E value	1.0e-21
Match length	90
% identity	90
NCBI Description	{dinucleotide repeats, microsatellite marker} [Dryobalanops lanceolata, Genomic, 230 nt]

Seq. No.	49152
Seq. ID	pxt700943724.h1
Method	BLASTX
NCBI GI	g4097573
BLAST score	172
E value	1.0e-12
Match length	52
% identity	63
NCBI Description	(U64917) GMFP7 [Glycine max]

Seq. No.	49153
Seq. ID	pxt700943742.h1
Method	BLASTX
NCBI GI	g4417293
BLAST score	267
E value	7.0e-24
Match length	76
% identity	70
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	49154
Seq. ID	pxt700943788.h1
Method	BLASTN
NCBI GI	g1732468
BLAST score	92
E value	2.0e-44
Match length	92
% identity	100
NCBI Description	Soybean mRNA for Mg chelatase subunit (46 kD), complete cds

Seq. No.	49155
Seq. ID	pxt700943796.h1
Method	BLASTX
NCBI GI	g2739376
BLAST score	229
E value	2.0e-19
Match length	66
% identity	64
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	49156
Seq. ID	pxt700943843.h1
Method	BLASTX
NCBI GI	g3183088
BLAST score	146
E value	1.0e-09
Match length	58
% identity	53
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No.	49157
Seq. ID	pxt700943922.h1
Method	BLASTN
NCBI GI	g3204107
BLAST score	134
E value	2.0e-69
Match length	233
% identity	93
NCBI Description	Cicer arietinum mRNA for putative cytidine or deoxycytidylate deaminase, partial

Seq. No.	49158
Seq. ID	pxt700943934.h1
Method	BLASTN
NCBI GI	g18644
BLAST score	239
E value	1.0e-132
Match length	243
% identity	100
NCBI Description	Soybean mRNA for HMG-1 like protein

Seq. No.	49159
Seq. ID	pxt700943953.h1
Method	BLASTN
NCBI GI	g602564
BLAST score	43
E value	3.0e-15
Match length	123
% identity	84
NCBI Description	C.paradisi (Macf) INO1 gene

Seq. No.	49160
Seq. ID	pxt700943978.h1
Method	BLASTN
NCBI GI	g4220624
BLAST score	68
E value	3.0e-30
Match length	116
% identity	90
NCBI Description	Vicia faba VHA2 mRNA for p-type H+-ATPase, complete cds

Seq. No.	49161
Seq. ID	pxt700943986.h1
Method	BLASTX
NCBI GI	g2642165
BLAST score	159
E value	2.0e-11
Match length	40
% identity	60
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49162
Seq. ID	pxt700944018.h1
Method	BLASTX
NCBI GI	g4455221

BLAST score	248
E value	2.0e-21
Match length	87
% identity	57
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	49163
Seq. ID	pxt700944027.h1
Method	BLASTX
NCBI GI	g1420936
BLAST score	270
E value	4.0e-24
Match length	85
% identity	41
NCBI Description	(U61396) Vigna unguiculata aspartic proteinase mRNA, complete cds. [Vigna unguiculata]

Seq. No.	49164
Seq. ID	pxt700944056.h1
Method	BLASTX
NCBI GI	g587564
BLAST score	200
E value	2.0e-28
Match length	78
% identity	85
NCBI Description	(X80235) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	49165
Seq. ID	pxt700944072.h1
Method	BLASTX
NCBI GI	g4185511
BLAST score	315
E value	2.0e-29
Match length	69
% identity	87
NCBI Description	(AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No.	49166
Seq. ID	pxt700944090.h1
Method	BLASTN
NCBI GI	g3511284
BLAST score	76
E value	8.0e-35
Match length	214
% identity	86
NCBI Description	Populus alba x Populus tremula cellulose synthase (cel1) mRNA, complete cds

Seq. No.	49167
Seq. ID	pxt700944120.h1
Method	BLASTX
NCBI GI	g4557058
BLAST score	144
E value	2.0e-18
Match length	82

% identity	52
NCBI Description	(AC007154) aldehyde oxidase [Arabidopsis thaliana]

Seq. No.	49168
Seq. ID	pxt700944139.h1
Method	BLASTX
NCBI GI	g2459412
BLAST score	172
E value	1.0e-12
Match length	82
% identity	44
NCBI Description	(AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No.	49169
Seq. ID	pxt700944140.h1
Method	BLASTX
NCBI GI	g2213613
BLAST score	137
E value	1.0e-08
Match length	40
% identity	55
NCBI Description	(AC000103) F21J9.7 [Arabidopsis thaliana]

Seq. No.	49170
Seq. ID	pxt700944145.h1
Method	BLASTX
NCBI GI	g4193320
BLAST score	191
E value	6.0e-15
Match length	51
% identity	67
NCBI Description	(AF045473) histone deacetylase [Zea mays]

Seq. No.	49171
Seq. ID	pxt700944165.h1
Method	BLASTX
NCBI GI	g2062173
BLAST score	282
E value	1.0e-25
Match length	76
% identity	71
NCBI Description	(AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No.	49172
Seq. ID	pxt700944205.h1
Method	BLASTX
NCBI GI	g4530126
BLAST score	316
E value	2.0e-29
Match length	86
% identity	71
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	49173
Seq. ID	pxt700944241.h1

Method	BLASTN
NCBI GI	g829118
BLAST score	110
E value	4.0e-55
Match length	214
% identity	88
NCBI Description	P.vulgaris gene for cyclophilin

Seq. No.	49174
Seq. ID	pxt700944304.h1
Method	BLASTX
NCBI GI	g2462134
BLAST score	253
E value	4.0e-22
Match length	88
% identity	51
NCBI Description	(Y13368) reverse transcriptase [Beta vulgaris]

Seq. No.	49175
Seq. ID	pxt700944338.h1
Method	BLASTX
NCBI GI	g3292829
BLAST score	277
E value	6.0e-25
Match length	83
% identity	61
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	49176
Seq. ID	pxt700944348.h1
Method	BLASTX
NCBI GI	g3482924
BLAST score	140
E value	6.0e-09
Match length	69
% identity	45
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	49177
Seq. ID	pxt700944364.h1
Method	BLASTX
NCBI GI	g2154715
BLAST score	338
E value	4.0e-32
Match length	83
% identity	83
NCBI Description	(Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No.	49178
Seq. ID	pxt700944384.h1
Method	BLASTX
NCBI GI	g728905
BLAST score	178
E value	2.0e-13
Match length	82
% identity	46

NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi_171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi_595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]

Seq. No.	49179
Seq. ID	pxt700944422.h1
Method	BLASTX
NCBI GI	g2960069
BLAST score	244
E value	5.0e-21
Match length	88
% identity	53
NCBI Description	(Y12777) acyl-CoA synthetase-like protein [Homo sapiens]

Seq. No.	49180
Seq. ID	pxt700944430.h1
Method	BLASTX
NCBI GI	g1666096
BLAST score	207
E value	1.0e-16
Match length	86
% identity	49
NCBI Description	(Y09113) dioxygenase [Marah macrocarpus]

Seq. No.	49181
Seq. ID	pxt700944456.h1
Method	BLASTX
NCBI GI	g3935185
BLAST score	174
E value	1.0e-22
Match length	83
% identity	70
NCBI Description	(AC004557) F17L21.28 [Arabidopsis thaliana]

Seq. No.	49182
Seq. ID	pxt700944562.h1
Method	BLASTX
NCBI GI	g3395436
BLAST score	183
E value	4.0e-14
Match length	51
% identity	73
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	49183
Seq. ID	pxt700944591.h1
Method	BLASTX
NCBI GI	g3757515
BLAST score	156
E value	9.0e-11
Match length	63
% identity	49
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49184
Seq. ID	pxt700944596.h1
Method	BLASTX
NCBI GI	g2104951
BLAST score	270
E value	4.0e-24
Match length	76
% identity	71
NCBI Description	(U96717) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	49185
Seq. ID	pxt700944612.h1
Method	BLASTX
NCBI GI	g2323344
BLAST score	354
E value	5.0e-34
Match length	84
% identity	76
NCBI Description	(AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]

Seq. No.	49186
Seq. ID	pxt700944648.h1
Method	BLASTN
NCBI GI	g516853
BLAST score	250
E value	1.0e-138
Match length	250
% identity	31
NCBI Description	Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No.	49187
Seq. ID	pxt700944656.h1
Method	BLASTX
NCBI GI	g3252866
BLAST score	266
E value	1.0e-23
Match length	83
% identity	64
NCBI Description	(AF033535) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	49188
Seq. ID	pxt700944661.h1
Method	BLASTX
NCBI GI	g3885328
BLAST score	137
E value	2.0e-10
Match length	73
% identity	49
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	49189
Seq. ID	pxt700944715.h1
Method	BLASTN
NCBI GI	g255572
BLAST score	90

E value	3.0e-43
Match length	199
% identity	90
NCBI Description	small auxin up RNA gene cluster: orf 15A [Glycine max=soybeans, cv. Wayne, Genomic, 637 nt]

Seq. No.	49190
Seq. ID	pxt700944744.h1
Method	BLASTX
NCBI GI	g4263792
BLAST score	167
E value	4.0e-12
Match length	72
% identity	81
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	49191
Seq. ID	pxt700944785.h1
Method	BLASTX
NCBI GI	g3273757
BLAST score	355
E value	4.0e-34
Match length	83
% identity	69
NCBI Description	(AF061852) iron superoxide dismutase 3 [Arabidopsis thaliana]

Seq. No.	49192
Seq. ID	pxt700944842.h1
Method	BLASTN
NCBI GI	g463251
BLAST score	87
E value	2.0e-41
Match length	155
% identity	89
NCBI Description	M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5

Seq. No.	49193
Seq. ID	pxt700944855.h1
Method	BLASTX
NCBI GI	g3850566
BLAST score	192
E value	6.0e-15
Match length	49
% identity	67
NCBI Description	(AC005278) F15K9.3 [Arabidopsis thaliana]

Seq. No.	49194
Seq. ID	pxt700944873.h1
Method	BLASTX
NCBI GI	g1673406
BLAST score	235
E value	5.0e-20
Match length	68
% identity	63
NCBI Description	(X91491) Xanthophyll epoxidase [Capsicum annuum]

Seq. No.	49195
Seq. ID	pxt700944877.h1
Method	BLASTN
NCBI GI	g20412
BLAST score	82
E value	2.0e-38
Match length	162
% identity	88
NCBI Description	P.amygdalus mRNA for alpha-tubulin

Seq. No.	49196
Seq. ID	pxt700944893.h1
Method	BLASTX
NCBI GI	g2853078
BLAST score	149
E value	3.0e-10
Match length	68
% identity	31
NCBI Description	(AL021768) TMV resistance protein N-like [Arabidopsis thaliana]

Seq. No.	49197
Seq. ID	pxt700944921.h1
Method	BLASTN
NCBI GI	g1566699
BLAST score	34
E value	9.0e-10
Match length	42
% identity	95
NCBI Description	C.papaya mRNA for metallothionein-like protein

Seq. No.	49198
Seq. ID	pxt700944935.h1
Method	BLASTN
NCBI GI	g1370143
BLAST score	40
E value	2.0e-13
Match length	44
% identity	98
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAB11B

Seq. No.	49199
Seq. ID	pxt700944955.h1
Method	BLASTX
NCBI GI	g4115337
BLAST score	288
E value	3.0e-26
Match length	85
% identity	12
NCBI Description	(L81141) ubiquitin [Pisum sativum]

Seq. No.	49200
Seq. ID	pxt700945028.h1
Method	BLASTX
NCBI GI	g4263827
BLAST score	116
E value	3.0e-11

Match length	80
% identity	47
NCBI Description	(AC006067) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	49201
Seq. ID	pxt700945051.h1
Method	BLASTN
NCBI GI	g710433
BLAST score	40
E value	2.0e-13
Match length	196
% identity	83
NCBI Description	Glycine max low molecular weight heat shock protein Hsp22.3 (Gmhsp22.3) mRNA, complete cds

Seq. No.	49202
Seq. ID	pxt700945076.h1
Method	BLASTX
NCBI GI	g3776573
BLAST score	215
E value	8.0e-30
Match length	85
% identity	85
NCBI Description	(AC005388) Similar to nodulins and lipase homolog F14J9.5 gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis thaliana]

Seq. No.	49203
Seq. ID	pxt700945079.h1
Method	BLASTX
NCBI GI	g3258569
BLAST score	196
E value	2.0e-15
Match length	60
% identity	62
NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	49204
Seq. ID	pxt700945129.h1
Method	BLASTX
NCBI GI	g3668089
BLAST score	169
E value	7.0e-19
Match length	76
% identity	65
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	49205
Seq. ID	pxt700945149.h1
Method	BLASTN
NCBI GI	g310568
BLAST score	193
E value	1.0e-104
Match length	227

% identity	97
NCBI Description	Glycine max homeobox-containing (Sbh1) mRNA, complete cds

Seq. No.	49206
Seq. ID	pxt700945181.h1
Method	BLASTX
NCBI GI	g3135992
BLAST score	189
E value	1.0e-20
Match length	56
% identity	80
NCBI Description	(AL023589) histone deacetylase [Schizosaccharomyces pombe] >gi_4159997 (AF064206) putative histone deacetylase [Schizosaccharomyces pombe]

Seq. No.	49207
Seq. ID	pxt700945211.h1
Method	BLASTX
NCBI GI	g2851508
BLAST score	151
E value	8.0e-15
Match length	64
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	49208
Seq. ID	pxt700945223.h1
Method	BLASTX
NCBI GI	g2804280
BLAST score	455
E value	8.0e-46
Match length	87
% identity	87
NCBI Description	(AB003687) 6-4 photolyase [Arabidopsis thaliana] >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase [Arabidopsis thaliana]

Seq. No.	49209
Seq. ID	pxt700945293.h1
Method	BLASTX
NCBI GI	g4033838
BLAST score	163
E value	1.0e-11
Match length	56
% identity	55
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No.	49210
Seq. ID	pxt700945316.h1
Method	BLASTX
NCBI GI	g1865677
BLAST score	353
E value	7.0e-34

Match length	87
% identity	77
NCBI Description	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	49211
Seq. ID	pxt700945325.h1
Method	BLASTX
NCBI GI	g4415917
BLAST score	335
E value	1.0e-31
Match length	88
% identity	47
NCBI Description	(AC006282) putative protein containing zinc finger domain [Arabidopsis thaliana]

Seq. No.	49212
Seq. ID	pxt700945336.h1
Method	BLASTX
NCBI GI	g3258576
BLAST score	134
E value	1.0e-10
Match length	41
% identity	70
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	49213
Seq. ID	pxt700945352.h1
Method	BLASTN
NCBI GI	g2905771
BLAST score	144
E value	2.0e-75
Match length	156
% identity	98
NCBI Description	Glycine max glyceraldehyde-3 phosphate dehydrogenase (GAPDH) mRNA, partial cds

Seq. No.	49214
Seq. ID	pxt700945387.h1
Method	BLASTN
NCBI GI	g2267582
BLAST score	76
E value	8.0e-35
Match length	172
% identity	86
NCBI Description	Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA, complete cds

Seq. No.	49215
Seq. ID	pxt700945408.h1
Method	BLASTX
NCBI GI	g4204095
BLAST score	253
E value	4.0e-22
Match length	86
% identity	55
NCBI Description	(AF030260) CYP94A1 [Vicia sativa]

Seq. No.	49216
Seq. ID	pxt700945417.h1
Method	BLASTN
NCBI GI	g3128139
BLAST score	41
E value	6.0e-14
Match length	118
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No.	49217
Seq. ID	pxt700945433.h1
Method	BLASTN
NCBI GI	g4324966
BLAST score	51
E value	7.0e-20
Match length	135
% identity	84
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No.	49218
Seq. ID	pxt700945441.h1
Method	BLASTX
NCBI GI	g4218122
BLAST score	162
E value	1.0e-11
Match length	51
% identity	75
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	49219
Seq. ID	pxt700945445.h1
Method	BLASTN
NCBI GI	g602564
BLAST score	49
E value	9.0e-19
Match length	129
% identity	84
NCBI Description	C.paradisi (Macf) INO1 gene

Seq. No.	49220
Seq. ID	pxt700945471.h1
Method	BLASTX
NCBI GI	g2435522
BLAST score	201
E value	3.0e-16
Match length	56
% identity	59
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	49221
Seq. ID	pxt700945481.h1
Method	BLASTN
NCBI GI	g2827081

BLAST score	78
E value	5.0e-36
Match length	138
% identity	89
NCBI Description	Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA, complete cds

Seq. No.	49222
Seq. ID	pxt700945491.h1
Method	BLASTX
NCBI GI	g3738339
BLAST score	338
E value	3.0e-32
Match length	78
% identity	81
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	49223
Seq. ID	pxt700945552.h1
Method	BLASTX
NCBI GI	g4220535
BLAST score	144
E value	1.0e-09
Match length	34
% identity	82
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	49224
Seq. ID	pxt700945587.h1
Method	BLASTX
NCBI GI	g1565223
BLAST score	254
E value	3.0e-22
Match length	88
% identity	58
NCBI Description	(Y08301) MCM2-related protein [Arabidopsis thaliana]

Seq. No.	49225
Seq. ID	pxt700945606.h1
Method	BLASTX
NCBI GI	g4539314
BLAST score	171
E value	2.0e-12
Match length	49
% identity	63
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	49226
Seq. ID	pxt700945692.h1
Method	BLASTX
NCBI GI	g3914468
BLAST score	99
E value	5.0e-09
Match length	33
% identity	89
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

>gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot
>gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus carota]

Seq. No.	49227
Seq. ID	pxt700945750.h1
Method	BLASTX
NCBI GI	g4406759
BLAST score	266
E value	1.0e-23
Match length	67
% identity	79
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49228
Seq. ID	pxt700945790.h1
Method	BLASTN
NCBI GI	g11957
BLAST score	47
E value	2.0e-17
Match length	67
% identity	46
NCBI Description	Rice complete chloroplast genome

Seq. No.	49229
Seq. ID	pxt700945796.h1
Method	BLASTX
NCBI GI	g2444174
BLAST score	353
E value	7.0e-34
Match length	81
% identity	84
NCBI Description	(U94781) unconventional myosin [Helianthus annuus]

Seq. No.	49230
Seq. ID	pxt700945803.h1
Method	BLASTN
NCBI GI	g3413472
BLAST score	91
E value	7.0e-44
Match length	170
% identity	89
NCBI Description	Glycine max mRNA for tyrosine phosphatase

Seq. No.	49231
Seq. ID	pxt700945834.h1
Method	BLASTX
NCBI GI	g3355490
BLAST score	150
E value	3.0e-10
Match length	59
% identity	54
NCBI Description	(AC004218) putative dolichyl-phosphate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	49232
Seq. ID	pxt700945845.h1

Method	BLASTN
NCBI GI	g166915
BLAST score	54
E value	6.0e-22
Match length	78
% identity	92
NCBI Description	Arabidopsis thaliana alpha-4 tubulin (TUA4) gene, complete cds

Seq. No.	49233
Seq. ID	pxt700945858.h1
Method	BLASTX
NCBI GI	g3415115
BLAST score	184
E value	4.0e-16
Match length	73
% identity	64
NCBI Description	(AF081202) villin 2 [Arabidopsis thaliana]

Seq. No.	49234
Seq. ID	pxt700945889.h1
Method	BLASTX
NCBI GI	g3142291
BLAST score	249
E value	7.0e-22
Match length	61
% identity	67
NCBI Description	(AC002411) Contains similarity to adenylate cyclase gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes from this gene. [Arabidopsis thaliana]

Seq. No.	49235
Seq. ID	pxt700945902.h1
Method	BLASTX
NCBI GI	g4249380
BLAST score	155
E value	1.0e-10
Match length	69
% identity	54
NCBI Description	(AC005966) ESTs gb_Z37637, gb_AA042498 and gb_AA042269 come from this gene. [Arabidopsis thaliana]

Seq. No.	49236
Seq. ID	pxt700945913.h1
Method	BLASTX
NCBI GI	g3176691
BLAST score	202
E value	4.0e-16
Match length	80
% identity	59
NCBI Description	(AC003671) Contains homology to serine/threonine protein kinase gb_X99618 from Mycobacterium tuberculosis. ESTs gb_F14403, gb_F14404, and gb_N96730 come from this gene. [Arabidopsis thaliana]

Seq. No.	49237
Seq. ID	pxt700945924.h1

Method	BLASTN
NCBI GI	g510545
BLAST score	157
E value	3.0e-83
Match length	249
% identity	91
NCBI Description	P.sativum mRNA for starch branching enzyme I

Seq. No.	49238
Seq. ID	pxt700945988.h1
Method	BLASTX
NCBI GI	g4455356
BLAST score	241
E value	9.0e-21
Match length	80
% identity	56
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	49239
Seq. ID	pxt700946025.h1
Method	BLASTX
NCBI GI	g4204310
BLAST score	283
E value	1.0e-25
Match length	68
% identity	78
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	49240
Seq. ID	pxt700946026.h1
Method	BLASTX
NCBI GI	g2129473
BLAST score	154
E value	1.0e-10
Match length	79
% identity	38
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	49241
Seq. ID	pxt700946049.h1
Method	BLASTX
NCBI GI	g1707019
BLAST score	167
E value	4.0e-12
Match length	54
% identity	59
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49242
Seq. ID	pxt700946051.h1
Method	BLASTX
NCBI GI	g2245005
BLAST score	140
E value	7.0e-09
Match length	83

% identity	45
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49243
Seq. ID	pxt700946094.h1
Method	BLASTX
NCBI GI	g3786011
BLAST score	294
E value	5.0e-27
Match length	77
% identity	78
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	49244
Seq. ID	pxt700946119.h1
Method	BLASTX
NCBI GI	g3108209
BLAST score	149
E value	8.0e-19
Match length	55
% identity	82
NCBI Description	(AF028809) eukaryotic cap-binding protein [Arabidopsis thaliana]

Seq. No.	49245
Seq. ID	pxt700946207.h1
Method	BLASTN
NCBI GI	g3449326
BLAST score	34
E value	9.0e-10
Match length	74
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	49246
Seq. ID	pxt700946220.h1
Method	BLASTX
NCBI GI	g2253579
BLAST score	181
E value	1.0e-13
Match length	77
% identity	53
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49247
Seq. ID	pxt700946227.h1
Method	BLASTN
NCBI GI	g4098318
BLAST score	134
E value	2.0e-69
Match length	262
% identity	88
NCBI Description	Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds

Seq. No.	49248

Seq. ID	pxt700946261.h1
Method	BLASTX
NCBI GI	g2801555
BLAST score	170
E value	2.0e-12
Match length	84
% identity	40
NCBI Description	(AF042169) putative ATP-dependent mitochondrial RNA helicase [Homo sapiens] >gi_4507315_ref_NP_003162.1_pSUPV3L1_ suppressor of var1 (S.cerevisiae) 3-like

Seq. No.	49249
Seq. ID	pxt700946283.h1
Method	BLASTN
NCBI GI	g1944341
BLAST score	43
E value	4.0e-15
Match length	87
% identity	93
NCBI Description	Glycine max DNA for cysteine proteinase inhibitor, complete cds

Seq. No.	49250
Seq. ID	pxt700946357.h1
Method	BLASTX
NCBI GI	g2833378
BLAST score	156
E value	8.0e-11
Match length	83
% identity	43
NCBI Description	HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis thaliana] >gi_1582383_prf__2118367A hexokinase [Arabidopsis thaliana]

Seq. No.	49251
Seq. ID	pxt700946369.h1
Method	BLASTX
NCBI GI	g481812
BLAST score	188
E value	9.0e-15
Match length	66
% identity	28
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	49252
Seq. ID	pxt700946384.h1
Method	BLASTX
NCBI GI	g4263771
BLAST score	163
E value	1.0e-11
Match length	36
% identity	78
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	49253
Seq. ID	pxt700946402.h1
Method	BLASTN
NCBI GI	g4097568
BLAST score	60
E value	3.0e-25
Match length	194
% identity	83
NCBI Description	Glycine max farnesylated protein GMFP4 mRNA, partial cds

Seq. No.	49254
Seq. ID	pxt700946451.h1
Method	BLASTX
NCBI GI	g294845
BLAST score	183
E value	5.0e-14
Match length	62
% identity	53
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	49255
Seq. ID	pxt700946469.h1
Method	BLASTX
NCBI GI	g4508082
BLAST score	187
E value	2.0e-14
Match length	36
% identity	89
NCBI Description	(AC005882) Putative RNA polymerase II subunit Rpb10 [Arabidopsis thaliana]

Seq. No.	49256
Seq. ID	rca700995962.h1
Method	BLASTX
NCBI GI	g3776559
BLAST score	254
E value	3.0e-22
Match length	58
% identity	81
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	49257
Seq. ID	rca700995970.h1
Method	BLASTX
NCBI GI	g4106388
BLAST score	171
E value	9.0e-13
Match length	54
% identity	63
NCBI Description	(AF074849) unknown [Arabidopsis thaliana]

Seq. No.	49258

Seq. ID	rca700996005.h1
Method	BLASTN
NCBI GI	g17668
BLAST score	54
E value	1.0e-21
Match length	126
% identity	86
NCBI Description	A.thaliana mRNA for U2 SnRNP-specific A'protein

Seq. No.	49259
Seq. ID	rca700996012.h1
Method	BLASTX
NCBI GI	g3914006
BLAST score	402
E value	1.0e-39
Match length	89
% identity	85
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588 (U85495) LON2 [Zea mays]

Seq. No.	49260
Seq. ID	rca700996050.h1
Method	BLASTN
NCBI GI	g19183
BLAST score	53
E value	4.0e-21
Match length	129
% identity	86
NCBI Description	L.esculentum Cab9 gene for type I (26 kD) CP29 polypeptide

Seq. No.	49261
Seq. ID	rca700996071.h1
Method	BLASTX
NCBI GI	g134886
BLAST score	140
E value	6.0e-13
Match length	75
% identity	51
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN (SRP54) >gi_54194_emb_CAA34386_ (X16319) SRP 54K subunit (AA 1-504) [Mus musculus]

Seq. No.	49262
Seq. ID	rca700996113.h1
Method	BLASTX
NCBI GI	g4204697
BLAST score	167
E value	5.0e-12
Match length	36
% identity	86
NCBI Description	(AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]

Seq. No.	49263
Seq. ID	rca700996142.h1
Method	BLASTN
NCBI GI	g4406529

BLAST score	228
E value	1.0e-125
Match length	272
% identity	96
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	49264
Seq. ID	rca700996155.h1
Method	BLASTX
NCBI GI	g3913640
BLAST score	307
E value	2.0e-28
Match length	66
% identity	89
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041775_dbj_BAA25422_ (AB007193) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	49265
Seq. ID	rca700996224.h1
Method	BLASTN
NCBI GI	g4490717
BLAST score	64
E value	1.0e-27
Match length	116
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	49266
Seq. ID	rca700996273.h1
Method	BLASTX
NCBI GI	g2959767
BLAST score	177
E value	2.0e-13
Match length	50
% identity	74
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	49267
Seq. ID	rca700996282.h1
Method	BLASTX
NCBI GI	g3201617
BLAST score	241
E value	8.0e-21
Match length	78
% identity	54
NCBI Description	(AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49268
Seq. ID	rca700996316.h1
Method	BLASTX
NCBI GI	g1168328

BLAST score	141
E value	3.0e-20
Match length	80
% identity	61
NCBI Description	ACTIN-LIKE PROTEIN 3 >gi_629878_pir__S48844 actin-like protein - slime mold (Dictyostelium discoideum) >gi_2130164_pir__S69002 actin-like protein - slime mold (Dictyostelium discoideum) >gi_563346_emb_CAA86553_ (Z46418) actin-like protein [Dictyostelium discoideum]

Seq. No.	49269
Seq. ID	rca700996330.h1
Method	BLASTX
NCBI GI	g3688173
BLAST score	259
E value	4.0e-23
Match length	68
% identity	66
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	49270
Seq. ID	rca700996334.h1
Method	BLASTX
NCBI GI	g4454465
BLAST score	218
E value	5.0e-18
Match length	61
% identity	67
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	49271
Seq. ID	rca700996336.h1
Method	BLASTX
NCBI GI	g3746059
BLAST score	185
E value	4.0e-14
Match length	48
% identity	75
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	49272
Seq. ID	rca700996367.h1
Method	BLASTX
NCBI GI	g2642450
BLAST score	271
E value	5.0e-26
Match length	81
% identity	79
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	49273
Seq. ID	rca700996391.h1
Method	BLASTN

NCBI GI	g1277163
BLAST score	233
E value	1.0e-128
Match length	233
% identity	100
NCBI Description	Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No.	49274
Seq. ID	rca700996413.h1
Method	BLASTX
NCBI GI	g464769
BLAST score	179
E value	2.0e-13
Match length	82
% identity	49
NCBI Description	SUPEROXIDE DISMUTASE (CU-ZN) >gi_477155_pir__A48256 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Caenorhabditis elegans >gi_416350 (L20135) superoxide dismutase [Caenorhabditis elegans] >gi_441278_emb_CAA54318_ (X77020) copper/zinc superoxide dismutase [Caenorhabditis elegans]

Seq. No.	49275
Seq. ID	rca700996504.h1
Method	BLASTX
NCBI GI	g2688828
BLAST score	196
E value	2.0e-15
Match length	76
% identity	45
NCBI Description	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No.	49276
Seq. ID	rca700996526.h1
Method	BLASTX
NCBI GI	g3164126
BLAST score	202
E value	4.0e-16
Match length	85
% identity	44
NCBI Description	(D78598) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	49277
Seq. ID	rca700996769.h1
Method	BLASTX
NCBI GI	g1705884
BLAST score	157
E value	7.0e-11
Match length	62
% identity	44
NCBI Description	PROBABLE CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi_1204243_emb_CAA93616_ (Z69731) unknown [Schizosaccharomyces pombe]

Seq. No.	49278
Seq. ID	rca700996772.h1

Method	BLASTN
NCBI GI	g18551
BLAST score	198
E value	1.0e-107
Match length	226
% identity	97
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	49279
Seq. ID	rca700996901.h1
Method	BLASTX
NCBI GI	g3152608
BLAST score	136
E value	1.0e-08
Match length	35
% identity	74
NCBI Description	(AC004482) putative BEL1-like homeotic protein [Arabidopsis thaliana]

Seq. No.	49280
Seq. ID	rca700996914.h1
Method	BLASTX
NCBI GI	g1707015
BLAST score	155
E value	2.0e-14
Match length	84
% identity	48
NCBI Description	(U78721) protein phosphatase 2C isolog [Arabidopsis thaliana]

Seq. No.	49281
Seq. ID	rca700996978.h1
Method	BLASTN
NCBI GI	g4220644
BLAST score	38
E value	4.0e-12
Match length	70
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	49282
Seq. ID	rca700997001.h1
Method	BLASTX
NCBI GI	g4567197
BLAST score	174
E value	4.0e-13
Match length	65
% identity	42
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	49283
Seq. ID	rca700997024.h1
Method	BLASTX
NCBI GI	g3785975
BLAST score	136

E value	1.0e-08
Match length	49
% identity	35
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49284
Seq. ID	rca700997039.h1
Method	BLASTX
NCBI GI	g1707015
BLAST score	319
E value	4.0e-30
Match length	67
% identity	88
NCBI Description	(U78721) protein phosphatase 2C isolog [Arabidopsis thaliana]

Seq. No.	49285
Seq. ID	rca700997058.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	120
E value	3.0e-61
Match length	184
% identity	92
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	49286
Seq. ID	rca700997072.h1
Method	BLASTN
NCBI GI	g217908
BLAST score	51
E value	5.0e-20
Match length	83
% identity	90
NCBI Description	Pumpkin mRNA for glycolate oxidase, complete cds

Seq. No.	49287
Seq. ID	rca700997082.h1
Method	BLASTX
NCBI GI	g3335374
BLAST score	190
E value	7.0e-15
Match length	65
% identity	61
NCBI Description	(AC003028) glutaredoxin-like protein [Arabidopsis thaliana]

Seq. No.	49288
Seq. ID	rca700997096.h1
Method	BLASTX
NCBI GI	g4376203
BLAST score	196
E value	1.0e-15
Match length	70
% identity	46
NCBI Description	(U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]

Seq. No.	49289
Seq. ID	rca700997157.h1
Method	BLASTX
NCBI GI	g2827530
BLAST score	136
E value	3.0e-12
Match length	48
% identity	67
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	49290
Seq. ID	rca700997170.h1
Method	BLASTN
NCBI GI	g20740
BLAST score	115
E value	4.0e-58
Match length	218
% identity	92
NCBI Description	Pisum sativum mRNA for P protein, a part of glycine cleavage complex

Seq. No.	49291
Seq. ID	rca700997216.h1
Method	BLASTN
NCBI GI	g609174
BLAST score	49
E value	5.0e-19
Match length	97
% identity	88
NCBI Description	N.rustica mRNA for cathepsin B-like cysteine proteinase

Seq. No.	49292
Seq. ID	rca700997227.h1
Method	BLASTX
NCBI GI	g1653033
BLAST score	279
E value	3.0e-25
Match length	82
% identity	63
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	49293
Seq. ID	rca700997324.h1
Method	BLASTX
NCBI GI	g3249068
BLAST score	175
E value	6.0e-13
Match length	80
% identity	50
NCBI Description	(AC004473) Contains similarity to zinc-binding protein (PWA33) gb_L04190 from Pleurodeles waltlii. [Arabidopsis thaliana]

Seq. No.	49294
Seq. ID	rca700997350.h1
Method	BLASTX
NCBI GI	g2760326

BLAST score	235
E value	5.0e-20
Match length	79
% identity	52
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	49295
Seq. ID	rca700997362.h1
Method	BLASTX
NCBI GI	g2674203
BLAST score	338
E value	4.0e-32
Match length	83
% identity	77
NCBI Description	(AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No.	49296
Seq. ID	rca700997368.h1
Method	BLASTX
NCBI GI	g585880
BLAST score	145
E value	1.0e-09
Match length	44
% identity	66
NCBI Description	60S RIBOSOMAL PROTEIN L2A (RP2) >gi_625514_pir__S45887 ribosomal protein L4.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_498759_emb_CAA53687_ (X76078) ribosomal protein L2B [Saccharomyces cerevisiae] >gi_536244_emb_CAA84973_ (Z35900) ORF YBR031w [Saccharomyces cerevisiae] >gi_1587588_prf__2206497L ribosomal protein L2B [Saccharomyces cerevisiae]

Seq. No.	49297
Seq. ID	rca700997386.h1
Method	BLASTN
NCBI GI	g1066160
BLAST score	33
E value	3.0e-09
Match length	37
% identity	97
NCBI Description	Wheat gene for protein H2B153, complete cds

Seq. No.	49298
Seq. ID	rca700997416.h1
Method	BLASTN
NCBI GI	g2924257
BLAST score	61
E value	5.0e-26
Match length	105
% identity	90
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	49299
Seq. ID	rca700997469.h1
Method	BLASTX
NCBI GI	g4455203

BLAST score 142
E value 2.0e-09
Match length 73
% identity 5
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 49300
Seq. ID rca700997484.h1
Method BLASTX
NCBI GI g4454470
BLAST score 161
E value 2.0e-11
Match length 57
% identity 54
NCBI Description (AC006234) putative sugar transporter [Arabidopsis thaliana]

Seq. No. 49301
Seq. ID rca700997493.h1
Method BLASTX
NCBI GI g4056503
BLAST score 146
E value 8.0e-10
Match length 34
% identity 82
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 49302
Seq. ID rca700997539.h1
Method BLASTX
NCBI GI g2316016
BLAST score 159
E value 4.0e-11
Match length 55
% identity 56
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 49303
Seq. ID rca700997546.h1
Method BLASTX
NCBI GI g3868814
BLAST score 154
E value 2.0e-10
Match length 79
% identity 37
NCBI Description (AB013718) SRK46Bra [Brassica rapa]

Seq. No. 49304
Seq. ID rca700997582.h1
Method BLASTX
NCBI GI g4185139
BLAST score 284
E value 9.0e-26
Match length 86
% identity 63
NCBI Description (AC005724) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	49305
Seq. ID	rca700997588.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	221
E value	2.0e-18
Match length	76
% identity	55
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	49306
Seq. ID	rca700997682.h1
Method	BLASTX
NCBI GI	g4249391
BLAST score	180
E value	8.0e-14
Match length	58
% identity	50
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	49307
Seq. ID	rca700997693.h1
Method	BLASTX
NCBI GI	g4559351
BLAST score	129
E value	1.0e-09
Match length	70
% identity	53
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49308
Seq. ID	rca700997709.h1
Method	BLASTX
NCBI GI	g1752734
BLAST score	400
E value	3.0e-39
Match length	92
% identity	77
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	49309
Seq. ID	rca700997713.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	50
E value	3.0e-19
Match length	70
% identity	93
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	49310
Seq. ID	rca700997803.h1
Method	BLASTX
NCBI GI	g3335378

BLAST score	321
E value	5.0e-30
Match length	80
% identity	76
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	49311
Seq. ID	rca700997806.h1
Method	BLASTX
NCBI GI	g4432821
BLAST score	138
E value	7.0e-09
Match length	48
% identity	62
NCBI Description	(AC006593) putative transmembrane protein [Arabidopsis thaliana]

Seq. No.	49312
Seq. ID	rca700997868.h1
Method	BLASTX
NCBI GI	g2781357
BLAST score	249
E value	1.0e-21
Match length	87
% identity	54
NCBI Description	(AC003113) F24O1.13 [Arabidopsis thaliana]

Seq. No.	49313
Seq. ID	rca700997934.h1
Method	BLASTX
NCBI GI	g3402715
BLAST score	141
E value	4.0e-09
Match length	60
% identity	29
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	49314
Seq. ID	rca700997963.h1
Method	BLASTX
NCBI GI	g2827661
BLAST score	190
E value	7.0e-15
Match length	76
% identity	55
NCBI Description	(AL021637) hyuC-like protein [Arabidopsis thaliana]

Seq. No.	49315
Seq. ID	rca700997972.h1
Method	BLASTX
NCBI GI	g2632252
BLAST score	121
E value	1.0e-08
Match length	45
% identity	73
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	49316
Seq. ID	rca700997992.h1
Method	BLASTN
NCBI GI	g510545
BLAST score	138
E value	8.0e-72
Match length	269
% identity	89
NCBI Description	P.sativum mRNA for starch branching enzyme I

Seq. No.	49317
Seq. ID	rca700998057.h1
Method	BLASTX
NCBI GI	g2661840
BLAST score	159
E value	2.0e-11
Match length	41
% identity	78
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	49318
Seq. ID	rca700998077.h1
Method	BLASTX
NCBI GI	g3341679
BLAST score	111
E value	7.0e-11
Match length	46
% identity	80
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	49319
Seq. ID	rca700998118.h1
Method	BLASTX
NCBI GI	g1351711
BLAST score	226
E value	2.0e-19
Match length	69
% identity	72
NCBI Description	HYPOTHETICAL 143.7 KD PROTEIN C11D3.15 IN CHROMOSOME I >gi_1107904_emb_CAA92316_ (Z68166) unknown [Schizosaccharomyces pombe]

Seq. No.	49320
Seq. ID	rca700998130.h1
Method	BLASTN
NCBI GI	g1150683
BLAST score	58
E value	3.0e-24
Match length	102
% identity	89
NCBI Description	V.radiata atpB, rbcL and trnK genes

Seq. No.	49321
Seq. ID	rca700998163.h1
Method	BLASTX

NCBI GI	g2911067
BLAST score	435
E value	2.0e-43
Match length	91
% identity	90
NCBI Description	(AL021960) UV-damaged DNA-binding protein- like [Arabidopsis thaliana]

Seq. No.	49322
Seq. ID	rca700998265.h1
Method	BLASTN
NCBI GI	g3881977
BLAST score	58
E value	4.0e-24
Match length	169
% identity	85
NCBI Description	M.sativa mRNA for annexin-like protein

Seq. No.	49323
Seq. ID	rca700998274.h1
Method	BLASTX
NCBI GI	g4099833
BLAST score	165
E value	2.0e-22
Match length	78
% identity	60
NCBI Description	(U90265) bifunctional nuclease [Zinnia elegans]

Seq. No.	49324
Seq. ID	rca700998280.h1
Method	BLASTX
NCBI GI	g1096035
BLAST score	195
E value	5.0e-28
Match length	85
% identity	65
NCBI Description	ribosomal protein S7 [Tetrahymena thermophila]

Seq. No.	49325
Seq. ID	rca700998283.h1
Method	BLASTX
NCBI GI	g114290
BLAST score	112
E value	9.0e-14
Match length	59
% identity	68
NCBI Description	ARGININOSUCCINATE SYNTHASE (CITRULLINE--ASPARTATE LIGASE) >gi_68638_pir__AJMSRS argininosuccinate synthase (EC 6.3.4.5) - mouse >gi_309111 (M31690) argininosuccinate synthetase (EC 6.3.4.5) [Mus musculus]

Seq. No.	49326
Seq. ID	rca700998290.h1
Method	BLASTX
NCBI GI	g4572669
BLAST score	320
E value	1.0e-30

Match length	85
% identity	76
NCBI Description	(AC006954) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	49327
Seq. ID	rca700998339.h1
Method	BLASTX
NCBI GI	g3914002
BLAST score	241
E value	6.0e-21
Match length	56
% identity	82
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	49328
Seq. ID	rca700998341.h1
Method	BLASTX
NCBI GI	g999441
BLAST score	222
E value	8.0e-20
Match length	55
% identity	93
NCBI Description	(X86221) lycopene synthase [Capsicum annuum]

Seq. No.	49329
Seq. ID	rca700998509.h1
Method	BLASTX
NCBI GI	g4200122
BLAST score	200
E value	4.0e-16
Match length	65
% identity	54
NCBI Description	(AJ009555) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49330
Seq. ID	rca700998529.h1
Method	BLASTN
NCBI GI	g516853
BLAST score	154
E value	2.0e-81
Match length	218
% identity	33
NCBI Description	Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No.	49331
Seq. ID	rca700998545.h1
Method	BLASTX
NCBI GI	g3757888
BLAST score	226
E value	5.0e-19
Match length	70
% identity	67
NCBI Description	(AF072865) thioredoxin reductase [Rattus norvegicus]

Seq. No. 49332

Seq. ID	rca700998587.h1
Method	BLASTX
NCBI GI	g140564
BLAST score	151
E value	4.0e-10
Match length	72
% identity	40
NCBI Description	HYPOTHETICAL ZINC-TYPE ALCOHOL DEHYDROGENASE-LIKE PROTEIN IN PAU3 3'REGION >gi_83277_pir__S19417 probable alcohol dehydrogenase, zinc-containing (EC 1.1.1.-) - yeast (Saccharomyces cerevisiae) >gi_1907243_emb_CAA42237_ (X59720) YCR105w, len:361 [Saccharomyces cerevisiae]

Seq. No.	49333
Seq. ID	rca700998622.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	168
E value	1.0e-89
Match length	240
% identity	93
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	49334
Seq. ID	rca700998623.h1
Method	BLASTX
NCBI GI	g1935914
BLAST score	228
E value	3.0e-19
Match length	44
% identity	93
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	49335
Seq. ID	rca700998638.h1
Method	BLASTX
NCBI GI	g3056591
BLAST score	324
E value	2.0e-30
Match length	86
% identity	71
NCBI Description	(AC004255) T1F9.12 [Arabidopsis thaliana]

Seq. No.	49336
Seq. ID	rca700998644.h1
Method	BLASTX
NCBI GI	g3046694
BLAST score	322
E value	3.0e-30
Match length	82
% identity	73
NCBI Description	(AL022224) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	49337
Seq. ID	rca700998652.h1

Method	BLASTN
NCBI GI	g169036
BLAST score	40
E value	2.0e-13
Match length	60
% identity	92
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	49338
Seq. ID	rca700998692.h1
Method	BLASTN
NCBI GI	g170455
BLAST score	82
E value	1.0e-38
Match length	154
% identity	88
NCBI Description	Tomato heat shock cognate protein 80 gene, 3' end

Seq. No.	49339
Seq. ID	rca700998710.h1
Method	BLASTX
NCBI GI	g417716
BLAST score	342
E value	1.0e-32
Match length	86
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S28 >gi_422182_pir__A46703 ribosomal protein S23.e - yeast (Saccharomyces cerevisiae) >gi_172498 (M96570) ribosomal protein S28 [Saccharomyces cerevisiae] >gi_172500 (M96571) ribosomal protein S28 [Saccharomyces cerevisiae] >gi_1066485 (U40829) 40S ribosomal protein S28 (Swiss Prot. accession number P32827) [Saccharomyces cerevisiae] >gi_1323191_emb_CAA97128_ (Z72903) ORF YGR118w [Saccharomyces cerevisiae]

Seq. No.	49340
Seq. ID	rca700998742.h1
Method	BLASTX
NCBI GI	g1217967
BLAST score	360
E value	1.0e-34
Match length	83
% identity	82
NCBI Description	(X96431) high affinity sulphate transporter [Hordeum vulgare]

Seq. No.	49341
Seq. ID	rca700998773.h1
Method	BLASTN
NCBI GI	g343498
BLAST score	51
E value	6.0e-20
Match length	51
% identity	100
NCBI Description	Tobacco chloroplast Arg-tRNA and Asn-tRNA 4.5S and 5S rRNA genes

Seq. No.	49342
Seq. ID	rca700998787.h1
Method	BLASTX
NCBI GI	g3107905
BLAST score	168
E value	3.0e-12
Match length	72
% identity	33
NCBI Description	(D85101) leaf protein [Ipomoea nil]

Seq. No.	49343
Seq. ID	rca700998825.h1
Method	BLASTX
NCBI GI	g2832632
BLAST score	215
E value	7.0e-18
Match length	44
% identity	89
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49344
Seq. ID	rca700998888.h1
Method	BLASTX
NCBI GI	g2129550
BLAST score	201
E value	5.0e-16
Match length	42
% identity	86
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	49345
Seq. ID	rca700998957.h1
Method	BLASTX
NCBI GI	g3885341
BLAST score	209
E value	2.0e-24
Match length	81
% identity	60
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	49346
Seq. ID	rca700998977.h1
Method	BLASTX
NCBI GI	g4572569
BLAST score	180
E value	1.0e-13
Match length	56
% identity	57
NCBI Description	(AJ133789) alpha-glucosidase [Alicyclobacillus acidocaldarius]

Seq. No.	49347
Seq. ID	rca700998983.h1
Method	BLASTX
NCBI GI	g585649
BLAST score	191
E value	7.0e-15
Match length	63
% identity	59
NCBI Description	POLYMYXIN B RESISTANCE PROTEIN KINASE >gi_460913 (J02946) putative protein kinase [Saccharomyces cerevisiae] >gi_517224 (U12237) Sfs4p [Saccharomyces cerevisiae]

Seq. No.	49348
Seq. ID	rca700999004.h1
Method	BLASTX
NCBI GI	g2316016
BLAST score	190
E value	1.0e-14
Match length	82
% identity	55
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	49349
Seq. ID	rca700999050.h1
Method	BLASTX
NCBI GI	g2088650
BLAST score	109
E value	1.0e-09
Match length	65
% identity	62
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	49350
Seq. ID	rca700999165.h1
Method	BLASTX
NCBI GI	g4512654
BLAST score	151
E value	4.0e-13
Match length	60
% identity	70
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	49351
Seq. ID	rca700999272.h1
Method	BLASTX
NCBI GI	g2492843
BLAST score	193
E value	2.0e-15
Match length	71
% identity	59
NCBI Description	PROBABLE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) (GLUTAMATE OXALOACETATE TRANSAMINASE-1) >gi_1326254 (U58726) coded for by C. elegans cDNA cm20g8; strong similarity to cytoplasmic aspartate aminotransferase [Caenorhabditis elegans]

Seq. No.	49352
Seq. ID	rca700999386.h1
Method	BLASTX
NCBI GI	g4105147
BLAST score	174
E value	4.0e-13
Match length	58
% identity	62
NCBI Description	(AF043595) xyloglucan-specific endo-beta-1,4-glucanase precursor [Aspergillus aculeatus]

Seq. No.	49353
Seq. ID	rca700999402.h1
Method	BLASTN
NCBI GI	g2138331
BLAST score	36
E value	4.0e-11
Match length	78
% identity	94
NCBI Description	Emericella nidulans citrate synthase (citA) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	49354
Seq. ID	rca700999412.h1
Method	BLASTN
NCBI GI	g12158
BLAST score	82
E value	2.0e-38
Match length	174
% identity	87
NCBI Description	Pea gpa1 gene for subunit A of chloroplast glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)

Seq. No.	49355
Seq. ID	rca700999439.h1
Method	BLASTX
NCBI GI	g1707017
BLAST score	311
E value	5.0e-29
Match length	78
% identity	81
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	49356
Seq. ID	rca700999449.h1
Method	BLASTX
NCBI GI	g4335745
BLAST score	146
E value	8.0e-10
Match length	62
% identity	47
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 49357

Seq. ID	rca700999482.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	46
E value	7.0e-17
Match length	70
% identity	91
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	49358
Seq. ID	rca700999491.h1
Method	BLASTX
NCBI GI	g100226
BLAST score	235
E value	6.0e-20
Match length	91
% identity	45
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	49359
Seq. ID	rca700999496.h1
Method	BLASTX
NCBI GI	g4538944
BLAST score	168
E value	4.0e-12
Match length	61
% identity	49
NCBI Description	(AL049483) putative transcription factor [Arabidopsis thaliana]

Seq. No.	49360
Seq. ID	rca700999525.h1
Method	BLASTX
NCBI GI	g4580392
BLAST score	158
E value	7.0e-11
Match length	74
% identity	46
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49361
Seq. ID	rca700999537.h1
Method	BLASTX
NCBI GI	g4455329
BLAST score	152
E value	2.0e-10
Match length	30
% identity	93
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	49362
Seq. ID	rca700999590.h1
Method	BLASTX

NCBI GI	g1710530
BLAST score	304
E value	2.0e-28
Match length	53
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	49363
Seq. ID	rca700999596.h1
Method	BLASTX
NCBI GI	g3786314
BLAST score	325
E value	2.0e-30
Match length	94
% identity	65
NCBI Description	(AB012141) translation elongation factor3 [Candida glabrata]

Seq. No.	49364
Seq. ID	rca700999647.h1
Method	BLASTX
NCBI GI	g4455188
BLAST score	242
E value	7.0e-21
Match length	70
% identity	63
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	49365
Seq. ID	rca700999651.h1
Method	BLASTX
NCBI GI	g3582340
BLAST score	159
E value	4.0e-11
Match length	37
% identity	84
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	49366
Seq. ID	rca700999713.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	210
E value	1.0e-115
Match length	254
% identity	96
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	49367
Seq. ID	rca700999789.h1
Method	BLASTN
NCBI GI	g1498333
BLAST score	112

E value	3.0e-56
Match length	116
% identity	99
NCBI Description	Glycine max actin (Soy57) gene, partial cds

Seq. No.	49368
Seq. ID	rca700999802.h1
Method	BLASTN
NCBI GI	g1381085
BLAST score	70
E value	3.0e-31
Match length	134
% identity	88
NCBI Description	Pisum sativum imidazoleglycerol-phosphate dehydratase (PSHIS3) mRNA, complete cds

Seq. No.	49369
Seq. ID	rca700999815.h1
Method	BLASTX
NCBI GI	g3355465
BLAST score	305
E value	3.0e-28
Match length	77
% identity	74
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	49370
Seq. ID	rca700999840.h1
Method	BLASTX
NCBI GI	g3461821
BLAST score	229
E value	2.0e-19
Match length	85
% identity	54
NCBI Description	(AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]

Seq. No.	49371
Seq. ID	rca700999866.h1
Method	BLASTX
NCBI GI	g309673
BLAST score	291
E value	1.0e-26
Match length	80
% identity	81
NCBI Description	(L19651) light harvesting protein [Pisum sativum]

Seq. No.	49372
Seq. ID	rca700999916.h1
Method	BLASTN
NCBI GI	g3334662
BLAST score	46
E value	2.0e-17
Match length	86
% identity	88
NCBI Description	G.max mRNA for putative cytochrome P450, clone CP4

Seq. No.	49373
Seq. ID	rca700999986.h1
Method	BLASTX
NCBI GI	g1931655
BLAST score	143
E value	2.0e-09
Match length	43
% identity	58
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	49374
Seq. ID	rca700999993.h1
Method	BLASTX
NCBI GI	g1644291
BLAST score	159
E value	1.0e-14
Match length	52
% identity	73
NCBI Description	(Z73295) receptor-like protein kinase [Catharanthus roseus]

Seq. No.	49375
Seq. ID	rca701000005.h1
Method	BLASTX
NCBI GI	g1781299
BLAST score	167
E value	1.0e-16
Match length	54
% identity	69
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]

Seq. No.	49376
Seq. ID	rca701000081.h1
Method	BLASTX
NCBI GI	g3378661
BLAST score	155
E value	8.0e-11
Match length	41
% identity	71
NCBI Description	(Y13048) putative outward rectifying potassium channel StKCO1 [Solanum tuberosum]

Seq. No.	49377
Seq. ID	rca701000102.h1
Method	BLASTX
NCBI GI	g3402684
BLAST score	187
E value	2.0e-14
Match length	78
% identity	47
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49378
Seq. ID	rca701000133.h1
Method	BLASTN
NCBI GI	g1209887

BLAST score	71
E value	8.0e-32
Match length	211
% identity	90
NCBI Description	Glycine max nonsymbiotic hemoglobin gene, complete cds

Seq. No.	49379
Seq. ID	rca701000155.h1
Method	BLASTX
NCBI GI	g2980641
BLAST score	191
E value	8.0e-15
Match length	83
% identity	43
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	49380
Seq. ID	rca701000182.h1
Method	BLASTX
NCBI GI	g3184096
BLAST score	204
E value	2.0e-16
Match length	83
% identity	47
NCBI Description	(AL023777) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	49381
Seq. ID	rca701000211.h1
Method	BLASTX
NCBI GI	g2118328
BLAST score	154
E value	1.0e-10
Match length	62
% identity	55
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) A precursor, mitochondrial - cyclosporin fungus (SGC3) >gi_642359_emb_CAA88041_ (Z48002) cyclophilin, mitochondrial form [Tolypocladium inflatum]

Seq. No.	49382
Seq. ID	rca701000229.h1
Method	BLASTX
NCBI GI	g3386611
BLAST score	285
E value	6.0e-26
Match length	68
% identity	68
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	49383
Seq. ID	rca701000252.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	88
E value	2.0e-42
Match length	128
% identity	92

NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	49384
Seq. ID	rca701000394.h1
Method	BLASTX
NCBI GI	g3176711
BLAST score	242
E value	8.0e-21
Match length	76
% identity	62
NCBI Description	(AC002392) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	49385
Seq. ID	rca701000415.h1
Method	BLASTX
NCBI GI	g1931642
BLAST score	239
E value	4.0e-21
Match length	65
% identity	80
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	49386
Seq. ID	rca701000449.h1
Method	BLASTX
NCBI GI	g2894606
BLAST score	227
E value	3.0e-19
Match length	60
% identity	75
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	49387
Seq. ID	rca701000456.h1
Method	BLASTX
NCBI GI	g4417294
BLAST score	275
E value	9.0e-25
Match length	82
% identity	68
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49388
Seq. ID	rca701000510.h1
Method	BLASTX
NCBI GI	g1353352
BLAST score	229
E value	3.0e-19
Match length	87
% identity	63
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	49389
Seq. ID	rca701000559.h1

Method	BLASTN
NCBI GI	g293056
BLAST score	100
E value	4.0e-49
Match length	210
% identity	90
NCBI Description	Leishmania amazonensis heat shock protein 70 (hsp70) mRNA, complete cds

Seq. No.	49390
Seq. ID	rca701000678.h1
Method	BLASTN
NCBI GI	g169157
BLAST score	78
E value	5.0e-36
Match length	264
% identity	89
NCBI Description	Pisum sativum serine hydroxymethyltransferase mRNA, complete cds

Seq. No.	49391
Seq. ID	rca701000683.h1
Method	BLASTX
NCBI GI	g976402
BLAST score	352
E value	9.0e-34
Match length	84
% identity	73
NCBI Description	(U31932) amino acid permease 1 [Nicotiana sylvestris] >gi_1906549 (U64823) amino acid permease [Nicotiana sylvestris]

Seq. No.	49392
Seq. ID	rca701000692.h1
Method	BLASTX
NCBI GI	g3850818
BLAST score	300
E value	1.0e-27
Match length	76
% identity	72
NCBI Description	(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	49393
Seq. ID	rca701000729.h1
Method	BLASTN
NCBI GI	g3281845
BLAST score	43
E value	4.0e-15
Match length	83
% identity	88
NCBI Description	Arabidopsis thaliana mRNA for LATE ELONGATED HYPOCOTYL MYB transcription factor

Seq. No.	49394
Seq. ID	rca701000736.h1
Method	BLASTX

NCBI GI	g2511715
BLAST score	288
E value	2.0e-26
Match length	67
% identity	76
NCBI Description	(AF019380) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	49395
Seq. ID	rca701000820.h1
Method	BLASTX
NCBI GI	g2507307
BLAST score	310
E value	1.0e-28
Match length	96
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L3 (TRICHODERMIN RESISTANCE PROTEIN) (YL1) (RP1) >gi_2144768_pir__R5BY4E ribosomal protein L3.e, cytosolic - yeast (Saccharomyces cerevisiae) >gi_1420207_emb_CAA99256_ (Z74971) ORF YOR063w [Saccharomyces cerevisiae] >gi_2104875_emb_CAA94548_ (Z70678) YOR29-14 [Saccharomyces cerevisiae]

Seq. No.	49396
Seq. ID	rca701000857.h1
Method	BLASTX
NCBI GI	g3269291
BLAST score	299
E value	2.0e-27
Match length	89
% identity	65
NCBI Description	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	49397
Seq. ID	rca701000882.h1
Method	BLASTX
NCBI GI	g231660
BLAST score	117
E value	2.0e-09
Match length	92
% identity	47
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	49398
Seq. ID	rca701000943.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	170
E value	6.0e-91
Match length	249
% identity	92
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	49399
Seq. ID	rca701000966.h1

Method	BLASTX
NCBI GI	g1621535
BLAST score	168
E value	3.0e-12
Match length	39
% identity	79
NCBI Description	(U27231) HSP70 [Trichomonas vaginalis]

Seq. No.	49400
Seq. ID	rca701000977.h1
Method	BLASTX
NCBI GI	g2119933
BLAST score	164
E value	1.0e-11
Match length	37
% identity	84
NCBI Description	translation initiation factor eIF-4A.11 - common tobacco

Seq. No.	49401
Seq. ID	rca701001013.h1
Method	BLASTN
NCBI GI	g1814402
BLAST score	84
E value	2.0e-39
Match length	266
% identity	86
NCBI Description	Mesembryanthemum crystallinum methionine synthase (MetE) mRNA, complete cds

Seq. No.	49402
Seq. ID	rca701001026.h1
Method	BLASTX
NCBI GI	g3776557
BLAST score	356
E value	4.0e-34
Match length	94
% identity	77
NCBI Description	(AC005388) Contains similarity to gi_2924495 hypothetical protein Rv1920 from Mycobacterium tuberculosis genome gb_AL022020. [Arabidopsis thaliana]

Seq. No.	49403
Seq. ID	rca701001046.h1
Method	BLASTX
NCBI GI	g1514643
BLAST score	318
E value	1.0e-29
Match length	94
% identity	60
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	49404
Seq. ID	rca701001070.h1
Method	BLASTN
NCBI GI	g218188
BLAST score	128
E value	8.0e-66

Match length	212
% identity	39
NCBI Description	Rice mRNA for poly-ubiquitin, partial sequence

Seq. No.	49405
Seq. ID	rca701001111.h1
Method	BLASTX
NCBI GI	g3142300
BLAST score	359
E value	2.0e-34
Match length	76
% identity	54
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	49406
Seq. ID	rca701001143.h1
Method	BLASTX
NCBI GI	g2341045
BLAST score	163
E value	2.0e-11
Match length	89
% identity	37
NCBI Description	(AC000104) F19P19.16 [Arabidopsis thaliana]

Seq. No.	49407
Seq. ID	rca701001144.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	140
E value	5.0e-73
Match length	275
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	49408
Seq. ID	rca701001159.h1
Method	BLASTX
NCBI GI	g121115
BLAST score	205
E value	2.0e-16
Match length	75
% identity	55
NCBI Description	GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120) >gi_84108_pir__S05943 gelation factor - slime mold (Dictyostelium discoideum) >gi_7286_emb_CAA33471_ (X15430) gelation factor (AA 1 - 857) [Dictyostelium discoideum]

Seq. No.	49409
Seq. ID	rca701001191.h1
Method	BLASTX
NCBI GI	g115593
BLAST score	184
E value	5.0e-14

Match length	51
% identity	69
NCBI Description	F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT (CAP34) >gi_483087_pir__B61042 Ca2+-independent f-actin-capping protein 34K chain - slime mold (Dictyostelium discoideum) >gi_167682 (M25132) CAP34 protein [Dictyostelium discoideum]

Seq. No.	49410
Seq. ID	rca701001212.h1
Method	BLASTX
NCBI GI	g4455224
BLAST score	144
E value	3.0e-09
Match length	75
% identity	41
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	49411
Seq. ID	rca701001227.h1
Method	BLASTX
NCBI GI	g4063762
BLAST score	137
E value	5.0e-10
Match length	77
% identity	47
NCBI Description	(AC005561) putative retrotransposon [Arabidopsis thaliana]

Seq. No.	49412
Seq. ID	rca701001234.h1
Method	BLASTN
NCBI GI	g984307
BLAST score	88
E value	2.0e-42
Match length	124
% identity	93
NCBI Description	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso

Seq. No.	49413
Seq. ID	rca701001255.h1
Method	BLASTN
NCBI GI	g4455262
BLAST score	36
E value	3.0e-11
Match length	104
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	49414
Seq. ID	rca701001260.h1
Method	BLASTX
NCBI GI	g3540195

BLAST score	327
E value	9.0e-31
Match length	88
% identity	36
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	49415
Seq. ID	rca701001275.h1
Method	BLASTX
NCBI GI	g4185131
BLAST score	151
E value	3.0e-15
Match length	81
% identity	62
NCBI Description	(AC005724) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	49416
Seq. ID	rca701001311.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	84
E value	2.0e-39
Match length	200
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49417
Seq. ID	rca701001323.h1
Method	BLASTX
NCBI GI	g3831469
BLAST score	143
E value	4.0e-09
Match length	96
% identity	30
NCBI Description	(AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49418
Seq. ID	rca701001355.h1
Method	BLASTX
NCBI GI	g2190187
BLAST score	213
E value	2.0e-17
Match length	70
% identity	60
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	49419
Seq. ID	rca701001416.h1
Method	BLASTN
NCBI GI	g343022
BLAST score	159
E value	2.0e-84
Match length	257

% identity	94
NCBI Description	Pea chloroplast photosystem II gene encoding the D2 and 44kd chlorophyll a-binding proteins, complete cds

Seq. No.	49420
Seq. ID	rca701001429.h1
Method	BLASTX
NCBI GI	g3269287
BLAST score	196
E value	2.0e-30
Match length	90
% identity	76
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	49421
Seq. ID	rca701001484.h1
Method	BLASTX
NCBI GI	g1345837
BLAST score	239
E value	2.0e-20
Match length	86
% identity	53
NCBI Description	PHYTOENE DEHYDROGENASE (PHYTOENE DESATURASE) >gi_433145 (U03903) phytoene dehydrogenase [Cercospora nicotianae]

Seq. No.	49422
Seq. ID	rca701001486.h1
Method	BLASTX
NCBI GI	g2244890
BLAST score	104
E value	1.0e-09
Match length	64
% identity	50
NCBI Description	(Z97338) unnamed protein product [Arabidopsis thaliana]

Seq. No.	49423
Seq. ID	rca701001577.h1
Method	BLASTX
NCBI GI	g2911047
BLAST score	146
E value	3.0e-14
Match length	60
% identity	75
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	49424
Seq. ID	rca701001584.h1
Method	BLASTX
NCBI GI	g1871187
BLAST score	143
E value	3.0e-09
Match length	60
% identity	35
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	49425
Seq. ID	rca701001589.h1

Method	BLASTX
NCBI GI	g4378663
BLAST score	193
E value	5.0e-29
Match length	81
% identity	68
NCBI Description	(AF107765) cytochrome P450 [Prunus dulcis]

Seq. No.	49426
Seq. ID	rca701001616.h1
Method	BLASTX
NCBI GI	g3047111
BLAST score	227
E value	3.0e-19
Match length	59
% identity	66
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	49427
Seq. ID	rca701001637.h1
Method	BLASTX
NCBI GI	g1710055
BLAST score	155
E value	1.0e-10
Match length	53
% identity	57
NCBI Description	RDS1 PROTEIN >gi_1363621_pir__S58477 rds1 protein - fission yeast (Schizosaccharomyces pombe) >gi_1184029_emb_CAA54544_ (X77328) rds1 [Schizosaccharomyces pombe]

Seq. No.	49428
Seq. ID	rca701001676.h1
Method	BLASTN
NCBI GI	g1065907
BLAST score	138
E value	7.0e-72
Match length	210
% identity	91
NCBI Description	Pisum sativum chloroplast processing enzyme mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	49429
Seq. ID	rca701001891.h1
Method	BLASTX
NCBI GI	g3877973
BLAST score	151
E value	5.0e-20
Match length	81
% identity	55
NCBI Description	(Z81095) Similarity to Rat Acyl-CoA oxidase I (SW:CAO1_RAT); cDNA EST EMBL:D71772 comes from this gene; cDNA EST EMBL:D74459 comes from this gene; cDNA EST yk470g3.3 comes from this gene; cDNA EST yk470g3.5 comes from this gene

Seq. No.	49430
Seq. ID	rca701001925.h1

Method	BLASTX
NCBI GI	g3763927
BLAST score	149
E value	4.0e-10
Match length	35
% identity	77
NCBI Description	(AC004450) putative carboxyphosphoenolpyruvate mutase [Arabidopsis thaliana]

Seq. No.	49431
Seq. ID	rca701001948.h1
Method	BLASTX
NCBI GI	g4056552
BLAST score	193
E value	3.0e-15
Match length	50
% identity	70
NCBI Description	(AL034583) putative nucleotide binding protein [Schizosaccharomyces pombe]

Seq. No.	49432
Seq. ID	rca701001988.h1
Method	BLASTN
NCBI GI	g4336433
BLAST score	34
E value	6.0e-10
Match length	133
% identity	82
NCBI Description	Lotus japonicus nodule-enhanced protein phosphatase type 2C (NPP2C1) mRNA, complete cds

Seq. No.	49433
Seq. ID	rca701002038.h1
Method	BLASTX
NCBI GI	g2501578
BLAST score	280
E value	3.0e-25
Match length	62
% identity	92
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	49434
Seq. ID	rca701002093.h1
Method	BLASTX
NCBI GI	g3646453
BLAST score	172
E value	7.0e-13
Match length	63
% identity	56
NCBI Description	(AL031603) putative succinate dehydrogenase cytochrome b subunit precursor [Schizosaccharomyces pombe]

Seq. No.	49435
Seq. ID	rca701002122.h1

Method	BLASTX
NCBI GI	g2980770
BLAST score	245
E value	3.0e-21
Match length	75
% identity	52
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	49436
Seq. ID	rca701002210.h1
Method	BLASTX
NCBI GI	g3150405
BLAST score	182
E value	5.0e-14
Match length	63
% identity	59
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	49437
Seq. ID	rca701002231.h1
Method	BLASTX
NCBI GI	g585957
BLAST score	238
E value	1.0e-20
Match length	62
% identity	68
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT >gi_346439_pir__A44170 membrane-bound ribosome-associated translocating polypeptide Sec61p - dog >gi_164070 (M96629) homologue to sec61 [Canis familiaris]

Seq. No.	49438
Seq. ID	rca701002234.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	36
E value	6.0e-11
Match length	48
% identity	94
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	49439
Seq. ID	rca701002309.h1
Method	BLASTN
NCBI GI	g1419473
BLAST score	35
E value	2.0e-10
Match length	88
% identity	93
NCBI Description	A.thaliana chloroplast ndhA gene

Seq. No.	49440
Seq. ID	rca701002310.h1
Method	BLASTX
NCBI GI	g1076632
BLAST score	390

E value	3.0e-38
Match length	85
% identity	88
NCBI Description	protein kinase - common tobacco >gi_506534_emb_CAA50374_ (X71057) protein kinase [Nicotiana tabacum]

Seq. No.	49441
Seq. ID	rca701002370.h1
Method	BLASTX
NCBI GI	g266731
BLAST score	140
E value	9.0e-14
Match length	57
% identity	75
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303 phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea >gi_217980_dbj_BAA00885_ (D10001) phenylalanine ammonia-lyase [Pisum sativum] >gi_217982_dbj_BAA00886_ (D10002) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No.	49442
Seq. ID	rca701002372.h1
Method	BLASTX
NCBI GI	g2194125
BLAST score	409
E value	2.0e-40
Match length	80
% identity	86
NCBI Description	(AC002062) ESTs gb_R30459,gb_N38441 come from this gene. [Arabidopsis thaliana]

Seq. No.	49443
Seq. ID	rca701002375.h1
Method	BLASTX
NCBI GI	g2316024
BLAST score	371
E value	6.0e-36
Match length	87
% identity	79
NCBI Description	(U96400) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	49444
Seq. ID	rca701002387.h1
Method	BLASTX
NCBI GI	g3337367
BLAST score	284
E value	7.0e-26
Match length	75
% identity	68
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49445
Seq. ID	rca701002395.h1
Method	BLASTX
NCBI GI	g1408322
BLAST score	217
E value	4.0e-18

Match length	61
% identity	67
NCBI Description	(D86351) cytochrome P-450 (CYP93A2) [Glycine max]

Seq. No.	49446
Seq. ID	rca701002419.h1
Method	BLASTX
NCBI GI	g4138724
BLAST score	136
E value	2.0e-11
Match length	83
% identity	48
NCBI Description	(AJ001061) hexose transporter [Vitis vinifera]

Seq. No.	49447
Seq. ID	rca701002454.h1
Method	BLASTX
NCBI GI	g2133295
BLAST score	177
E value	5.0e-15
Match length	86
% identity	52
NCBI Description	maackiain detoxification protein 1 - fungus (Nectria haematococca) >gi_1019889 (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]

Seq. No.	49448
Seq. ID	rca701002473.h1
Method	BLASTN
NCBI GI	g2511696
BLAST score	47
E value	1.0e-17
Match length	162
% identity	83
NCBI Description	Phaseolus vulgaris Moldavian encoding asparagine-specific endopeptidase precursor (clone cp6b)

Seq. No.	49449
Seq. ID	rca701002488.h1
Method	BLASTN
NCBI GI	g1419473
BLAST score	117
E value	3.0e-59
Match length	168
% identity	93
NCBI Description	A.thaliana chloroplast ndhA gene

Seq. No.	49450
Seq. ID	rca701002491.h1
Method	BLASTX
NCBI GI	g1019946
BLAST score	146
E value	8.0e-19
Match length	60
% identity	81
NCBI Description	(U37060) ascorbate peroxidase [Gossypium hirsutum]

Seq. No.	49451
Seq. ID	rca701002492.h1
Method	BLASTX
NCBI GI	g1708236
BLAST score	147
E value	1.0e-09
Match length	56
% identity	59
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	49452
Seq. ID	rca701002505.h1
Method	BLASTX
NCBI GI	g166949
BLAST score	185
E value	4.0e-14
Match length	58
% identity	59
NCBI Description	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]

Seq. No.	49453
Seq. ID	rca701002507.h1
Method	BLASTX
NCBI GI	g2160173
BLAST score	162
E value	2.0e-11
Match length	69
% identity	5
NCBI Description	(AC000132) Similar to N. tabacum salt-inducible protein (gb_U08285). [Arabidopsis thaliana]

Seq. No.	49454
Seq. ID	rca701002621.h1
Method	BLASTN
NCBI GI	g3452090
BLAST score	79
E value	1.0e-36
Match length	123
% identity	91
NCBI Description	Glycine max mRNA for rudimentary enhancer, partial

Seq. No.	49455
Seq. ID	rca701002631.h1
Method	BLASTX
NCBI GI	g1311386
BLAST score	281
E value	2.0e-25
Match length	79
% identity	62

NCBI Description	Cyanogenic Beta-Glucosidase Mol_id: 1; Molecule: Cyanogenic Beta-Glucosidase; Chain: Null; Ec: 3.2.1.21

Seq. No.	49456
Seq. ID	rca701002660.h1
Method	BLASTX
NCBI GI	g2130944
BLAST score	264
E value	1.0e-23
Match length	71
% identity	75
NCBI Description	(AB004060) sulfate transporter [Arabidopsis thaliana] >gi_2262137_gb_AAC78252.1_AAC78252 (AC002330) sulfate transporter protein [Arabidopsis thaliana]

Seq. No.	49457
Seq. ID	rca701002673.h1
Method	BLASTX
NCBI GI	g2833380
BLAST score	231
E value	9.0e-20
Match length	49
% identity	88
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2) (PRS II) >gi_2146772_pir__S71262 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) II - Arabidopsis thaliana (fragment) >gi_1064885_emb_CAA63552_ (X92974) phosphoribosyl pyrophosphate synthetase II [Arabidopsis thaliana]

Seq. No.	49458
Seq. ID	rlr700895314.h1
Method	BLASTX
NCBI GI	g1711036
BLAST score	208
E value	8.0e-17
Match length	76
% identity	60
NCBI Description	(U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No.	49459
Seq. ID	rlr700895329.h1
Method	BLASTX
NCBI GI	g730645
BLAST score	201
E value	5.0e-16
Match length	64
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	49460
Seq. ID	rlr700895340.h1
Method	BLASTX
NCBI GI	g1709001
BLAST score	92
E value	3.0e-09
Match length	65
% identity	60
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_2129888_pir__S66351 methionine adenosyltransferase (EC 2.5.1.6) 1 - garden pea (fragment) >gi_609223_emb_CAA57580_ (X82076) methionine adenosyltransferase [Pisum sativum]

Seq. No.	49461
Seq. ID	rlr700895353.h1
Method	BLASTX
NCBI GI	g3805956
BLAST score	361
E value	8.0e-35
Match length	80
% identity	81
NCBI Description	(Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	49462
Seq. ID	rlr700895371.h1
Method	BLASTX
NCBI GI	g1619321
BLAST score	136
E value	1.0e-09
Match length	80
% identity	44
NCBI Description	(Y07563) hin1 [Nicotiana tabacum]

Seq. No.	49463
Seq. ID	rlr700895420.h1
Method	BLASTX
NCBI GI	g4335773
BLAST score	164
E value	5.0e-19
Match length	78
% identity	73
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	49464
Seq. ID	rlr700895473.h1
Method	BLASTX
NCBI GI	g2181186
BLAST score	280
E value	3.0e-25
Match length	84
% identity	63
NCBI Description	(X97323) outward rectifying potassium channel KCO1 [Arabidopsis thaliana] >gi_2230761_emb_CAA69158_ (Y07825) kco1 [Arabidopsis thaliana]

Seq. No.	49465
Seq. ID	rlr700895485.h1
Method	BLASTX
NCBI GI	g1850546
BLAST score	138
E value	1.0e-08
Match length	42
% identity	67
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	49466
Seq. ID	rlr700895587.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	212
E value	1.0e-116
Match length	224
% identity	99
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	49467
Seq. ID	rlr700895592.h1
Method	BLASTX
NCBI GI	g3924596
BLAST score	189
E value	9.0e-15
Match length	62
% identity	66
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	49468
Seq. ID	rlr700895663.h1
Method	BLASTN
NCBI GI	g4049332
BLAST score	57
E value	1.0e-23
Match length	141
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	49469
Seq. ID	rlr700895705.h1
Method	BLASTX
NCBI GI	g2804278
BLAST score	311
E value	2.0e-33
Match length	87
% identity	85
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	49470
Seq. ID	rlr700895726.h1
Method	BLASTX

NCBI GI g4432846
BLAST score 182
E value 8.0e-14
Match length 86
% identity 49
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 49471
Seq. ID rlr700895871.h1
Method BLASTN
NCBI GI g2924257
BLAST score 62
E value 2.0e-26
Match length 106
% identity 90
NCBI Description Tobacco chloroplast genome DNA

Seq. No. 49472
Seq. ID rlr700895904.h1
Method BLASTX
NCBI GI g3850573
BLAST score 236
E value 3.0e-20
Match length 82
% identity 58
NCBI Description (AC005278) Similar to gi_1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb_D90908. ESTs gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from this gene. [Arabidopsis thaliana]

Seq. No. 49473
Seq. ID rlr700895907.h1
Method BLASTX
NCBI GI g2914707
BLAST score 200
E value 6.0e-16
Match length 81
% identity 5
NCBI Description (AC003974) putative disease resistance protein (Cf-2.2) [Arabidopsis thaliana] >gi_3298554 (AC004681) putative disease resistance protein [Arabidopsis thaliana]

Seq. No. 49474
Seq. ID rlr700895940.h1
Method BLASTX
NCBI GI g2827466
BLAST score 162
E value 1.0e-11
Match length 67
% identity 46
NCBI Description (AF044253) potassium channel beta 2 subunit [Homo sapiens]

Seq. No. 49475
Seq. ID rlr700895946.h1
Method BLASTX
NCBI GI g2288986
BLAST score 150

E value	4.0e-10
Match length	35
% identity	74
NCBI Description	(AC002335) glyoxalase II isolog [Arabidopsis thaliana]

Seq. No.	49476
Seq. ID	rlr700896008.h1
Method	BLASTX
NCBI GI	g2245136
BLAST score	201
E value	5.0e-16
Match length	70
% identity	61
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	49477
Seq. ID	rlr700896016.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	70
E value	3.0e-31
Match length	158
% identity	86
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49478
Seq. ID	rlr700896131.h1
Method	BLASTX
NCBI GI	g3894169
BLAST score	216
E value	8.0e-18
Match length	51
% identity	73
NCBI Description	(AC005312) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49479
Seq. ID	rlr700896167.h1
Method	BLASTX
NCBI GI	g3335350
BLAST score	203
E value	3.0e-17
Match length	82
% identity	67
NCBI Description	(AC004512) Similar to gb_Z84386 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus. [Arabidopsis thaliana]

Seq. No.	49480
Seq. ID	rlr700896224.h1
Method	BLASTX
NCBI GI	g2894603
BLAST score	151
E value	1.0e-12
Match length	55

% identity	64
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	49481
Seq. ID	rlr700896232.h1
Method	BLASTX
NCBI GI	g3183617
BLAST score	215
E value	9.0e-18
Match length	45
% identity	84
NCBI Description	(AJ005586) MYB-related transcription factor [Antirrhinum majus]

Seq. No.	49482
Seq. ID	rlr700896256.h1
Method	BLASTX
NCBI GI	g3643593
BLAST score	229
E value	2.0e-19
Match length	52
% identity	87
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49483
Seq. ID	rlr700896274.h1
Method	BLASTX
NCBI GI	g3935181
BLAST score	386
E value	7.0e-38
Match length	77
% identity	92
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	49484
Seq. ID	rlr700896308.h1
Method	BLASTX
NCBI GI	g4335742
BLAST score	148
E value	8.0e-10
Match length	48
% identity	60
NCBI Description	(AC006248) putative AR781 [Arabidopsis thaliana]

Seq. No.	49485
Seq. ID	rlr700896337.h1
Method	BLASTX
NCBI GI	g2497366
BLAST score	232
E value	9.0e-20
Match length	77
% identity	61
NCBI Description	INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 >gi_2137851_pir__I49127 unknown intracellular protein - mouse >gi_558903 (U15635) unknown intracellular protein [Mus musculus]

Seq. No.	49486
Seq. ID	rlr700896429.h1
Method	BLASTX
NCBI GI	g3882321
BLAST score	184
E value	5.0e-14
Match length	83
% identity	51
NCBI Description	(AB018343) KIAA0800 protein [Homo sapiens]

Seq. No.	49487
Seq. ID	rlr700896434.h1
Method	BLASTN
NCBI GI	g2565339
BLAST score	86
E value	8.0e-41
Match length	210
% identity	85
NCBI Description	Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete cds

Seq. No.	49488
Seq. ID	rlr700896459.h1
Method	BLASTX
NCBI GI	g1922938
BLAST score	304
E value	4.0e-28
Match length	84
% identity	70
NCBI Description	(AC000106) Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb_Z29094). [Arabidopsis thaliana]

Seq. No.	49489
Seq. ID	rlr700896469.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	91
E value	9.0e-44
Match length	195
% identity	87
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49490
Seq. ID	rlr700896546.h1
Method	BLASTN
NCBI GI	g169056
BLAST score	78
E value	5.0e-36
Match length	209
% identity	84
NCBI Description	P.sativum carbonic anhydrase mRNA, complete cds

Seq. No.	49491
Seq. ID	rlr700896559.h1
Method	BLASTN

NCBI GI	g170059
BLAST score	172
E value	4.0e-92
Match length	209
% identity	96
NCBI Description	Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete cds

Seq. No.	49492
Seq. ID	rlr700896594.h1
Method	BLASTX
NCBI GI	g2642433
BLAST score	220
E value	2.0e-18
Match length	78
% identity	19
NCBI Description	(AC002391) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	49493
Seq. ID	rlr700896663.h1
Method	BLASTX
NCBI GI	g81755
BLAST score	286
E value	6.0e-26
Match length	87
% identity	7
NCBI Description	33K hydroxyproline-rich glycoprotein - soybean (fragment)

Seq. No.	49494
Seq. ID	rlr700896705.h1
Method	BLASTX
NCBI GI	g1945279
BLAST score	324
E value	2.0e-30
Match length	82
% identity	68
NCBI Description	(Y11350) myb factor [Oryza sativa]

Seq. No.	49495
Seq. ID	rlr700896714.h1
Method	BLASTX
NCBI GI	g729092
BLAST score	416
E value	3.0e-41
Match length	89
% identity	84
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) >gi_477484_pir__A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana >gi_304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	49496
Seq. ID	rlr700896781.h1
Method	BLASTX
NCBI GI	g4455280
BLAST score	143

E value	3.0e-09
Match length	61
% identity	46
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	49497
Seq. ID	rlr700896805.h1
Method	BLASTX
NCBI GI	g4191774
BLAST score	363
E value	5.0e-35
Match length	84
% identity	76
NCBI Description	(AC005917) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	49498
Seq. ID	rlr700896843.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	137
E value	3.0e-71
Match length	201
% identity	92
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	49499
Seq. ID	rlr700896888.h1
Method	BLASTX
NCBI GI	g1418990
BLAST score	171
E value	1.0e-12
Match length	52
% identity	58
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	49500
Seq. ID	rlr700896895.h1
Method	BLASTX
NCBI GI	g2832658
BLAST score	163
E value	1.0e-11
Match length	75
% identity	47
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	49501
Seq. ID	rlr700896980.h1
Method	BLASTN
NCBI GI	g21981
BLAST score	41
E value	5.0e-14
Match length	41
% identity	100
NCBI Description	V.angustifolia 25S/18S rRNA intergenic spacer DNA

Seq. No.	49502

Seq. ID	rlr700897085.h1
Method	BLASTN
NCBI GI	g3273242
BLAST score	61
E value	7.0e-26
Match length	113
% identity	88
NCBI Description	Oryza sativa mRNA for NLS receptor, complete cds

Seq. No.	49503
Seq. ID	rlr700897142.h1
Method	BLASTX
NCBI GI	g3043529
BLAST score	145
E value	2.0e-21
Match length	86
% identity	58
NCBI Description	(AJ002204) polyamine oxidase [Zea mays]

Seq. No.	49504
Seq. ID	rlr700897161.h1
Method	BLASTN
NCBI GI	g463251
BLAST score	70
E value	3.0e-31
Match length	137
% identity	89
NCBI Description	M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5

Seq. No.	49505
Seq. ID	rlr700897181.h1
Method	BLASTN
NCBI GI	g255407
BLAST score	185
E value	1.0e-100
Match length	220
% identity	17
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	49506
Seq. ID	rlr700897209.h1
Method	BLASTX
NCBI GI	g1669655
BLAST score	211
E value	3.0e-17
Match length	49
% identity	73
NCBI Description	(X95962) CER3 [Arabidopsis thaliana]

Seq. No.	49507
Seq. ID	rlr700897212.h1
Method	BLASTN
NCBI GI	g455949
BLAST score	55
E value	3.0e-22

Match length	55
% identity	100
NCBI Description	18S rRNA {3' region} [Glycine max=soybeans, var. Pella 86, leaves, rRNA Partial, 111 nt]

Seq. No.	49508
Seq. ID	rlr700897283.h1
Method	BLASTN
NCBI GI	g2444413
BLAST score	189
E value	1.0e-102
Match length	241
% identity	95
NCBI Description	Gleditsia australis NADH dehydrogenase-like protein (ndhF) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No.	49509
Seq. ID	rlr700897301.h1
Method	BLASTN
NCBI GI	g1370284
BLAST score	69
E value	1.0e-30
Match length	165
% identity	85
NCBI Description	P.sativum mRNA for glutathione reductase

Seq. No.	49510
Seq. ID	rlr700897392.h1
Method	BLASTX
NCBI GI	g2213608
BLAST score	180
E value	1.0e-13
Match length	76
% identity	42
NCBI Description	(AC000103) F21J9.2 [Arabidopsis thaliana]

Seq. No.	49511
Seq. ID	rlr700897396.h1
Method	BLASTX
NCBI GI	g3421104
BLAST score	212
E value	2.0e-17
Match length	48
% identity	83
NCBI Description	(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]

Seq. No.	49512
Seq. ID	rlr700897421.h1
Method	BLASTN
NCBI GI	g166421
BLAST score	90
E value	4.0e-43
Match length	166
% identity	89
NCBI Description	Medicago sativa ubiquitin carrier protein mRNA, complete

cds

Seq. No.	49513
Seq. ID	rlr700897451.h1
Method	BLASTX
NCBI GI	g2598589
BLAST score	270
E value	4.0e-24
Match length	90
% identity	59
NCBI Description	(Y15367) MtN19 [Medicago truncatula]

Seq. No.	49514
Seq. ID	rlr700897525.h1
Method	BLASTX
NCBI GI	g3776029
BLAST score	331
E value	3.0e-31
Match length	90
% identity	89
NCBI Description	(AJ010476) RNA helicase [Arabidopsis thaliana]

Seq. No.	49515
Seq. ID	rlr700897567.h1
Method	BLASTX
NCBI GI	g2252831
BLAST score	262
E value	4.0e-23
Match length	88
% identity	60
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	49516
Seq. ID	rlr700897586.h1
Method	BLASTX
NCBI GI	g4510345
BLAST score	180
E value	1.0e-13
Match length	33
% identity	94
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	49517
Seq. ID	rlr700897587.h1
Method	BLASTN
NCBI GI	g3510337
BLAST score	51
E value	7.0e-20
Match length	167
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	49518
Seq. ID	rlr700897641.h1
Method	BLASTX
NCBI GI	g2062173

BLAST score 328
E value 6.0e-31
Match length 86
% identity 83
NCBI Description (AC001645) cell division protein FtsH isolog [Arabidopsis thaliana]

Seq. No. 49519
Seq. ID rlr700897644.h1
Method BLASTX
NCBI GI g4455225
BLAST score 372
E value 5.0e-36
Match length 77
% identity 82
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 49520
Seq. ID rlr700897679.h1
Method BLASTX
NCBI GI g4138343
BLAST score 139
E value 6.0e-09
Match length 36
% identity 75
NCBI Description (AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]

Seq. No. 49521
Seq. ID rlr700897695.h1
Method BLASTX
NCBI GI g2347088
BLAST score 156
E value 5.0e-11
Match length 51
% identity 59
NCBI Description (U72765) non-specific lipid transfer protein PvLTP-24 [Phaseolus vulgaris]

Seq. No. 49522
Seq. ID rlr700897780.h1
Method BLASTX
NCBI GI g4512657
BLAST score 163
E value 1.0e-11
Match length 61
% identity 48
NCBI Description (AC006931) putative APG protein [Arabidopsis thaliana] >gi_4544463_gb_AAD22370.1_AC006580_2 (AC006580) putative APG isolog protein [Arabidopsis thaliana]

Seq. No. 49523
Seq. ID rlr700897860.h1
Method BLASTX
NCBI GI g1168609
BLAST score 300
E value 1.0e-27
Match length 78

% identity	72
NCBI Description	AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf__1917337A ubiquitin-activating enzyme E1 [Arabidopsis thaliana]

Seq. No.	49524
Seq. ID	rlr700897931.h1
Method	BLASTX
NCBI GI	g3036805
BLAST score	161
E value	2.0e-11
Match length	32
% identity	88
NCBI Description	(AL022373) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	49525
Seq. ID	rlr700898043.h1
Method	BLASTX
NCBI GI	g4115536
BLAST score	204
E value	2.0e-16
Match length	50
% identity	78
NCBI Description	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No.	49526
Seq. ID	rlr700898141.h1
Method	BLASTN
NCBI GI	g170073
BLAST score	42
E value	8.0e-15
Match length	78
% identity	95
NCBI Description	Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No.	49527
Seq. ID	rlr700898146.h1
Method	BLASTX
NCBI GI	g3834323
BLAST score	347
E value	4.0e-33
Match length	87
% identity	68
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	49528
Seq. ID	rlr700898156.h1
Method	BLASTX
NCBI GI	g1142619
BLAST score	185
E value	2.0e-23
Match length	78

% identity	73
NCBI Description	(U18348) phaseolin G-box binding protein PG1 [Phaseolus vulgaris]

Seq. No.	49529
Seq. ID	rlr700898178.h1
Method	BLASTN
NCBI GI	g497119
BLAST score	58
E value	4.0e-24
Match length	102
% identity	90
NCBI Description	Pisum sativum monodehydroascorbate reductase mRNA, complete cds

Seq. No.	49530
Seq. ID	rlr700898322.h1
Method	BLASTN
NCBI GI	g609224
BLAST score	62
E value	2.0e-26
Match length	146
% identity	86
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	49531
Seq. ID	rlr700898334.h1
Method	BLASTX
NCBI GI	g730583
BLAST score	168
E value	4.0e-12
Match length	48
% identity	73
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	49532
Seq. ID	rlr700898354.h1
Method	BLASTN
NCBI GI	g1208702
BLAST score	79
E value	1.0e-36
Match length	161
% identity	99
NCBI Description	Glycine max histone H3 gene, partial cds, clone H3-DMAX

Seq. No.	49533
Seq. ID	rlr700898375.h1
Method	BLASTN
NCBI GI	g12182
BLAST score	73
E value	2.0e-33
Match length	116
% identity	91

NCBI Description	P.sativum chloroplast DNA of the single ribosomal RNA operon

Seq. No.	49534
Seq. ID	rlr700898383.h1
Method	BLASTX
NCBI GI	g3122333
BLAST score	159
E value	4.0e-11
Match length	44
% identity	66
NCBI Description	PUTATIVE 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI) >gi_2648330 (AE000954) 3-isopropylmalate dehydratase, large subunit (leuC) [Archaeoglobus fulgidus]

Seq. No.	49535
Seq. ID	rlr700898455.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	57
E value	2.0e-23
Match length	165
% identity	85
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	49536
Seq. ID	rlr700898456.h1
Method	BLASTX
NCBI GI	g2829918
BLAST score	152
E value	2.0e-10
Match length	57
% identity	58
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	49537
Seq. ID	rlr700898470.h1
Method	BLASTN
NCBI GI	g169984
BLAST score	54
E value	9.0e-22
Match length	148
% identity	92
NCBI Description	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.6-L)

Seq. No.	49538
Seq. ID	rlr700898484.h1
Method	BLASTN
NCBI GI	g2055229
BLAST score	40
E value	2.0e-13
Match length	100
% identity	85

NCBI Description	Soybean mRNA for SRC2, complete cds
Seq. No.	49539
Seq. ID	rlr700898493.h1
Method	BLASTX
NCBI GI	g3935169
BLAST score	162
E value	1.0e-11
Match length	35
% identity	86
NCBI Description	(AC004557) F17L21.12 [Arabidopsis thaliana]
Seq. No.	49540
Seq. ID	rlr700898533.h1
Method	BLASTX
NCBI GI	g1117778
BLAST score	408
E value	3.0e-40
Match length	88
% identity	85
NCBI Description	(D49366) 4-coumarate:CoA ligase [Lithospermum erythrorhizon]
Seq. No.	49541
Seq. ID	rlr700898561.h1
Method	BLASTX
NCBI GI	g2072986
BLAST score	188
E value	9.0e-15
Match length	39
% identity	90
NCBI Description	(U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi_2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana]
Seq. No.	49542
Seq. ID	rlr700898569.h1
Method	BLASTX
NCBI GI	g3928150
BLAST score	262
E value	3.0e-23
Match length	64
% identity	80
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]
Seq. No.	49543
Seq. ID	rlr700898590.h1
Method	BLASTX
NCBI GI	g3153889
BLAST score	393
E value	1.0e-38
Match length	85
% identity	85
NCBI Description	(AF065444) root iron transporter protein [Pisum sativum]
Seq. No.	49544
Seq. ID	rlr700898691.h1

Method	BLASTN
NCBI GI	g3241927
BLAST score	45
E value	2.0e-16
Match length	61
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	49545
Seq. ID	rlr700898772.h1
Method	BLASTN
NCBI GI	g296408
BLAST score	225
E value	1.0e-124
Match length	248
% identity	98
NCBI Description	G.max ADR12 mRNA

Seq. No.	49546
Seq. ID	rlr700898773.h1
Method	BLASTX
NCBI GI	g2493895
BLAST score	153
E value	2.0e-10
Match length	71
% identity	51
NCBI Description	CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_1071911_pir__S46438 cysteine synthase (EC 4.2.99.8) - watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine synthase [Citrullus lanatus]

Seq. No.	49547
Seq. ID	rlr700898925.h1
Method	BLASTX
NCBI GI	g1297359
BLAST score	172
E value	4.0e-21
Match length	67
% identity	71
NCBI Description	(U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]

Seq. No.	49548
Seq. ID	rlr700898932.h1
Method	BLASTX
NCBI GI	g3858937
BLAST score	116
E value	5.0e-10
Match length	67
% identity	61
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	49549
Seq. ID	rlr700899019.h1
Method	BLASTN
NCBI GI	g3021337

BLAST score	97
E value	2.0e-47
Match length	229
% identity	86
NCBI Description	Cicer arietinum mRNA for cytosolic fructose-1,6-bisphosphate aldolase

Seq. No.	49550
Seq. ID	rlr700899096.h1
Method	BLASTX
NCBI GI	g1946366
BLAST score	290
E value	2.0e-26
Match length	86
% identity	71
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	49551
Seq. ID	rlr700899111.h1
Method	BLASTX
NCBI GI	g2493318
BLAST score	168
E value	2.0e-18
Match length	64
% identity	76
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	49552
Seq. ID	rlr700899133.h1
Method	BLASTX
NCBI GI	g3319682
BLAST score	454
E value	1.0e-45
Match length	93
% identity	31
NCBI Description	(Y17720) SPINDLY protein [Petunia x hybrida]

Seq. No.	49553
Seq. ID	rlr700899140.h1
Method	BLASTX
NCBI GI	g3482932
BLAST score	338
E value	4.0e-32
Match length	84
% identity	74
NCBI Description	(AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	49554
Seq. ID	rlr700899141.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	248
E value	1.0e-137
Match length	248
% identity	100

NCBI Description	G.max ADR6 mRNA
Seq. No.	49555
Seq. ID	rlr700899152.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	273
E value	1.0e-152
Match length	273
% identity	26
NCBI Description	Glycine max gene for ubiquitin, complete cds
Seq. No.	49556
Seq. ID	rlr700899232.h1
Method	BLASTX
NCBI GI	g3044218
BLAST score	238
E value	2.0e-20
Match length	53
% identity	79
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]
Seq. No.	49557
Seq. ID	rlr700899338.h1
Method	BLASTX
NCBI GI	g1841462
BLAST score	166
E value	4.0e-12
Match length	69
% identity	58
NCBI Description	(Y10991) Elongation factor 2 [Nicotiana tabacum]
Seq. No.	49558
Seq. ID	rlr700899358.h1
Method	BLASTN
NCBI GI	g1706957
BLAST score	43
E value	3.0e-15
Match length	75
% identity	89
NCBI Description	Gossypium hirsutum cellulose synthase (celA2) mRNA, partial cds
Seq. No.	49559
Seq. ID	rlr700899371.h1
Method	BLASTN
NCBI GI	g1053044
BLAST score	87
E value	2.0e-41
Match length	126
% identity	99
NCBI Description	Glycine max histone H3 gene, partial cds, clone S1
Seq. No.	49560
Seq. ID	rlr700899393.h1
Method	BLASTX
NCBI GI	g132849

BLAST score	148
E value	5.0e-10
Match length	39
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L2 >gi_20001_emb_CAA44362.1_ (X62500) 60S ribosomal protein L2 [Nicotiana tabacum]

Seq. No.	49561
Seq. ID	rlr700899590.h1
Method	BLASTN
NCBI GI	g3192930
BLAST score	104
E value	1.0e-51
Match length	108
% identity	99
NCBI Description	Glycine max clone a2 malate dehydrogenase (Mdh-1) mRNA, nuclear gene encoding mitochondrial protein, partial cds

Seq. No.	49562
Seq. ID	rlr700899642.h1
Method	BLASTN
NCBI GI	g4159705
BLAST score	32
E value	1.0e-08
Match length	90
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence [Arabidopsis thaliana]

Seq. No.	49563
Seq. ID	rlr700899659.h1
Method	BLASTX
NCBI GI	g3142291
BLAST score	244
E value	5.0e-21
Match length	82
% identity	57
NCBI Description	(AC002411) Contains similarity to adenylate cyclase gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes from this gene. [Arabidopsis thaliana]

Seq. No.	49564
Seq. ID	rlr700899670.h1
Method	BLASTX
NCBI GI	g1805261
BLAST score	214
E value	1.0e-17
Match length	86
% identity	49
NCBI Description	(U75347) fatty acid synthase, alpha subunit [Emericella nidulans]

Seq. No.	49565
Seq. ID	rlr700899678.h1
Method	BLASTX
NCBI GI	g4510396
BLAST score	142

E value	4.0e-09
Match length	51
% identity	57
NCBI Description	(AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49566
Seq. ID	rlr700899771.h1
Method	BLASTX
NCBI GI	g115765
BLAST score	213
E value	2.0e-17
Match length	57
% identity	65
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	49567
Seq. ID	rlr700899914.h1
Method	BLASTX
NCBI GI	g2660670
BLAST score	359
E value	1.0e-34
Match length	86
% identity	80
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	49568
Seq. ID	rlr700899915.h1
Method	BLASTX
NCBI GI	g4572681
BLAST score	180
E value	1.0e-13
Match length	79
% identity	42
NCBI Description	(AC006954) putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana]

Seq. No.	49569
Seq. ID	rlr700899924.h1
Method	BLASTN
NCBI GI	g2924728
BLAST score	46
E value	6.0e-17
Match length	78
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	49570
Seq. ID	rlr700899933.h1

Method	BLASTX
NCBI GI	g3075398
BLAST score	176
E value	4.0e-13
Match length	58
% identity	55
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	49571
Seq. ID	rlr700899985.h1
Method	BLASTX
NCBI GI	g1922248
BLAST score	150
E value	4.0e-10
Match length	73
% identity	45
NCBI Description	(Y10087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49572
Seq. ID	rlr700899993.h1
Method	BLASTX
NCBI GI	g4204095
BLAST score	345
E value	6.0e-33
Match length	79
% identity	80
NCBI Description	(AF030260) CYP94A1 [Vicia sativa]

Seq. No.	49573
Seq. ID	rlr700900134.h1
Method	BLASTX
NCBI GI	g3193316
BLAST score	381
E value	3.0e-37
Match length	84
% identity	86
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	49574
Seq. ID	rlr700900145.h1
Method	BLASTX
NCBI GI	g3150404
BLAST score	374
E value	2.0e-36
Match length	80
% identity	31
NCBI Description	(AC004165) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	49575
Seq. ID	rlr700900182.h1
Method	BLASTX
NCBI GI	g2104536
BLAST score	230
E value	2.0e-19
Match length	44

% identity	84
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	49576
Seq. ID	rlr700900211.h1
Method	BLASTX
NCBI GI	g3785986
BLAST score	202
E value	3.0e-17
Match length	68
% identity	75
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No.	49577
Seq. ID	rlr700900230.h1
Method	BLASTX
NCBI GI	g1709758
BLAST score	213
E value	1.0e-17
Match length	65
% identity	63
NCBI Description	PROTEASOME COMPONENT C2 (MACROPAIN SUBUNIT C2) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2) >gi_1066151_dbj_BAA07128_ (D37886) proteasome C2 subunit [Oryza sativa]

Seq. No.	49578
Seq. ID	rlr700900244.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	204
E value	1.0e-111
Match length	252
% identity	95
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	49579
Seq. ID	rlr700900250.h1
Method	BLASTX
NCBI GI	g541943
BLAST score	193
E value	4.0e-15
Match length	40
% identity	95
NCBI Description	metallothionein - soybean >gi_228682_prf__1808316A metallothionein-like protein [Glycine max]

Seq. No.	49580
Seq. ID	rlr700900266.h1
Method	BLASTX
NCBI GI	g1717952
BLAST score	301
E value	9.0e-28
Match length	73
% identity	75

NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 4 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 4) (RISP4) >gi_530054 (L16812) Rieske iron-sulfur protein [Nicotiana tabacum]
Seq. No.	49581
Seq. ID	rlr700900437.h1
Method	BLASTN
NCBI GI	g4165340
BLAST score	39
E value	1.0e-12
Match length	95
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	49582
Seq. ID	rlr700900472.h1
Method	BLASTX
NCBI GI	g4056485
BLAST score	107
E value	3.0e-09
Match length	74
% identity	26
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.	49583
Seq. ID	rlr700900477.h1
Method	BLASTX
NCBI GI	g1197461
BLAST score	166
E value	4.0e-12
Match length	31
% identity	100
NCBI Description	(X78819) casein kinase I [Arabidopsis thaliana]
Seq. No.	49584
Seq. ID	rlr700900505.h1
Method	BLASTX
NCBI GI	g3135269
BLAST score	162
E value	2.0e-11
Match length	79
% identity	47
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]
Seq. No.	49585
Seq. ID	rlr700900524.h1
Method	BLASTX
NCBI GI	g4580392
BLAST score	149
E value	6.0e-10
Match length	60
% identity	43
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]
Seq. No.	49586
Seq. ID	rlr700900540.h1

Method	BLASTX
NCBI GI	g417828
BLAST score	193
E value	4.0e-15
Match length	65
% identity	65
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 >gi_320775_pir__S31245 translation initiation factor eIF-2A - yeast (Saccharomyces cerevisiae) >gi_172787 (M77514) SUI1 protein [Saccharomyces cerevisiae] >gi_1255973_emb_CAA65499_ (X96722) ORF N0905 [Saccharomyces cerevisiae] >gi_1302282_emb_CAA96150_ (Z71520) ORF YNL244c [Saccharomyces cerevisiae]

Seq. No.	49587
Seq. ID	rlr700900574.h1
Method	BLASTN
NCBI GI	g872115
BLAST score	52
E value	2.0e-20
Match length	116
% identity	86
NCBI Description	G.max gmsti mRNA

Seq. No.	49588
Seq. ID	rlr700900588.h1
Method	BLASTN
NCBI GI	g2264304
BLAST score	42
E value	1.0e-14
Match length	74
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	49589
Seq. ID	rlr700900611.h1
Method	BLASTX
NCBI GI	g3548805
BLAST score	292
E value	1.0e-26
Match length	71
% identity	73
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	49590
Seq. ID	rlr700900660.h1
Method	BLASTX
NCBI GI	g2262100
BLAST score	267
E value	5.0e-24
Match length	50
% identity	98
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	49591
Seq. ID	rlr700900669.h1
Method	BLASTX

NCBI GI g2781433
BLAST score 270
E value 4.0e-24
Match length 81
% identity 85
NCBI Description (AF030052) RSW1-like cellulose synthase catalytic subunit [Oryza sativa subsp. japonica]

Seq. No. 49592
Seq. ID rlr700900709.h1
Method BLASTN
NCBI GI g18551
BLAST score 60
E value 2.0e-25
Match length 80
% identity 94
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No. 49593
Seq. ID rlr700900826.h1
Method BLASTN
NCBI GI g1663540
BLAST score 140
E value 5.0e-73
Match length 255
% identity 89
NCBI Description Glycine max clone RLG3 disease resistance protein homolog gene, partial cds

Seq. No. 49594
Seq. ID rlr700900903.h1
Method BLASTN
NCBI GI g16508
BLAST score 59
E value 1.0e-24
Match length 159
% identity 85
NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No. 49595
Seq. ID rlr700900932.h1
Method BLASTX
NCBI GI g4206122
BLAST score 380
E value 5.0e-37
Match length 87
% identity 91
NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No. 49596
Seq. ID rlr700900970.h1
Method BLASTN
NCBI GI g2687435

BLAST score	148
E value	8.0e-78
Match length	236
% identity	91
NCBI Description	Hamamelis virginiana large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	49597
Seq. ID	rlr700900977.h1
Method	BLASTX
NCBI GI	g3269289
BLAST score	151
E value	3.0e-10
Match length	44
% identity	66
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	49598
Seq. ID	rlr700900987.h1
Method	BLASTN
NCBI GI	g4490701
BLAST score	35
E value	2.0e-10
Match length	95
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	49599
Seq. ID	rlr700900993.h1
Method	BLASTN
NCBI GI	g3241923
BLAST score	39
E value	9.0e-13
Match length	104
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	49600
Seq. ID	rlr700901109.h1
Method	BLASTX
NCBI GI	g100347
BLAST score	207
E value	1.0e-16
Match length	71
% identity	73
NCBI Description	monosaccharide transport protein MST1 - common tobacco >gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter [Nicotiana tabacum]

Seq. No.	49601
Seq. ID	rlr700901130.h1
Method	BLASTX
NCBI GI	g2160160
BLAST score	147
E value	1.0e-09

Match length	37
% identity	76
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	49602
Seq. ID	rlr700901133.h1
Method	BLASTX
NCBI GI	g2738756
BLAST score	300
E value	1.0e-27
Match length	74
% identity	78
NCBI Description	(AF016282) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	49603
Seq. ID	rlr700901159.h1
Method	BLASTX
NCBI GI	g2435519
BLAST score	303
E value	6.0e-28
Match length	89
% identity	65
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	49604
Seq. ID	rlr700901166.h1
Method	BLASTX
NCBI GI	g2347199
BLAST score	139
E value	1.0e-08
Match length	28
% identity	89
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	49605
Seq. ID	rlr700901321.h1
Method	BLASTX
NCBI GI	g2960364
BLAST score	342
E value	1.0e-32
Match length	71
% identity	86
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	49606
Seq. ID	rlr700901351.h1
Method	BLASTX
NCBI GI	g4544449
BLAST score	311
E value	6.0e-29
Match length	84
% identity	63
NCBI Description	(AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No.	49607
Seq. ID	rlr700901379.h1
Method	BLASTN
NCBI GI	g388206
BLAST score	37
E value	1.0e-11
Match length	69
% identity	88
NCBI Description	Lycopersicon esculentum ubiquitin carrier protein (Ubc) mRNA, complete cds. >gi_2086269_gb_I38279_I38279 Sequence 109 from patent US

Seq. No.	49608
Seq. ID	rlr700901443.h1
Method	BLASTX
NCBI GI	g3786015
BLAST score	161
E value	2.0e-11
Match length	79
% identity	49
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49609
Seq. ID	rlr700901482.h1
Method	BLASTX
NCBI GI	g3820648
BLAST score	181
E value	9.0e-14
Match length	79
% identity	59
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	49610
Seq. ID	rlr700901513.h1
Method	BLASTX
NCBI GI	g2462834
BLAST score	206
E value	1.0e-16
Match length	87
% identity	44
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49611
Seq. ID	rlr700901520.h1
Method	BLASTN
NCBI GI	g296408
BLAST score	239
E value	1.0e-132
Match length	259
% identity	98
NCBI Description	G.max ADR12 mRNA

Seq. No.	49612
Seq. ID	rlr700901533.h1
Method	BLASTN
NCBI GI	g18764

BLAST score	71
E value	8.0e-32
Match length	79
% identity	99
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	49613
Seq. ID	rlr700901534.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	70
E value	3.0e-31
Match length	158
% identity	86
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49614
Seq. ID	rlr700901568.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	101
E value	9.0e-50
Match length	259
% identity	93
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	49615
Seq. ID	rlr700901570.h1
Method	BLASTX
NCBI GI	g3913871
BLAST score	389
E value	4.0e-38
Match length	84
% identity	90
NCBI Description	FERROCHELATASE, CHLOROPLAST PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) (FERROCHELATASE-II) >gi_1946377 (U93215) ferrochelatase precusor isolog [Arabidopsis thaliana] >gi_2347202 (AC002338) ferrochelatase precusor isolog [Arabidopsis thaliana]

Seq. No.	49616
Seq. ID	rlr700901573.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	66
E value	7.0e-29
Match length	158
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49617
Seq. ID	rlr700901724.h1
Method	BLASTN

NCBI GI	g2905771
BLAST score	144
E value	2.0e-75
Match length	156
% identity	98
NCBI Description	Glycine max glyceraldehyde-3 phosphate dehydrogenase (GAPDH) mRNA, partial cds

Seq. No.	49618
Seq. ID	rlr700901740.h1
Method	BLASTN
NCBI GI	g167066
BLAST score	55
E value	3.0e-22
Match length	79
% identity	92
NCBI Description	Hordeum vulgare L-lactate dehydrogenase mRNA, complete cds

Seq. No.	49619
Seq. ID	rlr700901741.h1
Method	BLASTX
NCBI GI	g4056568
BLAST score	250
E value	8.0e-22
Match length	64
% identity	23
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	49620
Seq. ID	rlr700901753.h1
Method	BLASTX
NCBI GI	g3355490
BLAST score	369
E value	8.0e-36
Match length	80
% identity	85
NCBI Description	(AC004218) putative dolichyl-phosphate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	49621
Seq. ID	rlr700901758.h1
Method	BLASTX
NCBI GI	g3935167
BLAST score	227
E value	2.0e-25
Match length	82
% identity	73
NCBI Description	(AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No.	49622
Seq. ID	rlr700901839.h1
Method	BLASTN
NCBI GI	g1070007
BLAST score	47
E value	2.0e-17
Match length	142
% identity	84

NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP6) >gi_3715067_emb_A59876.1_A59876 Sequence 5 from Patent WO9707222

Seq. No.	49623
Seq. ID	rlr700901868.h1
Method	BLASTN
NCBI GI	g18703
BLAST score	33
E value	3.0e-09
Match length	89
% identity	84
NCBI Description	G.max mRNA for nodulin

Seq. No.	49624
Seq. ID	rlr700901902.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	223
E value	1.0e-18
Match length	59
% identity	78
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	49625
Seq. ID	rlr700901925.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	66
E value	7.0e-29
Match length	158
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49626
Seq. ID	rlr700901935.h1
Method	BLASTX
NCBI GI	g3135265
BLAST score	267
E value	7.0e-24
Match length	65
% identity	75
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	49627
Seq. ID	rlr700901996.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	50
E value	3.0e-19
Match length	70
% identity	93
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	49628

Seq. ID	rlr700902007.h1
Method	BLASTX
NCBI GI	g3255943
BLAST score	205
E value	3.0e-24
Match length	66
% identity	85
NCBI Description	(AJ007333) PP2A1 protein [Catharanthus roseus]

Seq. No.	49629
Seq. ID	rlr700902026.h1
Method	BLASTN
NCBI GI	g170393
BLAST score	51
E value	7.0e-20
Match length	103
% identity	87
NCBI Description	Tomato chlorophyll a-binding protein (Cab10A) gene, complete cds

Seq. No.	49630
Seq. ID	rlr700902147.h1
Method	BLASTX
NCBI GI	g3935157
BLAST score	165
E value	8.0e-12
Match length	76
% identity	43
NCBI Description	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No.	49631
Seq. ID	rlr700902159.h1
Method	BLASTN
NCBI GI	g4324966
BLAST score	249
E value	1.0e-138
Match length	249
% identity	100
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No.	49632
Seq. ID	rlr700902164.h1
Method	BLASTX
NCBI GI	g431162
BLAST score	230
E value	1.0e-19
Match length	76
% identity	53
NCBI Description	(D21822) ORF [Lilium longiflorum]

Seq. No.	49633
Seq. ID	rlr700902192.h1
Method	BLASTX
NCBI GI	g4558557
BLAST score	256
E value	2.0e-22
Match length	83

% identity	59
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	49634
Seq. ID	rlr700902317.h1
Method	BLASTX
NCBI GI	g4467147
BLAST score	243
E value	7.0e-21
Match length	51
% identity	92
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	49635
Seq. ID	rlr700902322.h1
Method	BLASTX
NCBI GI	g4115377
BLAST score	190
E value	1.0e-14
Match length	50
% identity	74
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	49636
Seq. ID	rlr700902352.h1
Method	BLASTN
NCBI GI	g296408
BLAST score	115
E value	2.0e-58
Match length	143
% identity	95
NCBI Description	G.max ADR12 mRNA

Seq. No.	49637
Seq. ID	rlr700902376.h1
Method	BLASTX
NCBI GI	g4091817
BLAST score	194
E value	3.0e-15
Match length	69
% identity	59
NCBI Description	(AF055375) ribosomal protein L14 [Schizosaccharomyces pombe]

Seq. No.	49638
Seq. ID	rlr700902415.h1
Method	BLASTX
NCBI GI	g4190952
BLAST score	260
E value	6.0e-23
Match length	68
% identity	69
NCBI Description	(AB022689) similar to hsr203J [Lycopersicon esculentum]

Seq. No.	49639
Seq. ID	rlr700902421.h1

Method	BLASTN
NCBI GI	g2606080
BLAST score	43
E value	4.0e-15
Match length	63
% identity	92
NCBI Description	Glycine max sucrose synthase (SS) mRNA, complete cds

Seq. No.	49640
Seq. ID	rlr700902428.h1
Method	BLASTN
NCBI GI	g2564044
BLAST score	35
E value	2.0e-10
Match length	115
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	49641
Seq. ID	rlr700902431.h1
Method	BLASTN
NCBI GI	g4127861
BLAST score	55
E value	2.0e-22
Match length	79
% identity	92
NCBI Description	Glycine max mRNA for glyoxalase I

Seq. No.	49642
Seq. ID	rlr700902460.h1
Method	BLASTN
NCBI GI	g2564044
BLAST score	35
E value	2.0e-10
Match length	93
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	49643
Seq. ID	rlr700902477.h1
Method	BLASTX
NCBI GI	g4469020
BLAST score	161
E value	1.0e-11
Match length	33
% identity	85
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	49644
Seq. ID	rlr700902480.h1
Method	BLASTN
NCBI GI	g1163180
BLAST score	53
E value	3.0e-21

Match length	53
% identity	100
NCBI Description	Glycine max arginine decarboxylase mRNA, complete cds

Seq. No.	49645
Seq. ID	rlr700902488.h1
Method	BLASTN
NCBI GI	g18761
BLAST score	42
E value	6.0e-15
Match length	114
% identity	84
NCBI Description	Soybean stem mRNA for 31 kD glycoprotein

Seq. No.	49646
Seq. ID	rrt700645939.h1
Method	BLASTX
NCBI GI	g3582442
BLAST score	246
E value	3.0e-21
Match length	90
% identity	58
NCBI Description	(AB017335) kinesin-like DNA binding protein [Homo sapiens]

Seq. No.	49647
Seq. ID	rrt700645952.h1
Method	BLASTN
NCBI GI	g624220
BLAST score	88
E value	6.0e-42
Match length	171
% identity	88
NCBI Description	Oryza sativa signal recognition particle 19 kDa protein subunit SRP19 mRNA, complete cds

Seq. No.	49648
Seq. ID	rrt700645981.h1
Method	BLASTX
NCBI GI	g1752734
BLAST score	262
E value	4.0e-23
Match length	86
% identity	57
NCBI Description	(D78510) beta-glucan-elicitor receptor [Glycine max]

Seq. No.	49649
Seq. ID	rrt700646007.h1
Method	BLASTN
NCBI GI	g20138
BLAST score	44
E value	1.0e-15
Match length	68
% identity	93
NCBI Description	O.sativa random single-copy DNA fragment 08RG108F

Seq. No.	49650
Seq. ID	rrt700646021.h1

Method	BLASTX
NCBI GI	g2108252
BLAST score	378
E value	1.0e-36
Match length	91
% identity	44
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	49651
Seq. ID	rrt700646040.h1
Method	BLASTX
NCBI GI	g2827666
BLAST score	166
E value	7.0e-12
Match length	43
% identity	72
NCBI Description	(AL021637) hypothetical protein [Arabidopsis thaliana] >gi_2982429_emb_CAA18237_ (AL022224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49652
Seq. ID	rrt700646056.h1
Method	BLASTN
NCBI GI	g544699
BLAST score	63
E value	2.0e-27
Match length	74
% identity	96
NCBI Description	LHC Ib-21=light-harvesting complex I [Hordeum vulgare=barley, Prato, mRNA Chloroplast, 878 nt]

Seq. No.	49653
Seq. ID	rrt700646064.h1
Method	BLASTX
NCBI GI	g3377820
BLAST score	245
E value	2.0e-21
Match length	62
% identity	79
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	49654
Seq. ID	rrt700646072.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	47
E value	2.0e-17
Match length	59
% identity	95
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	49655
Seq. ID	rrt700646073.h1

Method	BLASTX
NCBI GI	g1709990
BLAST score	209
E value	7.0e-17
Match length	50
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L35A

Seq. No.	49656
Seq. ID	rrt700646082.h1
Method	BLASTX
NCBI GI	g2253010
BLAST score	236
E value	2.0e-20
Match length	56
% identity	77
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	49657
Seq. ID	rry700808415.h1
Method	BLASTX
NCBI GI	g4006886
BLAST score	260
E value	6.0e-23
Match length	76
% identity	63
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	49658
Seq. ID	rry700808420.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	265
E value	1.0e-147
Match length	265
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	49659
Seq. ID	rry700808460.h1
Method	BLASTN
NCBI GI	g255580
BLAST score	111
E value	1.0e-55
Match length	215
% identity	88
NCBI Description	small auxin up RNA gene cluster: orf 10A5 [Glycine max=soybeans, cv. Wayne, Genomic, 646 nt]

Seq. No.	49660
Seq. ID	rry700808473.h1
Method	BLASTX
NCBI GI	g2245118
BLAST score	155
E value	7.0e-11
Match length	38

% identity	74
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49661
Seq. ID	rry700808477.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	253
E value	1.0e-140
Match length	257
% identity	100
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	49662
Seq. ID	rry700808488.h1
Method	BLASTX
NCBI GI	g3329366
BLAST score	243
E value	6.0e-21
Match length	74
% identity	61
NCBI Description	(AF031243) nodule-specific protein Nlj70 [Lotus japonicus]

Seq. No.	49663
Seq. ID	rry700808489.h1
Method	BLASTX
NCBI GI	g1076685
BLAST score	212
E value	2.0e-17
Match length	55
% identity	76
NCBI Description	SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ (D30038) SPF1 protein [Ipomoea batatas]

Seq. No.	49664
Seq. ID	sat701002716.h2
Method	BLASTX
NCBI GI	g2832660
BLAST score	167
E value	3.0e-12
Match length	43
% identity	67
NCBI Description	(AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No.	49665
Seq. ID	sat701002727.h2
Method	BLASTX
NCBI GI	g4091117
BLAST score	156
E value	1.0e-10
Match length	38
% identity	76
NCBI Description	(AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No.	49666
Seq. ID	sat701002729.h2

Method	BLASTX
NCBI GI	g984756
BLAST score	189
E value	1.0e-14
Match length	90
% identity	54
NCBI Description	(Z54153) chilling-inducible protein [Oryza sativa]

Seq. No.	49667
Seq. ID	sat701002739.h2
Method	BLASTX
NCBI GI	g2213608
BLAST score	176
E value	4.0e-13
Match length	88
% identity	39
NCBI Description	(AC000103) F21J9.2 [Arabidopsis thaliana]

Seq. No.	49668
Seq. ID	sat701002740.h2
Method	BLASTX
NCBI GI	g4139230
BLAST score	199
E value	1.0e-15
Match length	90
% identity	53
NCBI Description	(AF109243) mismatch repair protein [Arabidopsis thaliana]

Seq. No.	49669
Seq. ID	sat701002841.h1
Method	BLASTN
NCBI GI	g410285
BLAST score	108
E value	7.0e-54
Match length	171
% identity	91
NCBI Description	Pisum sativum rho (ras-related) GTP-binding protein mRNA, complete cds

Seq. No.	49670
Seq. ID	sat701002858.h1
Method	BLASTN
NCBI GI	g2209357
BLAST score	81
E value	8.0e-38
Match length	190
% identity	86
NCBI Description	Mangifera indica beta-D-galactosidase (SP26) mRNA, partial cds

Seq. No.	49671
Seq. ID	sat701002911.h1
Method	BLASTX
NCBI GI	g2281088
BLAST score	181
E value	1.0e-13
Match length	69

% identity	52
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	49672
Seq. ID	sat701002957.h1
Method	BLASTX
NCBI GI	g2465925
BLAST score	194
E value	4.0e-15
Match length	91
% identity	46
NCBI Description	(AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	49673
Seq. ID	sat701003029.h1
Method	BLASTX
NCBI GI	g3879583
BLAST score	179
E value	2.0e-13
Match length	83
% identity	47
NCBI Description	(Z81587) cDNA EST yk213d3.5 comes from this gene [Caenorhabditis elegans] >gi_3880444_emb_CAB04894_ (Z82062) cDNA EST yk213d3.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	49674
Seq. ID	sat701003031.h1
Method	BLASTX
NCBI GI	g1703478
BLAST score	339
E value	1.0e-34
Match length	84
% identity	88
NCBI Description	(U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana]

Seq. No.	49675
Seq. ID	sat701003063.h1
Method	BLASTX
NCBI GI	g2688299
BLAST score	248
E value	1.0e-21
Match length	83
% identity	55
NCBI Description	(AE001145) prolyl-tRNA synthetase (proS) [Borrelia burgdorferi]

Seq. No.	49676
Seq. ID	sat701003163.h1
Method	BLASTX
NCBI GI	g3415113
BLAST score	132
E value	2.0e-11
Match length	95

% identity	37
NCBI Description	(AF081201) villin 1 [Arabidopsis thaliana]

Seq. No.	49677
Seq. ID	sat701003211.h1
Method	BLASTX
NCBI GI	g2129635
BLAST score	330
E value	4.0e-31
Match length	96
% identity	64
NCBI Description	light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_ (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No.	49678
Seq. ID	sat701003243.h1
Method	BLASTX
NCBI GI	g4262225
BLAST score	405
E value	7.0e-40
Match length	90
% identity	79
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	49679
Seq. ID	sat701003253.h1
Method	BLASTX
NCBI GI	g2598575
BLAST score	258
E value	1.0e-22
Match length	85
% identity	56
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	49680
Seq. ID	sat701003302.h1
Method	BLASTX
NCBI GI	g881917
BLAST score	136
E value	1.0e-08
Match length	50
% identity	60
NCBI Description	(U14624) 3-hydroxy-3-methylglutaryl coenzyme A reductase [Artemisia annua]

Seq. No.	49681
Seq. ID	sat701003329.h1
Method	BLASTX
NCBI GI	g1931619
BLAST score	160
E value	2.0e-11
Match length	45
% identity	71
NCBI Description	(U93208) glyceraldehyde 3-phosphate dehydrogenase [Lycopersicon esculentum]

Seq. No.	49682
Seq. ID	sat701003334.h1
Method	BLASTN
NCBI GI	g169936
BLAST score	75
E value	3.0e-34
Match length	95
% identity	95
NCBI Description	Glycine max chalcone synthase (chs7) gene, complete cds

Seq. No.	49683
Seq. ID	sat701003350.h1
Method	BLASTN
NCBI GI	g3702737
BLAST score	32
E value	1.0e-08
Match length	56
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	49684
Seq. ID	sat701003377.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	300
E value	1.0e-27
Match length	73
% identity	82
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	49685
Seq. ID	sat701003380.h1
Method	BLASTX
NCBI GI	g4455316
BLAST score	239
E value	2.0e-20
Match length	70
% identity	60
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	49686
Seq. ID	sat701003410.h1
Method	BLASTX
NCBI GI	g3860247
BLAST score	235
E value	4.0e-20
Match length	62
% identity	77
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	49687
Seq. ID	sat701003434.h1
Method	BLASTX
NCBI GI	g2262105
BLAST score	169

E value	2.0e-19
Match length	69
% identity	66
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	49688
Seq. ID	sat701003435.h1
Method	BLASTX
NCBI GI	g4099482
BLAST score	139
E value	2.0e-16
Match length	73
% identity	55
NCBI Description	(U87791) eRFS [Homo sapiens]

Seq. No.	49689
Seq. ID	sat701003482.h1
Method	BLASTX
NCBI GI	g1076746
BLAST score	259
E value	5.0e-23
Match length	73
% identity	70
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	49690
Seq. ID	sat701003507.h1
Method	BLASTX
NCBI GI	g2160694
BLAST score	291
E value	1.0e-26
Match length	82
% identity	66
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	49691
Seq. ID	sat701003586.h1
Method	BLASTN
NCBI GI	g170772
BLAST score	60
E value	3.0e-25
Match length	176
% identity	84
NCBI Description	Triticum aestivum S-adenosyl-L-homocysteine hydrolase (SH6.2) mRNA, complete cds

Seq. No.	49692
Seq. ID	sat701003621.h1
Method	BLASTX
NCBI GI	g3135254
BLAST score	300
E value	1.0e-27
Match length	88
% identity	60

NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49693
Seq. ID	sat701003692.h1
Method	BLASTX
NCBI GI	g627469
BLAST score	188
E value	2.0e-14
Match length	87
% identity	8
NCBI Description	hypothetical protein 2 - human (fragment)

Seq. No.	49694
Seq. ID	sat701003736.h1
Method	BLASTN
NCBI GI	g1326160
BLAST score	62
E value	2.0e-26
Match length	138
% identity	93
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	49695
Seq. ID	sat701003747.h1
Method	BLASTX
NCBI GI	g2369766
BLAST score	164
E value	1.0e-11
Match length	56
% identity	59
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	49696
Seq. ID	sat701003772.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	184
E value	3.0e-99
Match length	220
% identity	96
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	49697
Seq. ID	sat701003779.h1
Method	BLASTX
NCBI GI	g2739309
BLAST score	190
E value	6.0e-23
Match length	86
% identity	31
NCBI Description	(Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No.	49698
Seq. ID	sat701003793.h1
Method	BLASTX
NCBI GI	g2052029

BLAST score	196
E value	1.0e-18
Match length	61
% identity	71
NCBI Description	(Y10820) glutathione transferase [Glycine max]

Seq. No.	49699
Seq. ID	sat701003802.h1
Method	BLASTX
NCBI GI	g3341697
BLAST score	170
E value	2.0e-12
Match length	39
% identity	85
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49700
Seq. ID	sat701003804.h1
Method	BLASTX
NCBI GI	g4191793
BLAST score	201
E value	5.0e-16
Match length	86
% identity	55
NCBI Description	(AC005917) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	49701
Seq. ID	sat701003822.h1
Method	BLASTN
NCBI GI	g4263753
BLAST score	34
E value	9.0e-10
Match length	58
% identity	90
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	49702
Seq. ID	sat701003827.h1
Method	BLASTN
NCBI GI	g14146
BLAST score	120
E value	4.0e-61
Match length	196
% identity	90
NCBI Description	Oenothera elata subsp. hookeri plastid DNA for psbB, psbH and psbN genes for chlorophyll a-binding apoprotein, 10 kDa phosphoprotein, and unknown protein of photosystem II, respectively

Seq. No.	49703
Seq. ID	sat701003837.h1
Method	BLASTX
NCBI GI	g2804280
BLAST score	288
E value	3.0e-26

Match length	85
% identity	65
NCBI Description	(AB003687) 6-4 photolyase [Arabidopsis thaliana] >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase [Arabidopsis thaliana]

Seq. No.	49704
Seq. ID	sat701003838.h1
Method	BLASTX
NCBI GI	g1176658
BLAST score	240
E value	1.0e-20
Match length	88
% identity	58
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	49705
Seq. ID	sat701003870.h1
Method	BLASTX
NCBI GI	g3327870
BLAST score	226
E value	6.0e-19
Match length	56
% identity	73
NCBI Description	(AB012913) COP1-Interacting ProteinI 7 (CIP7) [Arabidopsis thaliana]

Seq. No.	49706
Seq. ID	sat701003877.h1
Method	BLASTX
NCBI GI	g3068704
BLAST score	349
E value	2.0e-33
Match length	85
% identity	76
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	49707
Seq. ID	sat701003936.h1
Method	BLASTX
NCBI GI	g4510348
BLAST score	256
E value	1.0e-22
Match length	73
% identity	60
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	49708
Seq. ID	sat701004078.h1
Method	BLASTN
NCBI GI	g1150931
BLAST score	44
E value	1.0e-15
Match length	56
% identity	95

NCBI Description	M.sativa mRNA for cyclin protein

Seq. No.	49709
Seq. ID	sat701004084.h1
Method	BLASTX
NCBI GI	g2947066
BLAST score	155
E value	1.0e-10
Match length	63
% identity	17
NCBI Description	(AC002521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49710
Seq. ID	sat701004167.h1
Method	BLASTX
NCBI GI	g231799
BLAST score	149
E value	6.0e-10
Match length	60
% identity	55
NCBI Description	CHALCONE SYNTHASE 7 (NARINGENIN-CHALCONE SYNTHASE 7) >gi_478407_pir__JQ2250 naringenin-chalcone synthase (EC 2.3.1.74) - soybean >gi_169937 (M98871) chalcone synthase [Glycine max]

Seq. No.	49711
Seq. ID	sat701004252.h1
Method	BLASTX
NCBI GI	g4377180
BLAST score	172
E value	1.0e-12
Match length	77
% identity	42
NCBI Description	(AE001667) Phosphoglycerate Mutase [Chlamydia pneumoniae]

Seq. No.	49712
Seq. ID	sat701004254.h1
Method	BLASTX
NCBI GI	g2244866
BLAST score	207
E value	7.0e-17
Match length	79
% identity	53
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49713
Seq. ID	sat701004312.h1
Method	BLASTX
NCBI GI	g2281088
BLAST score	153
E value	2.0e-10
Match length	65
% identity	42
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	49714

Seq. ID	sat701004385.h1
Method	BLASTX
NCBI GI	g4335749
BLAST score	215
E value	9.0e-18
Match length	80
% identity	74
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	49715
Seq. ID	sat701004396.h1
Method	BLASTX
NCBI GI	g2244826
BLAST score	298
E value	2.0e-27
Match length	73
% identity	74
NCBI Description	(Z97336) replication control protein homolog [Arabidopsis thaliana]

Seq. No.	49716
Seq. ID	sat701004427.h1
Method	BLASTX
NCBI GI	g3738338
BLAST score	158
E value	6.0e-11
Match length	67
% identity	54
NCBI Description	(AC005170) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	49717
Seq. ID	sat701004429.h1
Method	BLASTX
NCBI GI	g3395440
BLAST score	174
E value	9.0e-13
Match length	49
% identity	53
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49718
Seq. ID	sat701004456.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	306
E value	3.0e-28
Match length	67
% identity	90
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	49719
Seq. ID	sat701004460.h1
Method	BLASTN
NCBI GI	g1518539
BLAST score	113
E value	7.0e-57

Match length	265
% identity	87
NCBI Description	Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No.	49720
Seq. ID	sat701004469.h1
Method	BLASTX
NCBI GI	g3600032
BLAST score	286
E value	6.0e-26
Match length	93
% identity	65
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	49721
Seq. ID	sat701004517.h1
Method	BLASTX
NCBI GI	g3935177
BLAST score	252
E value	3.0e-24
Match length	66
% identity	89
NCBI Description	(AC004557) F17L21.20 [Arabidopsis thaliana]

Seq. No.	49722
Seq. ID	sat701004539.h1
Method	BLASTX
NCBI GI	g2827662
BLAST score	218
E value	5.0e-18
Match length	87
% identity	52
NCBI Description	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	49723
Seq. ID	sat701004560.h1
Method	BLASTN
NCBI GI	g3322538
BLAST score	35
E value	2.0e-10
Match length	47
% identity	94
NCBI Description	Treponema pallidum section 24 of 87 of the complete genome

Seq. No.	49724
Seq. ID	sat701004578.h1
Method	BLASTX
NCBI GI	g1669341
BLAST score	235
E value	5.0e-20
Match length	87
% identity	60
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	49725
Seq. ID	sat701004591.h1
Method	BLASTN
NCBI GI	g1854444
BLAST score	88
E value	5.0e-42
Match length	180
% identity	87
NCBI Description	Vigna unguiculata mRNA for CPRD14 protein, complete cds

Seq. No.	49726
Seq. ID	sat701004595.h1
Method	BLASTX
NCBI GI	g3063446
BLAST score	260
E value	6.0e-23
Match length	85
% identity	61
NCBI Description	(AC003981) F22O13.8 [Arabidopsis thaliana]

Seq. No.	49727
Seq. ID	sat701004616.h1
Method	BLASTX
NCBI GI	g1771160
BLAST score	294
E value	6.0e-27
Match length	81
% identity	67
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	49728
Seq. ID	sat701004647.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	255
E value	1.0e-141
Match length	267
% identity	99
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	49729
Seq. ID	sat701004735.h1
Method	BLASTX
NCBI GI	g4455287
BLAST score	103
E value	3.0e-09
Match length	49
% identity	67
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	49730
Seq. ID	sat701004764.h1
Method	BLASTX

NCBI GI	g2702274
BLAST score	114
E value	1.0e-13
Match length	68
% identity	60
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]

Seq. No.	49731
Seq. ID	sat701004785.h1
Method	BLASTX
NCBI GI	g2443886
BLAST score	152
E value	3.0e-10
Match length	45
% identity	73
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	49732
Seq. ID	sat701004833.h1
Method	BLASTX
NCBI GI	g4539301
BLAST score	412
E value	9.0e-41
Match length	89
% identity	88
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	49733
Seq. ID	sat701004846.h1
Method	BLASTX
NCBI GI	g1351274
BLAST score	377
E value	1.0e-36
Match length	87
% identity	85
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_256120_bbs_114967 (S46215) triose phosphate isomerase, TPI [Lactuca sativa=lettuce, Peptide Partial, 195 aa] [Lactuca sativa]

Seq. No.	49734
Seq. ID	sat701004885.h1
Method	BLASTX
NCBI GI	g1236961
BLAST score	167
E value	5.0e-12
Match length	46
% identity	65
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	49735
Seq. ID	sat701004891.h1
Method	BLASTX
NCBI GI	g4115925
BLAST score	275
E value	1.0e-24

Match length	81
% identity	52
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	49736
Seq. ID	sat701004927.h1
Method	BLASTX
NCBI GI	g3702341
BLAST score	226
E value	6.0e-19
Match length	86
% identity	50
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49737
Seq. ID	sat701004960.h1
Method	BLASTX
NCBI GI	g2342730
BLAST score	255
E value	2.0e-22
Match length	88
% identity	65
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49738
Seq. ID	sat701005050.h1
Method	BLASTX
NCBI GI	g3176662
BLAST score	270
E value	4.0e-24
Match length	72
% identity	78
NCBI Description	(AC004393) Similar to mannosyl-oligosaccharide glucosidase gb_X87237 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	49739
Seq. ID	sat701005202.h1
Method	BLASTN
NCBI GI	g1545804
BLAST score	43
E value	3.0e-15
Match length	43
% identity	100
NCBI Description	Nicotiana tabacum mRNA for cytochrome P450 like_TBP, complete cds

Seq. No.	49740
Seq. ID	sat701005244.h1
Method	BLASTX
NCBI GI	g1709006
BLAST score	486
E value	2.0e-49
Match length	94
% identity	95

NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_726032 (U17241) S-adenosylmethionine synthetase [Actinidia chinensis]

Seq. No.	49741
Seq. ID	sat701005283.h1
Method	BLASTX
NCBI GI	g2495184
BLAST score	391
E value	3.0e-38
Match length	89
% identity	83
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO) >gi_1877018_dbj_BAA11820_ (D83139) protoporphyrinogen oxidase [Arabidopsis thaliana]

Seq. No.	49742
Seq. ID	sat701005293.h1
Method	BLASTN
NCBI GI	g1326160
BLAST score	67
E value	2.0e-29
Match length	143
% identity	95
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	49743
Seq. ID	sat701005317.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	185
E value	1.0e-100
Match length	221
% identity	96
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	49744
Seq. ID	sat701005343.h1
Method	BLASTX
NCBI GI	g3080388
BLAST score	196
E value	2.0e-15
Match length	38
% identity	82
NCBI Description	(AL022603) myb-related protein [Arabidopsis thaliana] >gi_3402763_emb_CAA20209.1_ (AL031187) myb-related protein M4 [Arabidopsis thaliana]

Seq. No.	49745
Seq. ID	sat701005371.h1
Method	BLASTX
NCBI GI	g3402683
BLAST score	197
E value	1.0e-15
Match length	55

% identity	69
NCBI Description	(AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No.	49746
Seq. ID	sat701005372.h1
Method	BLASTX
NCBI GI	g3927831
BLAST score	151
E value	3.0e-10
Match length	73
% identity	70
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	49747
Seq. ID	sat701005437.h1
Method	BLASTX
NCBI GI	g4512658
BLAST score	153
E value	2.0e-10
Match length	49
% identity	61
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49748
Seq. ID	sat701005496.h1
Method	BLASTN
NCBI GI	g3264762
BLAST score	72
E value	2.0e-32
Match length	187
% identity	85
NCBI Description	Prunus armeniaca 40S ribosomal protein S4 (RPS4) mRNA, complete cds

Seq. No.	49749
Seq. ID	sat701005703.h1
Method	BLASTX
NCBI GI	g4127662
BLAST score	273
E value	2.0e-24
Match length	91
% identity	53
NCBI Description	(Y11176) fructosidase [Cichorium intybus]

Seq. No.	49750
Seq. ID	sat701005917.h1
Method	BLASTX
NCBI GI	g1171642
BLAST score	182
E value	9.0e-14
Match length	47
% identity	70
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK >gi_481206_pir__S38326 protein kinase - Arabidopsis thaliana >gi_166809 (L07248) protein kinase [Arabidopsis thaliana]

Seq. No.	49751
Seq. ID	sat701005928.h1
Method	BLASTX
NCBI GI	g4559333
BLAST score	254
E value	3.0e-22
Match length	84
% identity	48
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	49752
Seq. ID	sat701005950.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	258
E value	1.0e-143
Match length	262
% identity	100
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	49753
Seq. ID	sat701005952.h1
Method	BLASTX
NCBI GI	g4126473
BLAST score	183
E value	6.0e-14
Match length	86
% identity	50
NCBI Description	(AB014884) adenylyl cyclase associated protein [Gossypium hirsutum]

Seq. No.	49754
Seq. ID	sat701005971.h1
Method	BLASTX
NCBI GI	g1931642
BLAST score	350
E value	2.0e-33
Match length	85
% identity	81
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	49755
Seq. ID	sat701006026.h2
Method	BLASTX
NCBI GI	g2499708
BLAST score	288
E value	3.0e-26
Match length	63
% identity	78
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea mays]

Seq. No. 49756

Seq. ID	sat701006037.h2
Method	BLASTX
NCBI GI	g3415117
BLAST score	306
E value	1.0e-30
Match length	79
% identity	74
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	49757
Seq. ID	sat701006141.h1
Method	BLASTX
NCBI GI	g3183088
BLAST score	182
E value	9.0e-14
Match length	67
% identity	54
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	49758
Seq. ID	sat701006159.h1
Method	BLASTX
NCBI GI	g2582351
BLAST score	150
E value	5.0e-10
Match length	77
% identity	35
NCBI Description	(AF018639) unknown [Dictyostelium discoideum]

Seq. No.	49759
Seq. ID	sat701006219.h2
Method	BLASTX
NCBI GI	g2827621
BLAST score	146
E value	1.0e-09
Match length	25
% identity	100
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	49760
Seq. ID	sat701006261.h2
Method	BLASTX
NCBI GI	g2765244
BLAST score	148
E value	3.0e-14
Match length	80
% identity	51
NCBI Description	(Y12807) invertase inhibitor homolog [Arabidopsis thaliana]

Seq. No.	49761
Seq. ID	sat701006271.h2
Method	BLASTX
NCBI GI	g4049353
BLAST score	190

E value	7.0e-27
Match length	88
% identity	65
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	49762
Seq. ID	sat701006289.h2
Method	BLASTX
NCBI GI	g3183088
BLAST score	169
E value	3.0e-12
Match length	57
% identity	60
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	49763
Seq. ID	sat701006302.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	79
E value	4.0e-37
Match length	99
% identity	95
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	49764
Seq. ID	sat701006356.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	91
E value	4.0e-44
Match length	127
% identity	93
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	49765
Seq. ID	sat701006450.h1
Method	BLASTX
NCBI GI	g3461814
BLAST score	140
E value	4.0e-09
Match length	43
% identity	60
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49766
Seq. ID	sat701006456.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	82
E value	9.0e-39
Match length	126
% identity	91
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	49767
Seq. ID	sat701006473.h1
Method	BLASTN
NCBI GI	g2196549
BLAST score	150
E value	6.0e-79
Match length	182
% identity	96
NCBI Description	Glycine max mRNA for beta-amylase, complete cds

Seq. No.	49768
Seq. ID	sat701006572.h1
Method	BLASTN
NCBI GI	g1370143
BLAST score	94
E value	1.0e-45
Match length	174
% identity	94
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAB11B

Seq. No.	49769
Seq. ID	sat701006588.h1
Method	BLASTX
NCBI GI	g3915039
BLAST score	289
E value	2.0e-26
Match length	88
% identity	58
NCBI Description	SUGAR CARRIER PROTEIN C >gi_169718 (L08196) sugar carrier protein [Ricinus communis]

Seq. No.	49770
Seq. ID	sat701006595.h1
Method	BLASTX
NCBI GI	g2244814
BLAST score	198
E value	1.0e-15
Match length	62
% identity	63
NCBI Description	(Z97336) protein kinase [Arabidopsis thaliana]

Seq. No.	49771
Seq. ID	sat701006617.h1
Method	BLASTN
NCBI GI	g497899
BLAST score	46
E value	6.0e-17
Match length	110
% identity	85
NCBI Description	Populus trichocarpa * Populus deltoides (clone sam.Pdx.Pt.2) S-adenosyl methionine synthetase mRNA, complete cds

Seq. No.	49772
Seq. ID	sat701006645.h1
Method	BLASTX

NCBI GI	g3540195
BLAST score	157
E value	4.0e-11
Match length	55
% identity	25
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	49773
Seq. ID	sat701006677.h1
Method	BLASTX
NCBI GI	g3702338
BLAST score	142
E value	4.0e-09
Match length	45
% identity	60
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	49774
Seq. ID	sat701006774.h1
Method	BLASTX
NCBI GI	g4539459
BLAST score	170
E value	2.0e-12
Match length	65
% identity	45
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	49775
Seq. ID	sat701006812.h1
Method	BLASTN
NCBI GI	g3320378
BLAST score	112
E value	3.0e-56
Match length	272
% identity	85
NCBI Description	Medicago sativa putative JUN kinase activation domain binding protein mRNA, complete cds

Seq. No.	49776
Seq. ID	sat701006882.h1
Method	BLASTX
NCBI GI	g4220485
BLAST score	189
E value	2.0e-14
Match length	102
% identity	46
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	49777
Seq. ID	sat701006896.h1
Method	BLASTX
NCBI GI	g3128209
BLAST score	235
E value	3.0e-20
Match length	51
% identity	84

NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]
Seq. No.	49778
Seq. ID	sat701007010.h1
Method	BLASTX
NCBI GI	g4432840
BLAST score	189
E value	1.0e-14
Match length	80
% identity	47
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.	49779
Seq. ID	sat701007046.h1
Method	BLASTX
NCBI GI	g3319682
BLAST score	307
E value	2.0e-28
Match length	73
% identity	21
NCBI Description	(Y17720) SPINDLY protein [Petunia x hybrida]
Seq. No.	49780
Seq. ID	sat701007132.h1
Method	BLASTX
NCBI GI	g4567227
BLAST score	291
E value	1.0e-26
Match length	80
% identity	64
NCBI Description	(AC007119) putative transport protein [Arabidopsis thaliana]
Seq. No.	49781
Seq. ID	sat701007135.h1
Method	BLASTX
NCBI GI	g730536
BLAST score	241
E value	6.0e-21
Match length	62
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal protein subunit L17 [Nicotiana tabacum]
Seq. No.	49782
Seq. ID	sat701007191.h1
Method	BLASTX
NCBI GI	g2498731
BLAST score	275
E value	9.0e-25
Match length	79
% identity	63
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	49783
Seq. ID	sat701007194.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	258
E value	9.0e-23
Match length	81
% identity	58
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	49784
Seq. ID	sat701007203.h2
Method	BLASTX
NCBI GI	g3860251
BLAST score	237
E value	2.0e-32
Match length	87
% identity	79
NCBI Description	(AC005824) putative permease [Arabidopsis thaliana]

Seq. No.	49785
Seq. ID	sat701007214.h2
Method	BLASTN
NCBI GI	g1675195
BLAST score	116
E value	1.0e-58
Match length	208
% identity	89
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	49786
Seq. ID	sat701007248.h2
Method	BLASTN
NCBI GI	g457569
BLAST score	78
E value	4.0e-36
Match length	162
% identity	88
NCBI Description	Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No.	49787
Seq. ID	sat701007251.h2
Method	BLASTX
NCBI GI	g2588818
BLAST score	244
E value	1.0e-28
Match length	74
% identity	86
NCBI Description	(D88927) cytosolic phosphoglucose isomerase [Dioscorea tokoro]

Seq. No.	49788
Seq. ID	sat701007264.h2
Method	BLASTX
NCBI GI	g82263
BLAST score	235

E value	3.0e-20
Match length	62
% identity	74
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	49789
Seq. ID	sat701007266.h2
Method	BLASTX
NCBI GI	g2829867
BLAST score	148
E value	5.0e-10
Match length	48
% identity	67
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	49790
Seq. ID	sat701007270.h2
Method	BLASTX
NCBI GI	g123656
BLAST score	178
E value	2.0e-13
Match length	50
% identity	72
NCBI Description	CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED PROTEIN >gi_285407_pir__A42582 heat shock protein SCE70 - spinach >gi_21338_emb_CAA43711_ (X61491) 70 kDa heat shock protein [Spinacia oleracea]

Seq. No.	49791
Seq. ID	sat701007284.h2
Method	BLASTX
NCBI GI	g4006882
BLAST score	240
E value	1.0e-21
Match length	86
% identity	62
NCBI Description	(Z99707) UDP-glucuronyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	49792
Seq. ID	sat701007291.h2
Method	BLASTN
NCBI GI	g2687433
BLAST score	34
E value	8.0e-10
Match length	98
% identity	84
NCBI Description	Tragopogon dubius large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	49793
Seq. ID	sat701007295.h2
Method	BLASTX
NCBI GI	g2058311
BLAST score	163
E value	1.0e-11

Match length	54
% identity	59
NCBI Description	(X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No.	49794
Seq. ID	sat701007309.h2
Method	BLASTX
NCBI GI	g4468984
BLAST score	158
E value	6.0e-11
Match length	70
% identity	43
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	49795
Seq. ID	sat701007325.h2
Method	BLASTN
NCBI GI	g3449327
BLAST score	41
E value	6.0e-14
Match length	175
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	49796
Seq. ID	sat701007327.h2
Method	BLASTX
NCBI GI	g4455683
BLAST score	163
E value	1.0e-11
Match length	83
% identity	43
NCBI Description	(AL035472) possible tRNA pseudouridine synthase B [Mycobacterium leprae]

Seq. No.	49797
Seq. ID	sat701007343.h2
Method	BLASTX
NCBI GI	g3023817
BLAST score	322
E value	3.0e-30
Match length	68
% identity	90
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	49798
Seq. ID	sat701007371.h2
Method	BLASTX
NCBI GI	g2894600
BLAST score	254
E value	3.0e-22
Match length	87
% identity	32
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	49799
Seq. ID	sat701007375.h2
Method	BLASTX
NCBI GI	g4006868
BLAST score	170
E value	2.0e-12
Match length	49
% identity	67
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	49800
Seq. ID	sat701007423.h2
Method	BLASTX
NCBI GI	g2832408
BLAST score	271
E value	3.0e-24
Match length	57
% identity	86
NCBI Description	(Y14209) R2R3-MYB transcription factor [Arabidopsis thaliana]

Seq. No.	49801
Seq. ID	sat701007443.h2
Method	BLASTX
NCBI GI	g1706958
BLAST score	189
E value	2.0e-31
Match length	89
% identity	76
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	49802
Seq. ID	sat701007457.h2
Method	BLASTX
NCBI GI	g3822223
BLAST score	162
E value	2.0e-11
Match length	52
% identity	54
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	49803
Seq. ID	sat701007460.h2
Method	BLASTX
NCBI GI	g2213594
BLAST score	352
E value	1.0e-33
Match length	91
% identity	73
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	49804
Seq. ID	sat701007484.h2
Method	BLASTN
NCBI GI	g1408459

BLAST score	44
E value	1.0e-15
Match length	104
% identity	86
NCBI Description	Arabidopsis thaliana type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit mRNA, complete cds

Seq. No.	49805
Seq. ID	sat701007504.h1
Method	BLASTX
NCBI GI	g4455158
BLAST score	292
E value	1.0e-26
Match length	59
% identity	90
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	49806
Seq. ID	sat701007511.h1
Method	BLASTX
NCBI GI	g4039155
BLAST score	235
E value	6.0e-20
Match length	67
% identity	60
NCBI Description	(AF104258) putative copper-inducible 35.6 kDa protein [Festuca rubra]

Seq. No.	49807
Seq. ID	sat701007536.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	165
E value	7.0e-88
Match length	219
% identity	95
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	49808
Seq. ID	sat701007643.h1
Method	BLASTX
NCBI GI	g2501555
BLAST score	259
E value	1.0e-24
Match length	79
% identity	75
NCBI Description	POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	49809
Seq. ID	sat701007661.h1
Method	BLASTN
NCBI GI	g4314374
BLAST score	45
E value	3.0e-16
Match length	101

% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	49810
Seq. ID	sat701007664.h1
Method	BLASTX
NCBI GI	g3269290
BLAST score	168
E value	3.0e-17
Match length	72
% identity	44
NCBI Description	(AL030978) putative receptor like kinase [Arabidopsis thaliana]

Seq. No.	49811
Seq. ID	sat701007669.h1
Method	BLASTX
NCBI GI	g3850587
BLAST score	244
E value	5.0e-21
Match length	92
% identity	61
NCBI Description	(AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	49812
Seq. ID	sat701007675.h1
Method	BLASTX
NCBI GI	g3702962
BLAST score	227
E value	6.0e-19
Match length	51
% identity	86
NCBI Description	(AF079484) rac GTP binding protein Arac7 [Arabidopsis thaliana]

Seq. No.	49813
Seq. ID	sat701007678.h1
Method	BLASTN
NCBI GI	g22758
BLAST score	35
E value	3.0e-10
Match length	43
% identity	95
NCBI Description	A.thaliana HAT4 gene

Seq. No.	49814
Seq. ID	sat701007715.h1
Method	BLASTN
NCBI GI	g169344
BLAST score	61
E value	7.0e-26
Match length	217
% identity	42
NCBI Description	P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA,

exon 2

Seq. No.	49815
Seq. ID	sat701007759.h1
Method	BLASTX
NCBI GI	g4454039
BLAST score	169
E value	3.0e-12
Match length	89
% identity	40
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	49816
Seq. ID	sat701007916.h1
Method	BLASTX
NCBI GI	g1730629
BLAST score	160
E value	3.0e-11
Match length	61
% identity	52
NCBI Description	HYPOTHETICAL 43.0 KD PROTEIN B0361.6 IN CHROMOSOME III >gi_458954 (U00031) similar to H. marismortui hypothetical 23.1 kd protein in HMAL3 5' region [Caenorhabditis elegans]

Seq. No.	49817
Seq. ID	sat701007918.h1
Method	BLASTX
NCBI GI	g3540184
BLAST score	149
E value	6.0e-10
Match length	68
% identity	14
NCBI Description	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No.	49818
Seq. ID	sat701007927.h1
Method	BLASTN
NCBI GI	g4019184
BLAST score	33
E value	4.0e-09
Match length	33
% identity	26
NCBI Description	, complete sequence [Mus musculus]

Seq. No.	49819
Seq. ID	sat701007948.h1
Method	BLASTX
NCBI GI	g3608150
BLAST score	219
E value	4.0e-18
Match length	53
% identity	75
NCBI Description	(AC005314) putative peroxidase [Arabidopsis thaliana]

Seq. No.	49820
Seq. ID	sat701007950.h1

Method	BLASTX
NCBI GI	g2864609
BLAST score	141
E value	6.0e-09
Match length	36
% identity	78
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	49821
Seq. ID	sat701008034.h1
Method	BLASTX
NCBI GI	g2570047
BLAST score	177
E value	3.0e-13
Match length	78
% identity	44
NCBI Description	(Y09234) MSTK2S kinase-like protein [Mus musculus]

Seq. No.	49822
Seq. ID	sat701008133.h1
Method	BLASTX
NCBI GI	g2444174
BLAST score	187
E value	3.0e-14
Match length	87
% identity	49
NCBI Description	(U94781) unconventional myosin [Helianthus annuus]

Seq. No.	49823
Seq. ID	sat701008134.h1
Method	BLASTX
NCBI GI	g2832682
BLAST score	189
E value	1.0e-14
Match length	61
% identity	66
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49824
Seq. ID	sat701008175.h1
Method	BLASTX
NCBI GI	g1669664
BLAST score	207
E value	1.0e-16
Match length	80
% identity	45
NCBI Description	(Z49706) GTP cyclohydrolase I [Dictyostelium discoideum]

Seq. No.	49825
Seq. ID	sat701008241.h1
Method	BLASTN
NCBI GI	g4104971
BLAST score	56
E value	7.0e-23
Match length	104

% identity	88
NCBI Description	Pisum sativum spermidine synthase 1 (SPDSYN1) mRNA, complete cds

Seq. No.	49826
Seq. ID	sat701008254.h1
Method	BLASTN
NCBI GI	g170061
BLAST score	64
E value	6.0e-28
Match length	112
% identity	89
NCBI Description	Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete cds

Seq. No.	49827
Seq. ID	sat701008261.h1
Method	BLASTX
NCBI GI	g4455199
BLAST score	168
E value	4.0e-12
Match length	92
% identity	45
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	49828
Seq. ID	sat701008290.h1
Method	BLASTX
NCBI GI	g3511285
BLAST score	186
E value	2.0e-14
Match length	49
% identity	76
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	49829
Seq. ID	sat701008293.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	257
E value	1.0e-143
Match length	275
% identity	99
NCBI Description	G.max ADR6 mRNA

Seq. No.	49830
Seq. ID	sat701008362.h1
Method	BLASTX
NCBI GI	g4519671
BLAST score	204
E value	2.0e-16
Match length	83
% identity	60
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No. 49831

Seq. ID	sat701008394.h1
Method	BLASTX
NCBI GI	g3377797
BLAST score	156
E value	5.0e-11
Match length	66
% identity	58
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	49832
Seq. ID	sat701008407.h1
Method	BLASTN
NCBI GI	g2564045
BLAST score	48
E value	4.0e-18
Match length	164
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	49833
Seq. ID	sat701008422.h1
Method	BLASTX
NCBI GI	g3702121
BLAST score	159
E value	3.0e-11
Match length	83
% identity	43
NCBI Description	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]

Seq. No.	49834
Seq. ID	sat701008431.h1
Method	BLASTN
NCBI GI	g170048
BLAST score	130
E value	4.0e-67
Match length	214
% identity	41
NCBI Description	Glycine max SbPRP1 gene encoding a proline-rich protein, complete cds

Seq. No.	49835
Seq. ID	sat701008439.h1
Method	BLASTX
NCBI GI	g4510348
BLAST score	140
E value	6.0e-09
Match length	67
% identity	43
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 49836

Seq. ID	sat701008470.h1
Method	BLASTX
NCBI GI	g3914212
BLAST score	227
E value	4.0e-19
Match length	83
% identity	55
NCBI Description	5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus norvegicus]

Seq. No.	49837
Seq. ID	sat701008488.h1
Method	BLASTX
NCBI GI	g3645899
BLAST score	168
E value	3.0e-12
Match length	68
% identity	47
NCBI Description	(U68408) 5' end not determined experimentally [Zea mays]

Seq. No.	49838
Seq. ID	sat701008502.h1
Method	BLASTX
NCBI GI	g3122858
BLAST score	379
E value	7.0e-37
Match length	88
% identity	82
NCBI Description	D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate dehydrogenase [Arabidopsis thaliana] >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]

Seq. No.	49839
Seq. ID	sat701008521.h1
Method	BLASTX
NCBI GI	g3063451
BLAST score	183
E value	4.0e-14
Match length	59
% identity	59
NCBI Description	(AC003981) F22O13.13 [Arabidopsis thaliana]

Seq. No.	49840
Seq. ID	sat701008548.h1
Method	BLASTN
NCBI GI	g497899
BLAST score	84
E value	1.0e-39
Match length	176
% identity	88
NCBI Description	Populus trichocarpa * Populus deltoides (clone sam.Pdx.Pt.2) S-adenosyl methionine synthetase mRNA, complete cds

Seq. No.	49841
Seq. ID	sat701008589.h1
Method	BLASTX
NCBI GI	g4262234
BLAST score	199
E value	6.0e-16
Match length	48
% identity	71
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	49842
Seq. ID	sat701008594.h1
Method	BLASTX
NCBI GI	g2244790
BLAST score	386
E value	1.0e-37
Match length	89
% identity	90
NCBI Description	(Z97336) kinesin homolog [Arabidopsis thaliana]

Seq. No.	49843
Seq. ID	sat701008679.h1
Method	BLASTX
NCBI GI	g3283072
BLAST score	288
E value	3.0e-26
Match length	89
% identity	63
NCBI Description	(AF056022) p60 katanin [Homo sapiens]

Seq. No.	49844
Seq. ID	sat701008682.h1
Method	BLASTN
NCBI GI	g3413472
BLAST score	75
E value	3.0e-34
Match length	146
% identity	88
NCBI Description	Glycine max mRNA for tyrosine phosphatase

Seq. No.	49845
Seq. ID	sat701008769.h1
Method	BLASTX
NCBI GI	g2827659
BLAST score	276
E value	9.0e-25
Match length	93
% identity	60
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	49846
Seq. ID	sat701008774.h1
Method	BLASTX
NCBI GI	g4559334
BLAST score	325
E value	2.0e-30
Match length	94

% identity	56
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	49847
Seq. ID	sat701008783.h1
Method	BLASTX
NCBI GI	g1352461
BLAST score	176
E value	5.0e-13
Match length	45
% identity	71
NCBI Description	IN2-2 PROTEIN

Seq. No.	49848
Seq. ID	sat701008801.h1
Method	BLASTX
NCBI GI	g2529677
BLAST score	253
E value	4.0e-22
Match length	80
% identity	76
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No.	49849
Seq. ID	sat701008812.h1
Method	BLASTN
NCBI GI	g4165340
BLAST score	56
E value	7.0e-23
Match length	213
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	49850
Seq. ID	sat701008843.h1
Method	BLASTX
NCBI GI	g3935145
BLAST score	193
E value	5.0e-15
Match length	70
% identity	56
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	49851
Seq. ID	sat701008857.h1
Method	BLASTN
NCBI GI	g2739005
BLAST score	41
E value	3.0e-14
Match length	69
% identity	90
NCBI Description	Glycine max cytochrome P450 monooxygenase CYP93C1p (CYP93C1) mRNA, complete cds

Seq. No.	49852

Seq. ID	sat701009013.h1
Method	BLASTX
NCBI GI	g4455187
BLAST score	170
E value	2.0e-12
Match length	81
% identity	53
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49853
Seq. ID	sat701009116.h1
Method	BLASTX
NCBI GI	g4510417
BLAST score	142
E value	4.0e-09
Match length	34
% identity	74
NCBI Description	(AC006929) putative BEL1 homeotic protein [Arabidopsis thaliana]

Seq. No.	49854
Seq. ID	sat701009148.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	108
E value	6.0e-54
Match length	152
% identity	93
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49855
Seq. ID	sat701009168.h1
Method	BLASTX
NCBI GI	g2160158
BLAST score	166
E value	6.0e-12
Match length	42
% identity	76
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	49856
Seq. ID	sat701009174.h1
Method	BLASTN
NCBI GI	g1208704
BLAST score	79
E value	1.0e-36
Match length	140
% identity	99
NCBI Description	Glycine soja histone H3 gene, partial cds, clone H3-DGS750

Seq. No.	49857
Seq. ID	sat701009249.h1
Method	BLASTX

NCBI GI g3482931
BLAST score 333
E value 2.0e-31
Match length 84
% identity 73
NCBI Description (AC003970) germin-like protein [Arabidopsis thaliana]

Seq. No. 49858
Seq. ID sat701009304.h1
Method BLASTX
NCBI GI g2121177
BLAST score 154
E value 1.0e-10
Match length 50
% identity 56
NCBI Description hypothetical protein (transposon Tn1000) - Escherichia coli >gi_43087_emb_CAA42758_ (X60200) ORF [Escherichia coli] >gi_303568_dbj_BAA03916_ (D16449) ORF [Escherichia coli]

Seq. No. 49859
Seq. ID sat701009339.h1
Method BLASTX
NCBI GI g4580529
BLAST score 286
E value 5.0e-26
Match length 85
% identity 64
NCBI Description (AF036308) scarecrow-like 13 [Arabidopsis thaliana]

Seq. No. 49860
Seq. ID sat701009343.h1
Method BLASTX
NCBI GI g4056431
BLAST score 258
E value 1.0e-23
Match length 78
% identity 71
NCBI Description (AC005990) Similar to gb_AJ002532 endo-polygalacturonase from Arabidopsis thaliana and is a member of the polygalacturonase family PF_00295. [Arabidopsis thaliana]

Seq. No. 49861
Seq. ID sat701009394.h1
Method BLASTX
NCBI GI g2257756
BLAST score 103
E value 2.0e-09
Match length 64
% identity 53
NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] >gi_3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays]

Seq. No. 49862
Seq. ID sat701009561.h1
Method BLASTN
NCBI GI g4097568

BLAST score	83
E value	5.0e-39
Match length	126
% identity	92
NCBI Description	Glycine max farnesylated protein GMFP4 mRNA, partial cds

Seq. No.	49863
Seq. ID	sat701009563.h1
Method	BLASTX
NCBI GI	g3482921
BLAST score	230
E value	1.0e-19
Match length	81
% identity	60
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No.	49864
Seq. ID	sat701009641.h1
Method	BLASTN
NCBI GI	g2811229
BLAST score	39
E value	1.0e-12
Match length	63
% identity	90
NCBI Description	Arabidopsis thaliana fimbrin 1 gene, partial cds

Seq. No.	49865
Seq. ID	sat701009665.h1
Method	BLASTX
NCBI GI	g2462748
BLAST score	276
E value	8.0e-25
Match length	59
% identity	85
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	49866
Seq. ID	sat701009685.h1
Method	BLASTX
NCBI GI	g136107
BLAST score	147
E value	1.0e-09
Match length	75
% identity	39
NCBI Description	TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL AMINOPEPTIDASE) >gi_1082875_pir__S54376 tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880 (M73047) tripeptidyl peptidase II [Homo sapiens] >gi_4507657_ref_NP_003282.1_pTPP2_ tripeptidyl peptidase II

Seq. No.	49867
Seq. ID	sat701009702.h1
Method	BLASTN
NCBI GI	g1370173
BLAST score	60
E value	2.0e-25

Match length	164
% identity	84
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAB1Y

Seq. No.	49868
Seq. ID	sat701009726.h1
Method	BLASTX
NCBI GI	g1707019
BLAST score	180
E value	1.0e-13
Match length	76
% identity	45
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49869
Seq. ID	sat701009744.h1
Method	BLASTX
NCBI GI	g4558666
BLAST score	139
E value	7.0e-09
Match length	61
% identity	48
NCBI Description	(AC007063) putative Na/H antiporter isolog [Arabidopsis thaliana]

Seq. No.	49870
Seq. ID	sat701009761.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	228
E value	1.0e-125
Match length	232
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	49871
Seq. ID	sat701009812.h1
Method	BLASTX
NCBI GI	g3688172
BLAST score	308
E value	2.0e-28
Match length	79
% identity	63
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	49872
Seq. ID	sat701009829.h1
Method	BLASTN
NCBI GI	g609224
BLAST score	120
E value	5.0e-61
Match length	272
% identity	86
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	49873
Seq. ID	sat701009842.h1
Method	BLASTX
NCBI GI	g4220462
BLAST score	216
E value	9.0e-18
Match length	43
% identity	93
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	49874
Seq. ID	sat701009854.h1
Method	BLASTX
NCBI GI	g2829868
BLAST score	322
E value	3.0e-30
Match length	84
% identity	73
NCBI Description	(AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No.	49875
Seq. ID	sat701009872.h1
Method	BLASTX
NCBI GI	g2854049
BLAST score	145
E value	2.0e-09
Match length	67
% identity	43
NCBI Description	(AF044260) receptor serine/threonine kinase; protein kinase [Oryza sativa]

Seq. No.	49876
Seq. ID	sat701009876.h1
Method	BLASTX
NCBI GI	g3779032
BLAST score	195
E value	3.0e-15
Match length	90
% identity	42
NCBI Description	(AC005171) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	49877
Seq. ID	sat701009945.h2
Method	BLASTX
NCBI GI	g3702343
BLAST score	154
E value	2.0e-10
Match length	66
% identity	56
NCBI Description	(AC005397) putative homeotic gene regulator [Arabidopsis thaliana]

Seq. No.	49878
Seq. ID	sat701009968.h2
Method	BLASTX

NCBI GI g4433048
BLAST score 168
E value 4.0e-12
Match length 41
% identity 78
NCBI Description (D26578) DNA-binding protein [Daucus carota]

Seq. No. 49879
Seq. ID sat701010053.h2
Method BLASTX
NCBI GI g2827715
BLAST score 247
E value 4.0e-28
Match length 76
% identity 23
NCBI Description (AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 49880
Seq. ID sat701010062.h2
Method BLASTX
NCBI GI g4539460
BLAST score 173
E value 8.0e-13
Match length 80
% identity 4
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 49881
Seq. ID sat701010078.h2
Method BLASTX
NCBI GI g2781348
BLAST score 223
E value 1.0e-18
Match length 79
% identity 57
NCBI Description (AC003113) F24O1.4 [Arabidopsis thaliana]

Seq. No. 49882
Seq. ID sat701010089.h2
Method BLASTX
NCBI GI g2289005
BLAST score 354
E value 4.0e-34
Match length 76
% identity 86
NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana] >gi_3763937 (AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No. 49883
Seq. ID sat701010130.h2
Method BLASTX
NCBI GI g4138343
BLAST score 360
E value 1.0e-34
Match length 86

% identity 80
NCBI Description (AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]

Seq. No. 49884
Seq. ID sat701010143.h2
Method BLASTX
NCBI GI g4539292
BLAST score 197
E value 8.0e-16
Match length 49
% identity 80
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 49885
Seq. ID sat701010167.h2
Method BLASTN
NCBI GI g457569
BLAST score 101
E value 1.0e-49
Match length 101
% identity 100
NCBI Description Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No. 49886
Seq. ID sat701010168.h2
Method BLASTX
NCBI GI g3980417
BLAST score 229
E value 3.0e-19
Match length 63
% identity 38
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 49887
Seq. ID sat701010213.h2
Method BLASTN
NCBI GI g170073
BLAST score 166
E value 2.0e-88
Match length 220
% identity 95
NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No. 49888
Seq. ID sat701010287.h2
Method BLASTX
NCBI GI g4406821
BLAST score 233
E value 9.0e-20
Match length 57
% identity 74
NCBI Description (AC006201) hypothetical protein [Arabidopsis thaliana]

Seq. No. 49889
Seq. ID sat701010337.h1
Method BLASTX

NCBI GI g3046815
BLAST score 361
E value 1.0e-34
Match length 78
% identity 81
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 49890
Seq. ID sat701010343.h1
Method BLASTX
NCBI GI g4539301
BLAST score 245
E value 4.0e-21
Match length 54
% identity 80
NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 49891
Seq. ID sat701010350.h1
Method BLASTX
NCBI GI g3935149
BLAST score 172
E value 1.0e-12
Match length 66
% identity 50
NCBI Description (AC005106) T25N20.13 [Arabidopsis thaliana]

Seq. No. 49892
Seq. ID sat701010361.h1
Method BLASTX
NCBI GI g3861070
BLAST score 265
E value 2.0e-23
Match length 87
% identity 56
NCBI Description (AJ235272) ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (clpP) [Rickettsia prowazekii]

Seq. No. 49893
Seq. ID sat701010364.h1
Method BLASTX
NCBI GI g400803
BLAST score 171
E value 2.0e-19
Match length 57
% identity 80
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir__A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Seq. No. 49894
Seq. ID sat701010386.h1
Method BLASTX

NCBI GI	g2829862
BLAST score	271
E value	3.0e-24
Match length	90
% identity	57
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	49895
Seq. ID	sat701010418.h1
Method	BLASTX
NCBI GI	g2194116
BLAST score	139
E value	1.0e-08
Match length	57
% identity	44
NCBI Description	(AC002062) F20P5.1 gene product [Arabidopsis thaliana]

Seq. No.	49896
Seq. ID	sat701010420.h1
Method	BLASTX
NCBI GI	g3641845
BLAST score	179
E value	1.0e-13
Match length	49
% identity	73
NCBI Description	(AJ223358) stelar K+ outward rectifying channel [Arabidopsis thaliana]

Seq. No.	49897
Seq. ID	sat701010512.h1
Method	BLASTX
NCBI GI	g2146731
BLAST score	155
E value	1.0e-10
Match length	93
% identity	22
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	49898
Seq. ID	sat701010515.h1
Method	BLASTX
NCBI GI	g3668089
BLAST score	184
E value	6.0e-14
Match length	92
% identity	40
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	49899
Seq. ID	sat701010533.h1
Method	BLASTX
NCBI GI	g4006920
BLAST score	230
E value	5.0e-38
Match length	95

% identity	82
NCBI Description	(Z99708) actin interacting protein [Arabidopsis thaliana]

Seq. No.	49900
Seq. ID	sat701010535.h1
Method	BLASTX
NCBI GI	g4467125
BLAST score	236
E value	5.0e-20
Match length	94
% identity	50
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	49901
Seq. ID	sat701010637.h1
Method	BLASTX
NCBI GI	g2511715
BLAST score	485
E value	3.0e-49
Match length	99
% identity	90
NCBI Description	(AF019380) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	49902
Seq. ID	sat701010640.h1
Method	BLASTX
NCBI GI	g3395440
BLAST score	396
E value	1.0e-38
Match length	104
% identity	65
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49903
Seq. ID	sat701010647.h1
Method	BLASTX
NCBI GI	g2459437
BLAST score	296
E value	5.0e-27
Match length	81
% identity	73
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49904
Seq. ID	sat701010658.h1
Method	BLASTN
NCBI GI	g3176097
BLAST score	98
E value	7.0e-48
Match length	285
% identity	84
NCBI Description	Medicago truncatula mRNA for annexin

Seq. No.	49905
Seq. ID	sat701010747.h1
Method	BLASTX

NCBI GI g4559333
BLAST score 148
E value 8.0e-10
Match length 72
% identity 44
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 49906
Seq. ID sat701010748.h1
Method BLASTX
NCBI GI g4544374
BLAST score 174
E value 8.0e-13
Match length 92
% identity 39
NCBI Description (AC006920) unknown protein [Arabidopsis thaliana]

Seq. No. 49907
Seq. ID sat701010777.h1
Method BLASTX
NCBI GI g2443887
BLAST score 284
E value 1.0e-25
Match length 82
% identity 70
NCBI Description (AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No. 49908
Seq. ID sat701010809.h1
Method BLASTX
NCBI GI g2911072
BLAST score 217
E value 5.0e-18
Match length 61
% identity 70
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 49909
Seq. ID sat701010912.h1
Method BLASTX
NCBI GI g4115377
BLAST score 179
E value 2.0e-13
Match length 77
% identity 47
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 49910
Seq. ID sat701010916.h1
Method BLASTX
NCBI GI g4490330
BLAST score 373
E value 3.0e-36
Match length 85
% identity 82
NCBI Description (AL035656) splicing factor-like protein [Arabidopsis

thaliana]

Seq. No.	49911
Seq. ID	sat701010919.h1
Method	BLASTX
NCBI GI	g729332
BLAST score	308
E value	1.0e-28
Match length	87
% identity	63
NCBI Description	DHP1 PROTEIN >gi_629894_pir__S43891 dhp1 protein - fission yeast (Schizosaccharomyces pombe) >gi_496393_dbj_BAA04601_ (D17752) Dhp1 protein [Schizosaccharomyces pombe] >gi_1177359_emb_CAA93235_ (Z69240) dna exoribonuclease [Schizosaccharomyces pombe]

Seq. No.	49912
Seq. ID	sat701010920.h1
Method	BLASTX
NCBI GI	g3249065
BLAST score	175
E value	6.0e-13
Match length	72
% identity	47
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	49913
Seq. ID	sat701010969.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	66
E value	8.0e-29
Match length	158
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	49914
Seq. ID	sat701010977.h1
Method	BLASTX
NCBI GI	g1931653
BLAST score	141
E value	5.0e-09
Match length	43
% identity	67
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	49915
Seq. ID	sat701010986.h1
Method	BLASTX
NCBI GI	g118926
BLAST score	187
E value	2.0e-14
Match length	61

% identity	57
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No.	49916
Seq. ID	sat701011035.h1
Method	BLASTX
NCBI GI	g2388937
BLAST score	270
E value	6.0e-24
Match length	56
% identity	82
NCBI Description	(Z98977) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	49917
Seq. ID	sat701011036.h1
Method	BLASTX
NCBI GI	g3451071
BLAST score	385
E value	2.0e-37
Match length	81
% identity	95
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	49918
Seq. ID	sat701011044.h1
Method	BLASTX
NCBI GI	g4028970
BLAST score	139
E value	1.0e-08
Match length	63
% identity	49
NCBI Description	(AF060248) pollenless3 [Arabidopsis thaliana]

Seq. No.	49919
Seq. ID	sat701011053.h1
Method	BLASTX
NCBI GI	g2160166
BLAST score	170
E value	3.0e-12
Match length	95
% identity	41
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	49920
Seq. ID	sat701011082.h1
Method	BLASTN
NCBI GI	g829118
BLAST score	132
E value	4.0e-68
Match length	248
% identity	88

NCBI Description	P.vulgaris gene for cyclophilin
Seq. No.	49921
Seq. ID	sat701011101.h1
Method	BLASTX
NCBI GI	g2244904
BLAST score	345
E value	8.0e-33
Match length	95
% identity	24
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]
Seq. No.	49922
Seq. ID	sat701011136.h1
Method	BLASTX
NCBI GI	g2497366
BLAST score	182
E value	9.0e-14
Match length	79
% identity	49
NCBI Description	INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 >gi_2137851_pir__I49127 unknown intracellular protein - mouse >gi_558903 (U15635) unknown intracellular protein [Mus musculus]
Seq. No.	49923
Seq. ID	sat701011165.h1
Method	BLASTX
NCBI GI	g3036792
BLAST score	406
E value	5.0e-40
Match length	88
% identity	86
NCBI Description	(AL022373) putative protein (fragment) [Arabidopsis thaliana]
Seq. No.	49924
Seq. ID	sat701011201.h1
Method	BLASTX
NCBI GI	g4104929
BLAST score	433
E value	3.0e-43
Match length	93
% identity	86
NCBI Description	(AF042195) auxin response factor 7 [Arabidopsis thaliana]
Seq. No.	49925
Seq. ID	sat701011291.h1
Method	BLASTN
NCBI GI	g516102
BLAST score	247
E value	1.0e-137
Match length	247
% identity	100
NCBI Description	Soybean phytochrome B (phyB) gene exons 1-5, complete cds

Seq. No.	49926
Seq. ID	sat701011452.h1
Method	BLASTX
NCBI GI	g3805962
BLAST score	166
E value	6.0e-12
Match length	38
% identity	76
NCBI Description	(Y13772) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	49927
Seq. ID	sat701011515.h1
Method	BLASTX
NCBI GI	g1917019
BLAST score	219
E value	4.0e-18
Match length	67
% identity	66
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.	49928
Seq. ID	sat701011673.h1
Method	BLASTX
NCBI GI	g470337
BLAST score	235
E value	5.0e-20
Match length	74
% identity	57
NCBI Description	(U00043) similar to entire D. melanogaster white protein; also similar to other atp-binding transport proteins [Caenorhabditis elegans]

Seq. No.	49929
Seq. ID	sat701011784.h1
Method	BLASTX
NCBI GI	g3367534
BLAST score	296
E value	3.0e-27
Match length	84
% identity	69
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	49930
Seq. ID	sat701011787.h1
Method	BLASTX
NCBI GI	g3901294
BLAST score	156
E value	9.0e-11
Match length	68
% identity	43
NCBI Description	(AF089711) rpp8 [Arabidopsis thaliana]

Seq. No.	49931
Seq. ID	sat701011830.h1
Method	BLASTX

NCBI GI	g3598857
BLAST score	213
E value	2.0e-17
Match length	69
% identity	62
NCBI Description	(AF072447) short-chain alcohol dehydrogenase [Ipomoea trifida]

Seq. No.	49932
Seq. ID	sat701011895.h1
Method	BLASTX
NCBI GI	g3924598
BLAST score	153
E value	2.0e-10
Match length	71
% identity	45
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	49933
Seq. ID	sat701011931.h1
Method	BLASTX
NCBI GI	g3033392
BLAST score	237
E value	4.0e-20
Match length	75
% identity	79
NCBI Description	(AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No.	49934
Seq. ID	sat701011990.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	277
E value	1.0e-154
Match length	277
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	49935
Seq. ID	sat701012014.h1
Method	BLASTX
NCBI GI	g2146731
BLAST score	295
E value	5.0e-27
Match length	76
% identity	28
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	49936
Seq. ID	sat701012057.h1
Method	BLASTX
NCBI GI	g3979853
BLAST score	159
E value	4.0e-11
Match length	57

% identity	44
NCBI Description	(AJ131181) DAF-18 protein [Caenorhabditis elegans] >gi_4050032 (AF098286) DAF-18 [Caenorhabditis elegans] >gi_4512113_gb_AAD21620.1_ (AF126286) PTEN phosphatidylinositol 3' phosphatase homolog DAF-18 [Caenorhabditis elegans]

Seq. No.	49937
Seq. ID	sat701012079.h1
Method	BLASTN
NCBI GI	g974781
BLAST score	109
E value	2.0e-54
Match length	208
% identity	91
NCBI Description	C.blumei kinetoplast met gene for cobalamine-independent methionine synthase

Seq. No.	49938
Seq. ID	sat701012091.h1
Method	BLASTN
NCBI GI	g169980
BLAST score	239
E value	1.0e-132
Match length	259
% identity	98
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	49939
Seq. ID	sat701012156.h1
Method	BLASTX
NCBI GI	g3367596
BLAST score	297
E value	3.0e-27
Match length	92
% identity	60
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	49940
Seq. ID	sat701012195.h1
Method	BLASTN
NCBI GI	g2606080
BLAST score	80
E value	3.0e-37
Match length	199
% identity	86
NCBI Description	Glycine max sucrose synthase (SS) mRNA, complete cds

Seq. No.	49941
Seq. ID	sat701012238.h1
Method	BLASTN
NCBI GI	g310560
BLAST score	272
E value	1.0e-151
Match length	279
% identity	100
NCBI Description	Soybean ascorbate peroxidase mRNA, complete cds

Seq. No.	49942
Seq. ID	sat701012292.h1
Method	BLASTX
NCBI GI	g2462134
BLAST score	166
E value	5.0e-17
Match length	86
% identity	47
NCBI Description	(Y13368) reverse transcriptase [Beta vulgaris]

Seq. No.	49943
Seq. ID	sat701012313.h1
Method	BLASTX
NCBI GI	g3249577
BLAST score	184
E value	3.0e-14
Match length	60
% identity	48
NCBI Description	(AF055573) fragile histidine triad protein [Mus musculus] >gi_3264590 (AF047699) fragile histidine triad protein [Mus musculus]

Seq. No.	49944
Seq. ID	sat701012389.h1
Method	BLASTX
NCBI GI	g509810
BLAST score	151
E value	8.0e-12
Match length	63
% identity	62
NCBI Description	(L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	49945
Seq. ID	sat701012412.h1
Method	BLASTX
NCBI GI	g584892
BLAST score	236
E value	4.0e-20
Match length	67
% identity	60
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) >gi_629805_pir__S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I [Oryza sativa]

Seq. No.	49946
Seq. ID	sat701012419.h1
Method	BLASTX
NCBI GI	g1076291
BLAST score	188
E value	1.0e-14
Match length	83
% identity	53
NCBI Description	amino acid transporter AAT1 - Arabidopsis thaliana >gi_2911069_emb_CAA17531_ (AL021960) amino acid transport protein AAT1 [Arabidopsis thaliana]

Seq. No.	49947
Seq. ID	sat701012504.h1
Method	BLASTN
NCBI GI	g255407
BLAST score	74
E value	9.0e-34
Match length	74
% identity	100
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	49948
Seq. ID	sat701012510.h1
Method	BLASTX
NCBI GI	g2281647
BLAST score	205
E value	2.0e-16
Match length	59
% identity	63
NCBI Description	(AF003104) AP2 domain containing protein RAP2.11 [Arabidopsis thaliana]

Seq. No.	49949
Seq. ID	sat701012544.h1
Method	BLASTX
NCBI GI	g3540195
BLAST score	304
E value	4.0e-28
Match length	75
% identity	39
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	49950
Seq. ID	sat701012567.h1
Method	BLASTN
NCBI GI	g498907
BLAST score	60
E value	3.0e-25
Match length	168
% identity	88
NCBI Description	Pisum sativum ribosomal protein L34 homolog (RPL34) mRNA, complete cds

Seq. No.	49951
Seq. ID	sat701012568.h1
Method	BLASTN
NCBI GI	g2058281
BLAST score	40
E value	2.0e-13
Match length	68
% identity	90
NCBI Description	A.thaliana mRNA for AtRanBP1a protein

Seq. No.	49952
Seq. ID	sat701012591.h1

Method	BLASTX
NCBI GI	g4204303
BLAST score	276
E value	8.0e-25
Match length	80
% identity	66
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	49953
Seq. ID	sat701012689.h1
Method	BLASTN
NCBI GI	g1778369
BLAST score	36
E value	3.0e-11
Match length	48
% identity	94
NCBI Description	Glycine max asparagine synthetase 2 (AS2) mRNA, complete cds

Seq. No.	49954
Seq. ID	sat701012690.h1
Method	BLASTX
NCBI GI	g3395428
BLAST score	150
E value	5.0e-10
Match length	69
% identity	43
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	49955
Seq. ID	sat701012722.h1
Method	BLASTX
NCBI GI	g2648023
BLAST score	207
E value	1.0e-16
Match length	80
% identity	49
NCBI Description	(Z97184) BING4 [Homo sapiens]

Seq. No.	49956
Seq. ID	sat701012770.h1
Method	BLASTX
NCBI GI	g2244827
BLAST score	271
E value	3.0e-24
Match length	64
% identity	39
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49957
Seq. ID	sat701012775.h1
Method	BLASTX
NCBI GI	g2864618
BLAST score	198
E value	1.0e-15
Match length	69

% identity	54
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	49958
Seq. ID	sat701012818.h1
Method	BLASTN
NCBI GI	g21103
BLAST score	64
E value	1.0e-27
Match length	100
% identity	91
NCBI Description	R.sativus mRNA for HMG-COA reductase (clone cRS8)

Seq. No.	49959
Seq. ID	sat701012845.h1
Method	BLASTX
NCBI GI	g2649345
BLAST score	305
E value	4.0e-28
Match length	85
% identity	68
NCBI Description	(AE001019) tryptophan synthase, subunit beta (trpB-1) [Archaeoglobus fulgidus]

Seq. No.	49960
Seq. ID	sat701012878.h1
Method	BLASTX
NCBI GI	g3355467
BLAST score	250
E value	3.0e-23
Match length	93
% identity	59
NCBI Description	(AC004218) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49961
Seq. ID	sat701012968.h1
Method	BLASTX
NCBI GI	g3451079
BLAST score	149
E value	7.0e-10
Match length	46
% identity	63
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	49962
Seq. ID	sat701013003.h1
Method	BLASTX
NCBI GI	g2129771
BLAST score	120
E value	3.0e-11
Match length	53
% identity	70
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	49963
Seq. ID	sat701013026.h1
Method	BLASTX
NCBI GI	g3319341
BLAST score	166
E value	7.0e-12
Match length	91
% identity	40
NCBI Description	(AF077407) similar to Medicago sativa nucleic acid binding protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]

Seq. No.	49964
Seq. ID	sat701013041.h1
Method	BLASTN
NCBI GI	g1808591
BLAST score	117
E value	3.0e-59
Match length	173
% identity	92
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	49965
Seq. ID	sat701013063.h1
Method	BLASTX
NCBI GI	g2462750
BLAST score	170
E value	2.0e-12
Match length	59
% identity	53
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	49966
Seq. ID	sat701013083.h1
Method	BLASTX
NCBI GI	g3420050
BLAST score	261
E value	5.0e-23
Match length	89
% identity	51
NCBI Description	(AC004680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49967
Seq. ID	sat701013086.h1
Method	BLASTX
NCBI GI	g2314805
BLAST score	272
E value	3.0e-24
Match length	87
% identity	68
NCBI Description	(U85045) 2-oxoglutarate-dependent dioxygenase [Pisum sativum] >gi_2316036 (AF001219) gibberellin 3 beta-hydroxylase [Pisum sativum]

Seq. No.	49968
Seq. ID	sat701013093.h1

Method	BLASTN
NCBI GI	g303900
BLAST score	38
E value	2.0e-12
Match length	130
% identity	41
NCBI Description	Soybean gene for ubiquitin, complete cds

Seq. No.	49969
Seq. ID	sat701013103.h1
Method	BLASTX
NCBI GI	g3688193
BLAST score	247
E value	2.0e-21
Match length	78
% identity	60
NCBI Description	(AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]

Seq. No.	49970
Seq. ID	sat701013168.h1
Method	BLASTX
NCBI GI	g2191144
BLAST score	394
E value	1.0e-38
Match length	91
% identity	81
NCBI Description	(AF007269) A_IG002N01.24 gene product [Arabidopsis thaliana]

Seq. No.	49971
Seq. ID	sat701013183.h1
Method	BLASTX
NCBI GI	g2506525
BLAST score	250
E value	1.0e-21
Match length	91
% identity	62
NCBI Description	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10) >gi_2129614_pir__S71449 homeotic protein GL2 - Arabidopsis thaliana >gi_1695244 (L32873) homeodomain protein [Arabidopsis thaliana]

Seq. No.	49972
Seq. ID	sat701013210.h1
Method	BLASTX
NCBI GI	g1899175
BLAST score	416
E value	3.0e-41
Match length	92
% identity	87
NCBI Description	(U90262) calcium-dependent calmodulin-independent protein kinase CDPK [Cucurbita pepo]

Seq. No.	49973
Seq. ID	sat701013242.h1
Method	BLASTX
NCBI GI	g4415912

BLAST score 184
E value 3.0e-14
Match length 68
% identity 51
NCBI Description (AC006282) putative protease [Arabidopsis thaliana]

Seq. No. 49974
Seq. ID sat701013309.h1
Method BLASTX
NCBI GI g1076314
BLAST score 138
E value 1.0e-08
Match length 32
% identity 84
NCBI Description cystathionine gamma-lyase (EC 4.4.1.1) 1 - Arabidopsis thaliana (fragment) >gi_499166_emb_CAA56143_ (X79707) CYS1 [Arabidopsis thaliana]

Seq. No. 49975
Seq. ID sat701013325.h1
Method BLASTN
NCBI GI g3982595
BLAST score 156
E value 1.0e-82
Match length 156
% identity 100
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 49976
Seq. ID sat701013420.h1
Method BLASTX
NCBI GI g3075393
BLAST score 250
E value 1.0e-21
Match length 91
% identity 62
NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No. 49977
Seq. ID sat701013429.h1
Method BLASTX
NCBI GI g3970652
BLAST score 295
E value 5.0e-27
Match length 75
% identity 67
NCBI Description (X77499) amino acid permease [Arabidopsis thaliana]

Seq. No. 49978
Seq. ID sat701013445.h1
Method BLASTX
NCBI GI g1777312
BLAST score 250
E value 1.0e-21
Match length 91
% identity 61
NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No.	49979
Seq. ID	sat701013504.h1
Method	BLASTX
NCBI GI	g3152583
BLAST score	239
E value	2.0e-20
Match length	87
% identity	59
NCBI Description	(AC002986) Contains similarity to inhibitor of apoptosis protein gb_U45881 from D. melanogaster. [Arabidopsis thaliana]

Seq. No.	49980
Seq. ID	sat701013521.h1
Method	BLASTX
NCBI GI	g3759184
BLAST score	180
E value	2.0e-13
Match length	54
% identity	70
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	49981
Seq. ID	sat701013533.h1
Method	BLASTX
NCBI GI	g1246403
BLAST score	206
E value	2.0e-16
Match length	52
% identity	71
NCBI Description	(X94698) TINY [Arabidopsis thaliana] >gi_3406035 (AC005405) TINY [Arabidopsis thaliana]

Seq. No.	49982
Seq. ID	sat701013548.h1
Method	BLASTX
NCBI GI	g2055228
BLAST score	180
E value	2.0e-13
Match length	51
% identity	21
NCBI Description	(AB000129) SRC1 [Glycine max]

Seq. No.	49983
Seq. ID	sat701013585.h1
Method	BLASTX
NCBI GI	g2827623
BLAST score	226
E value	7.0e-19
Match length	48
% identity	92
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	49984
Seq. ID	sat701013601.h1

Method	BLASTX
NCBI GI	g1561774
BLAST score	186
E value	3.0e-14
Match length	64
% identity	56
NCBI Description	(U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.	49985
Seq. ID	sat701013636.h1
Method	BLASTX
NCBI GI	g2623248
BLAST score	358
E value	1.0e-35
Match length	82
% identity	88
NCBI Description	(AF030882) SU1 isoamylase [Zea mays]

Seq. No.	49986
Seq. ID	sat701013640.h1
Method	BLASTX
NCBI GI	g4314376
BLAST score	122
E value	1.0e-08
Match length	64
% identity	52
NCBI Description	(AC006232) similar to PIG-L [Arabidopsis thaliana]

Seq. No.	49987
Seq. ID	sat701013644.h1
Method	BLASTX
NCBI GI	g3033389
BLAST score	183
E value	5.0e-14
Match length	77
% identity	4
NCBI Description	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No.	49988
Seq. ID	sat701013650.h1
Method	BLASTN
NCBI GI	g3449323
BLAST score	34
E value	9.0e-10
Match length	132
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZA15, complete sequence [Arabidopsis thaliana]

Seq. No.	49989
Seq. ID	sat701013728.h1
Method	BLASTX
NCBI GI	g4455293
BLAST score	198
E value	1.0e-15
Match length	76
% identity	57

NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	49990
Seq. ID	sat701013730.h1
Method	BLASTX
NCBI GI	g584892
BLAST score	185
E value	5.0e-17
Match length	64
% identity	67
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) >gi_629805_pir__S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I [Oryza sativa]

Seq. No.	49991
Seq. ID	sat701013768.h1
Method	BLASTX
NCBI GI	g3201680
BLAST score	352
E value	1.0e-33
Match length	89
% identity	79
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	49992
Seq. ID	sat701013775.h1
Method	BLASTX
NCBI GI	g2305222
BLAST score	234
E value	6.0e-20
Match length	78
% identity	58
NCBI Description	(AF012089) phenylalanyl tRNA synthetase [Drosophila melanogaster]

Seq. No.	49993
Seq. ID	sat701013785.h1
Method	BLASTX
NCBI GI	g2129613
BLAST score	223
E value	1.0e-18
Match length	88
% identity	52
NCBI Description	homeotic protein BEL1 - Arabidopsis thaliana >gi_1122533 (U39944) BELL1 [Arabidopsis thaliana]

Seq. No.	49994
Seq. ID	sat701013796.h1
Method	BLASTX
NCBI GI	g1706956
BLAST score	254
E value	3.0e-22
Match length	65
% identity	62
NCBI Description	(U58283) cellulose synthase [Gossypium hirsutum]

Seq. No.	49995
Seq. ID	sat701013811.h1
Method	BLASTX
NCBI GI	g4038037
BLAST score	158
E value	6.0e-11
Match length	87
% identity	4
NCBI Description	(AC005936) hypothetical protein [Arabidopsis thaliana]

Seq. No.	49996
Seq. ID	sat701013842.h1
Method	BLASTN
NCBI GI	g1161925
BLAST score	189
E value	1.0e-102
Match length	197
% identity	99
NCBI Description	Glycine max alpha-carboxyltransferase aCT-1 precursor mRNA, complete cds

Seq. No.	49997
Seq. ID	sat701013845.h1
Method	BLASTX
NCBI GI	g4185511
BLAST score	253
E value	4.0e-22
Match length	56
% identity	88
NCBI Description	(AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No.	49998
Seq. ID	sat701013852.h1
Method	BLASTX
NCBI GI	g3378491
BLAST score	267
E value	9.0e-24
Match length	81
% identity	65
NCBI Description	(AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No.	49999
Seq. ID	sat701013855.h1
Method	BLASTX
NCBI GI	g1087073
BLAST score	385
E value	1.0e-37
Match length	86
% identity	79
NCBI Description	(S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa] [Nicotiana tabacum]

Seq. No.	50000
Seq. ID	sat701013866.h1
Method	BLASTN

NCBI GI g516853
BLAST score 203
E value 1.0e-110
Match length 262
% identity 41
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 50001
Seq. ID sat701013868.h1
Method BLASTX
NCBI GI g3927830
BLAST score 326
E value 1.0e-30
Match length 77
% identity 74
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No. 50002
Seq. ID sat701013915.h1
Method BLASTN
NCBI GI g3298610
BLAST score 63
E value 5.0e-27
Match length 119
% identity 88
NCBI Description Arabidopsis thaliana BAC T2H3

Seq. No. 50003
Seq. ID sat701013939.h1
Method BLASTX
NCBI GI g3355480
BLAST score 195
E value 3.0e-15
Match length 80
% identity 41
NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No. 50004
Seq. ID sat701013952.h1
Method BLASTX
NCBI GI g3122313
BLAST score 389
E value 6.0e-38
Match length 95
% identity 75
NCBI Description LEC14B HOMOLOG >gi_2351587 (U82760) LEC14B homolog [Prunus armeniaca]

Seq. No. 50005
Seq. ID sat701013978.h1
Method BLASTX
NCBI GI g136057
BLAST score 204
E value 2.0e-16
Match length 70
% identity 57

NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	50006
Seq. ID	sat701014019.h1
Method	BLASTX
NCBI GI	g1703446
BLAST score	172
E value	1.0e-12
Match length	68
% identity	57
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	50007
Seq. ID	sat701014062.h1
Method	BLASTX
NCBI GI	g3075398
BLAST score	359
E value	2.0e-34
Match length	91
% identity	73
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	50008
Seq. ID	sat701014073.h1
Method	BLASTX
NCBI GI	g4538959
BLAST score	252
E value	5.0e-22
Match length	49
% identity	86
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]

Seq. No.	50009
Seq. ID	sat701014148.h1
Method	BLASTX
NCBI GI	g3831470
BLAST score	274
E value	9.0e-25
Match length	94
% identity	55
NCBI Description	(AC005700) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	50010
Seq. ID	sat701014174.h1
Method	BLASTX
NCBI GI	g3759184
BLAST score	419
E value	1.0e-41
Match length	92
% identity	83

NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	50011
Seq. ID	sat701014185.h1
Method	BLASTN
NCBI GI	g169360
BLAST score	33
E value	4.0e-09
Match length	69
% identity	87
NCBI Description	P.vulgaris PVPK-1 protein, complete cds

Seq. No.	50012
Seq. ID	sat701014225.h1
Method	BLASTX
NCBI GI	g2464901
BLAST score	229
E value	6.0e-22
Match length	72
% identity	78
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	50013
Seq. ID	sat701014261.h1
Method	BLASTX
NCBI GI	g3152613
BLAST score	159
E value	2.0e-11
Match length	47
% identity	70
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50014
Seq. ID	sat701014263.h1
Method	BLASTN
NCBI GI	g3695294
BLAST score	40
E value	2.0e-13
Match length	136
% identity	87
NCBI Description	Glycine max nodule-specific glutamine synthetase gene, complete cds

Seq. No.	50015
Seq. ID	sat701014290.h1
Method	BLASTX
NCBI GI	g116908
BLAST score	282
E value	2.0e-25
Match length	67
% identity	84
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_166420 (M63853) S-adenosyl-L-methionine: caffeic acid 3-0-methyltransferase [Medicago sativa]

Seq. No.	50016
Seq. ID	sat701014314.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	276
E value	1.0e-154
Match length	296
% identity	98
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	50017
Seq. ID	sat701014338.h1
Method	BLASTX
NCBI GI	g1161167
BLAST score	275
E value	1.0e-24
Match length	88
% identity	50
NCBI Description	(L42466) ethylene-forming enzyme [Picea glauca]

Seq. No.	50018
Seq. ID	sat701014343.h1
Method	BLASTX
NCBI GI	g3334667
BLAST score	138
E value	1.0e-08
Match length	80
% identity	38
NCBI Description	(Y10493) putative cytochrome P450 [Glycine max]

Seq. No.	50019
Seq. ID	sat701014395.h1
Method	BLASTX
NCBI GI	g2244965
BLAST score	213
E value	2.0e-17
Match length	51
% identity	82
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No.	50020
Seq. ID	sat701014403.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	123
E value	4.0e-63
Match length	139
% identity	97
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	50021
Seq. ID	sat701014495.h1
Method	BLASTN
NCBI GI	g3241920
BLAST score	35
E value	2.0e-10
Match length	47

% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	50022
Seq. ID	sat701014546.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	269
E value	1.0e-150
Match length	276
% identity	100
NCBI Description	G.max ADR6 mRNA

Seq. No.	50023
Seq. ID	sat701014587.h1
Method	BLASTX
NCBI GI	g4204695
BLAST score	193
E value	2.0e-29
Match length	90
% identity	68
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No.	50024
Seq. ID	sat701014631.h1
Method	BLASTN
NCBI GI	g1808591
BLAST score	88
E value	6.0e-42
Match length	196
% identity	86
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	50025
Seq. ID	sat701014639.h1
Method	BLASTX
NCBI GI	g3947735
BLAST score	172
E value	2.0e-12
Match length	55
% identity	55
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	50026
Seq. ID	sat701014660.h1
Method	BLASTX
NCBI GI	g4239692
BLAST score	317
E value	2.0e-29
Match length	71
% identity	82
NCBI Description	(AJ132745) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50027
Seq. ID	sat701014661.h1

Method	BLASTN
NCBI GI	g4097879
BLAST score	118
E value	8.0e-60
Match length	277
% identity	86
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	50028
Seq. ID	sat701014726.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	122
E value	3.0e-62
Match length	122
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	50029
Seq. ID	sat701014729.h1
Method	BLASTX
NCBI GI	g4467359
BLAST score	158
E value	6.0e-11
Match length	37
% identity	76
NCBI Description	(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No.	50030
Seq. ID	sat701014732.h1
Method	BLASTN
NCBI GI	g166379
BLAST score	74
E value	1.0e-33
Match length	192
% identity	70
NCBI Description	Alfalfa glucose-regulated endoplasmic reticular protein mRNA, complete cds

Seq. No.	50031
Seq. ID	sat701014866.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	89
E value	1.0e-42
Match length	149
% identity	90
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	50032
Seq. ID	sat701014880.h1
Method	BLASTX
NCBI GI	g2911049

BLAST score	144
E value	2.0e-09
Match length	60
% identity	48
NCBI Description	(AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]

Seq. No.	50033
Seq. ID	sat701014974.h1
Method	BLASTN
NCBI GI	g18737
BLAST score	218
E value	1.0e-119
Match length	274
% identity	10
NCBI Description	Glycine max RPRP3 gene for repetitive proline-rich protein

Seq. No.	50034
Seq. ID	sat701015072.h1
Method	BLASTN
NCBI GI	g1769894
BLAST score	64
E value	1.0e-27
Match length	175
% identity	85
NCBI Description	A.thaliana mRNA for CaLB protein

Seq. No.	50035
Seq. ID	sat701015081.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	38
E value	4.0e-12
Match length	171
% identity	91
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	50036
Seq. ID	sat701015236.h1
Method	BLASTX
NCBI GI	g1763230
BLAST score	330
E value	4.0e-31
Match length	85
% identity	76
NCBI Description	(U72145) 3-hydroxy-3-methylglutaryl coenzyme a reductase [Camptotheca acuminata]

Seq. No.	50037
Seq. ID	sat701015241.h1
Method	BLASTX
NCBI GI	g2618696
BLAST score	216
E value	9.0e-18
Match length	71
% identity	49

NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.	50038
Seq. ID	sat701015262.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	116
E value	1.0e-58
Match length	268
% identity	86
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds
Seq. No.	50039
Seq. ID	sat701015266.h1
Method	BLASTN
NCBI GI	g3158473
BLAST score	82
E value	1.0e-38
Match length	126
% identity	91
NCBI Description	Samanea saman aquaporin 1 (Aqp1) mRNA, complete cds
Seq. No.	50040
Seq. ID	sat701015284.h1
Method	BLASTX
NCBI GI	g2842481
BLAST score	279
E value	4.0e-25
Match length	76
% identity	39
NCBI Description	(AL021749) extensin-like protein [Arabidopsis thaliana]
Seq. No.	50041
Seq. ID	sat701015317.h1
Method	BLASTX
NCBI GI	g4378659
BLAST score	160
E value	8.0e-25
Match length	84
% identity	73
NCBI Description	(AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
Seq. No.	50042
Seq. ID	sat701015336.h1
Method	BLASTX
NCBI GI	g2911067
BLAST score	169
E value	2.0e-12
Match length	43
% identity	81
NCBI Description	(AL021960) UV-damaged DNA-binding protein- like [Arabidopsis thaliana]
Seq. No.	50043
Seq. ID	sat701015373.h1

Method	BLASTN
NCBI GI	g296444
BLAST score	236
E value	1.0e-130
Match length	243
% identity	100
NCBI Description	G.max ADR6 mRNA

Seq. No.	50044
Seq. ID	sat701015424.h1
Method	BLASTX
NCBI GI	g4006900
BLAST score	282
E value	1.0e-25
Match length	84
% identity	71
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50045
Seq. ID	sat701015444.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	144
E value	2.0e-75
Match length	183
% identity	95
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	50046
Seq. ID	sat701015485.h1
Method	BLASTX
NCBI GI	g2865416
BLAST score	370
E value	7.0e-36
Match length	80
% identity	81
NCBI Description	(AF039367) chromomethylase [Arabidopsis thaliana]

Seq. No.	50047
Seq. ID	sat701015492.h1
Method	BLASTX
NCBI GI	g1076289
BLAST score	175
E value	5.0e-13
Match length	74
% identity	41
NCBI Description	amino acid permease AAP5 - Arabidopsis thaliana >gi_608673_emb_CAA54632_ (X77501) amino acid permease [Arabidopsis thaliana]

Seq. No.	50048
Seq. ID	seb700647978.h1
Method	BLASTX
NCBI GI	g4220535
BLAST score	250
E value	2.0e-21
Match length	56

% identity	82
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	50049
Seq. ID	seb700648053.h1
Method	BLASTN
NCBI GI	g474009
BLAST score	34
E value	8.0e-10
Match length	54
% identity	91
NCBI Description	Rice mRNA, partial homologous to ribosomal protein S19 gene

Seq. No.	50050
Seq. ID	seb700648105.h1
Method	BLASTX
NCBI GI	g4107037
BLAST score	343
E value	2.0e-32
Match length	75
% identity	93
NCBI Description	(AB021862) HMG-CoA reductase [Cucumis melo]

Seq. No.	50051
Seq. ID	seb700648112.h1
Method	BLASTN
NCBI GI	g3021337
BLAST score	77
E value	2.0e-35
Match length	272
% identity	83
NCBI Description	Cicer arietinum mRNA for cytosolic fructose-1,6-bisphosphate aldolase

Seq. No.	50052
Seq. ID	seb700648140.h1
Method	BLASTX
NCBI GI	g2244740
BLAST score	144
E value	3.0e-09
Match length	39
% identity	72
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	50053
Seq. ID	seb700648153.h1
Method	BLASTN
NCBI GI	g18761
BLAST score	209
E value	1.0e-114
Match length	295
% identity	94
NCBI Description	Soybean stem mRNA for 31 kD glycoprotein

Seq. No.	50054
Seq. ID	seb700648195.h1

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Method	BLASTN
NCBI GI	g310575
BLAST score	76
E value	7.0e-35
Match length	95
% identity	96
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	50055
Seq. ID	seb700648210.h1
Method	BLASTN
NCBI GI	g18525
BLAST score	51
E value	2.0e-20
Match length	63
% identity	95
NCBI Description	Soybean actin SAc6 gene for leader exon and exon

Seq. No.	50056
Seq. ID	seb700648338.h1
Method	BLASTX
NCBI GI	g3236259
BLAST score	149
E value	4.0e-10
Match length	42
% identity	71
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	50057
Seq. ID	seb700648370.h1
Method	BLASTN
NCBI GI	g255407
BLAST score	68
E value	2.0e-30
Match length	104
% identity	91
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	50058
Seq. ID	seb700648409.h1
Method	BLASTN
NCBI GI	g475597
BLAST score	126
E value	7.0e-65
Match length	150
% identity	97
NCBI Description	Glycine max Century 84 BiP isoform C mRNA, partial cds

Seq. No.	50059
Seq. ID	seb700648439.h1
Method	BLASTN
NCBI GI	g4558461
BLAST score	52
E value	9.0e-21

Match length	80
% identity	91
NCBI Description	Medicago sativa subsp. X varia cell cycle switch protein (ccs52) mRNA, complete cds

Seq. No.	50060
Seq. ID	seb700648521.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	138
E value	9.0e-72
Match length	245
% identity	89
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50061
Seq. ID	seb700648555.h1
Method	BLASTN
NCBI GI	g1808591
BLAST score	74
E value	2.0e-33
Match length	164
% identity	87
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	50062
Seq. ID	seb700648579.h1
Method	BLASTN
NCBI GI	g170091
BLAST score	170
E value	7.0e-91
Match length	265
% identity	91
NCBI Description	Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No.	50063
Seq. ID	seb700648580.h1
Method	BLASTN
NCBI GI	g1568510
BLAST score	64
E value	8.0e-28
Match length	116
% identity	89
NCBI Description	N.tabacum mRNA for protein phosphatase 2A, 65kD regulatory subunit

Seq. No.	50064
Seq. ID	seb700648583.h1
Method	BLASTX
NCBI GI	g3023721
BLAST score	163
E value	2.0e-11
Match length	40
% identity	62
NCBI Description	FLOWERING TIME CONTROL PROTEIN FCA >gi_2204095_emb_CAB05391_ (Z82992) FCA gamma [Arabidopsis

thaliana]

Seq. No.	50065
Seq. ID	seb700648615.h1
Method	BLASTX
NCBI GI	g4539335
BLAST score	151
E value	5.0e-10
Match length	71
% identity	42
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	50066
Seq. ID	seb700648707.h1
Method	BLASTX
NCBI GI	g3927830
BLAST score	198
E value	2.0e-15
Match length	54
% identity	67
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50067
Seq. ID	seb700648736.h1
Method	BLASTN
NCBI GI	g170091
BLAST score	296
E value	1.0e-166
Match length	335
% identity	97
NCBI Description	Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No.	50068
Seq. ID	seb700648819.h1
Method	BLASTN
NCBI GI	g218112
BLAST score	81
E value	7.0e-38
Match length	148
% identity	89
NCBI Description	Rice mRNA for ribosomal protein L41 (340 gene), partial sequence >gi_3107899_dbj_D42832_D42832 Rice callus cDNA,

Seq. No.	50069
Seq. ID	seb700648833.h1
Method	BLASTX
NCBI GI	g100876
BLAST score	210
E value	3.0e-20
Match length	65
% identity	83
NCBI Description	globulin-2 precursor - maize >gi_228310_prf__1802402A globulin 2 [Zea mays]

Seq. No.	50070
Seq. ID	seb700648868.h1

Method	BLASTX
NCBI GI	g2598579
BLAST score	280
E value	4.0e-25
Match length	74
% identity	74
NCBI Description	(Y15295) L-ascorbate oxidase [Medicago truncatula]

Seq. No.	50071
Seq. ID	seb700648929.h1
Method	BLASTN
NCBI GI	g609224
BLAST score	45
E value	8.0e-17
Match length	93
% identity	87
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	50072
Seq. ID	seb700648984.h1
Method	BLASTN
NCBI GI	g397395
BLAST score	89
E value	6.0e-43
Match length	97
% identity	98
NCBI Description	Z.mays MNB1b mRNA for DNA-binding protein

Seq. No.	50073
Seq. ID	seb700649038.h1
Method	BLASTX
NCBI GI	g1929056
BLAST score	197
E value	2.0e-15
Match length	73
% identity	53
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	50074
Seq. ID	seb700649134.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	77
E value	1.0e-35
Match length	91
% identity	98
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50075
Seq. ID	seb700649203.h1
Method	BLASTN
NCBI GI	g312988
BLAST score	88
E value	3.0e-42

Match length 142
% identity 92
NCBI Description G.max mRNA for beta-tubulin, partial cds

Seq. No. 50076
Seq. ID seb700649213.h1
Method BLASTN
NCBI GI g31107
BLAST score 183
E value 8.0e-99
Match length 199
% identity 98
NCBI Description H.sapiens mRNA for elongation factor

Seq. No. 50077
Seq. ID seb700649216.h1
Method BLASTX
NCBI GI g3075398
BLAST score 183
E value 4.0e-14
Match length 50
% identity 64
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 50078
Seq. ID seb700649226.h1
Method BLASTX
NCBI GI g1155090
BLAST score 153
E value 3.0e-10
Match length 73
% identity 40
NCBI Description (X94986) beta glucosidase [Manihot esculenta]

Seq. No. 50079
Seq. ID seb700649262.h1
Method BLASTN
NCBI GI g414704
BLAST score 42
E value 9.0e-15
Match length 101
% identity 86
NCBI Description O.sativa mRNA for cytochrome b5

Seq. No. 50080
Seq. ID seb700649312.h1
Method BLASTN
NCBI GI g18764
BLAST score 272
E value 1.0e-151
Match length 310
% identity 97
NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 50081
Seq. ID seb700649338.h1
Method BLASTX

NCBI GI	g4567282
BLAST score	143
E value	5.0e-09
Match length	46
% identity	65
NCBI Description	(AC006841) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	50082
Seq. ID	seb700649373.h1
Method	BLASTN
NCBI GI	g1183936
BLAST score	52
E value	2.0e-20
Match length	91
% identity	90
NCBI Description	P.sativum 5S rRNA gene

Seq. No.	50083
Seq. ID	seb700649382.h1
Method	BLASTX
NCBI GI	g2119933
BLAST score	275
E value	1.0e-24
Match length	66
% identity	82
NCBI Description	translation initiation factor eIF-4A.11 - common tobacco

Seq. No.	50084
Seq. ID	seb700649386.h1
Method	BLASTX
NCBI GI	g2829912
BLAST score	196
E value	3.0e-15
Match length	60
% identity	67
NCBI Description	(AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]

Seq. No.	50085
Seq. ID	seb700649388.h1
Method	BLASTN
NCBI GI	g1217993
BLAST score	262
E value	1.0e-145
Match length	269
% identity	99
NCBI Description	Glycine max dynamin-like protein SDL12A mRNA, complete cds

Seq. No.	50086
Seq. ID	seb700649410.h1
Method	BLASTN
NCBI GI	g303900
BLAST score	238
E value	1.0e-131
Match length	342
% identity	28
NCBI Description	Soybean gene for ubiquitin, complete cds

Seq. No.	50087
Seq. ID	seb700649413.h1
Method	BLASTN
NCBI GI	g1381675
BLAST score	243
E value	1.0e-134
Match length	283
% identity	96
NCBI Description	Glycine max small GTP-binding protein (sra1) mRNA, partial cds

Seq. No.	50088
Seq. ID	seb700649508.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	194
E value	1.0e-105
Match length	246
% identity	28
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	50089
Seq. ID	seb700649584.h1
Method	BLASTX
NCBI GI	g2832408
BLAST score	182
E value	5.0e-14
Match length	41
% identity	80
NCBI Description	(Y14209) R2R3-MYB transcription factor [Arabidopsis thaliana]

Seq. No.	50090
Seq. ID	seb700649594.h1
Method	BLASTX
NCBI GI	g1170937
BLAST score	183
E value	7.0e-23
Match length	70
% identity	76
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	50091
Seq. ID	seb700649641.h1
Method	BLASTN
NCBI GI	g1843461
BLAST score	273
E value	1.0e-152
Match length	325
% identity	97
NCBI Description	Human keratin 1 gene, complete cds

Seq. No.	50092

Seq. ID	seb700649656.h1
Method	BLASTN
NCBI GI	g337500
BLAST score	88
E value	2.0e-42
Match length	100
% identity	97
NCBI Description	Human ribosomal protein S17 mRNA, complete cds. >gi_4506692_ref_NM_001021.1_RPS17_ Homo sapiens ribosomal protein S17 (RPS17) mRNA

Seq. No.	50093
Seq. ID	seb700649676.h1
Method	BLASTN
NCBI GI	g347454
BLAST score	120
E value	5.0e-61
Match length	253
% identity	39
NCBI Description	Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3' end

Seq. No.	50094
Seq. ID	seb700649684.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	87
E value	3.0e-41
Match length	215
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	50095
Seq. ID	seb700649715.h1
Method	BLASTN
NCBI GI	g170089
BLAST score	108
E value	4.0e-54
Match length	182
% identity	91
NCBI Description	G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No.	50096
Seq. ID	seb700649736.h1
Method	BLASTN
NCBI GI	g166915
BLAST score	59
E value	6.0e-25
Match length	97
% identity	96
NCBI Description	Arabidopsis thaliana alpha-4 tubulin (TUA4) gene, complete cds

Seq. No.	50097
Seq. ID	seb700649744.h1

Method	BLASTN
NCBI GI	g4193387
BLAST score	52
E value	2.0e-20
Match length	178
% identity	86
NCBI Description	Hevea brasiliensis translationally controlled tumor protein (TCTP) mRNA, complete cds

Seq. No.	50098
Seq. ID	seb700649753.h1
Method	BLASTN
NCBI GI	g3483561
BLAST score	45
E value	1.0e-16
Match length	113
% identity	85
NCBI Description	Homo sapiens full length insert cDNA clone ZC65B11

Seq. No.	50099
Seq. ID	seb700649776.h1
Method	BLASTN
NCBI GI	g4406704
BLAST score	112
E value	1.0e-56
Match length	120
% identity	98
NCBI Description	Homo sapiens clone 24870 mRNA sequence

Seq. No.	50100
Seq. ID	seb700649794.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	64
E value	6.0e-28
Match length	98
% identity	92
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50101
Seq. ID	seb700649805.h1
Method	BLASTX
NCBI GI	g3643598
BLAST score	167
E value	9.0e-14
Match length	75
% identity	57
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	50102
Seq. ID	seb700649807.h1
Method	BLASTX
NCBI GI	g2369714
BLAST score	242
E value	1.0e-32
Match length	103

% identity	75
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	50103
Seq. ID	seb700649823.h1
Method	BLASTN
NCBI GI	g1778369
BLAST score	59
E value	5.0e-25
Match length	117
% identity	91
NCBI Description	Glycine max asparagine synthetase 2 (AS2) mRNA, complete cds

Seq. No.	50104
Seq. ID	seb700649828.h1
Method	BLASTX
NCBI GI	g2462931
BLAST score	178
E value	6.0e-21
Match length	64
% identity	78
NCBI Description	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]

Seq. No.	50105
Seq. ID	seb700649914.h1
Method	BLASTX
NCBI GI	g2462925
BLAST score	165
E value	5.0e-12
Match length	40
% identity	80
NCBI Description	(AJ000053) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana]

Seq. No.	50106
Seq. ID	seb700650068.h1
Method	BLASTN
NCBI GI	g2204063
BLAST score	50
E value	2.0e-19
Match length	213
% identity	88
NCBI Description	Pisum sativum mRNA for F1 ATPase, complete cds

Seq. No.	50107
Seq. ID	seb700650120.h1
Method	BLASTN
NCBI GI	g1778369
BLAST score	32
E value	6.0e-09
Match length	32
% identity	100
NCBI Description	Glycine max asparagine synthetase 2 (AS2) mRNA, complete cds

Seq. No.	50108
Seq. ID	seb700650127.h1
Method	BLASTX
NCBI GI	g1865677
BLAST score	208
E value	4.0e-17
Match length	59
% identity	76
NCBI Description	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	50109
Seq. ID	seb700650345.h1
Method	BLASTX
NCBI GI	g2811029
BLAST score	353
E value	7.0e-34
Match length	82
% identity	79
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	50110
Seq. ID	seb700650425.h1
Method	BLASTN
NCBI GI	g3941321
BLAST score	65
E value	1.0e-28
Match length	121
% identity	88
NCBI Description	Medicago truncatula gamma-glutamylcysteine synthetase mRNA, nuclear gene encoding putative plastid protein, complete cds

Seq. No.	50111
Seq. ID	seb700650507.h1
Method	BLASTX
NCBI GI	g2462825
BLAST score	203
E value	3.0e-20
Match length	72
% identity	71
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	50112
Seq. ID	seb700650510.h1
Method	BLASTX
NCBI GI	g2911055
BLAST score	201
E value	8.0e-16
Match length	93
% identity	49
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	50113
Seq. ID	seb700650621.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	295
E value	1.0e-165
Match length	349
% identity	97
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	50114
Seq. ID	seb700650625.h1
Method	BLASTX
NCBI GI	g730456
BLAST score	224
E value	7.0e-19
Match length	66
% identity	68
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	50115
Seq. ID	seb700650671.h1
Method	BLASTN
NCBI GI	g1399379
BLAST score	147
E value	3.0e-77
Match length	250
% identity	90
NCBI Description	Glycine max S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase mRNA, complete cds

Seq. No.	50116
Seq. ID	seb700650787.h1
Method	BLASTX
NCBI GI	g3924605
BLAST score	237
E value	5.0e-20
Match length	115
% identity	44
NCBI Description	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No.	50117
Seq. ID	seb700650882.h1
Method	BLASTX
NCBI GI	g2191175
BLAST score	366
E value	4.0e-35
Match length	116
% identity	59
NCBI Description	(AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No.	50118
Seq. ID	seb700651004.h1
Method	BLASTX

NCBI GI g2921510
BLAST score 221
E value 5.0e-25
Match length 75
% identity 88
NCBI Description (AF037459) clp-like energy-dependent protease [Fritillaria agrestis]

Seq. No. 50119
Seq. ID seb700651032.h1
Method BLASTN
NCBI GI g1150683
BLAST score 82
E value 2.0e-38
Match length 262
% identity 83
NCBI Description V.radiata atpB, rbcL and trnK genes

Seq. No. 50120
Seq. ID seb700651058.h1
Method BLASTN
NCBI GI g1150683
BLAST score 62
E value 2.0e-26
Match length 245
% identity 83
NCBI Description V.radiata atpB, rbcL and trnK genes

Seq. No. 50121
Seq. ID seb700651095.h1
Method BLASTX
NCBI GI g2462822
BLAST score 284
E value 3.0e-30
Match length 84
% identity 27
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 50122
Seq. ID seb700651159.h1
Method BLASTX
NCBI GI g1709449
BLAST score 144
E value 2.0e-09
Match length 31
% identity 81
NCBI Description PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_1263302 (U51918) pyruvate dehydrogenase E1 alpha subunit [Pisum sativum]

Seq. No. 50123
Seq. ID seb700651179.h1
Method BLASTX
NCBI GI g2655008
BLAST score 155
E value 8.0e-11
Match length 44

% identity	59
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	50124
Seq. ID	seb700651230.h1
Method	BLASTX
NCBI GI	g3747050
BLAST score	205
E value	3.0e-16
Match length	58
% identity	69
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	50125
Seq. ID	seb700651261.h1
Method	BLASTX
NCBI GI	g1944575
BLAST score	507
E value	1.0e-51
Match length	119
% identity	76
NCBI Description	(Z94058) pectinesterase [Lycopersicon esculentum]

Seq. No.	50126
Seq. ID	seb700651357.h1
Method	BLASTX
NCBI GI	g3924594
BLAST score	311
E value	1.0e-28
Match length	92
% identity	23
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	50127
Seq. ID	seb700651374.h1
Method	BLASTX
NCBI GI	g2081612
BLAST score	258
E value	1.0e-22
Match length	96
% identity	55
NCBI Description	(D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza sativa]

Seq. No.	50128
Seq. ID	seb700651460.h1
Method	BLASTX
NCBI GI	g4335731
BLAST score	173
E value	2.0e-16
Match length	101
% identity	48
NCBI Description	(AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No.	50129
Seq. ID	seb700651467.h1
Method	BLASTX
NCBI GI	g2642154
BLAST score	318
E value	2.0e-29
Match length	110
% identity	55
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana]

Seq. No.	50130
Seq. ID	seb700651478.h1
Method	BLASTX
NCBI GI	g4263818
BLAST score	251
E value	1.0e-21
Match length	72
% identity	62
NCBI Description	(AC006067) unknown protein [Arabidopsis thaliana]

Seq. No.	50131
Seq. ID	seb700651483.h1
Method	BLASTN
NCBI GI	g414675
BLAST score	36
E value	8.0e-11
Match length	68
% identity	88
NCBI Description	L.esculentum (ERT 15) ripening-related mRNA

Seq. No.	50132
Seq. ID	seb700651556.h1
Method	BLASTX
NCBI GI	g3024020
BLAST score	380
E value	1.0e-43
Match length	97
% identity	92
NCBI Description	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]

Seq. No.	50133
Seq. ID	seb700651591.h1
Method	BLASTX
NCBI GI	g4432841
BLAST score	163
E value	2.0e-11
Match length	111
% identity	26
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50134
Seq. ID	seb700651712.h1
Method	BLASTX

NCBI GI g4160573
BLAST score 147
E value 1.0e-09
Match length 101
% identity 36
NCBI Description (AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]

Seq. No. 50135
Seq. ID seb700651853.h1
Method BLASTN
NCBI GI g2598656
BLAST score 100
E value 2.0e-49
Match length 172
% identity 94
NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No. 50136
Seq. ID seb700651854.h1
Method BLASTX
NCBI GI g4097547
BLAST score 233
E value 1.0e-19
Match length 70
% identity 50
NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

Seq. No. 50137
Seq. ID seb700651877.h1
Method BLASTX
NCBI GI g4567310
BLAST score 249
E value 1.0e-21
Match length 79
% identity 71
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 50138
Seq. ID seb700651942.h1
Method BLASTX
NCBI GI g1086252
BLAST score 187
E value 3.0e-14
Match length 54
% identity 59
NCBI Description sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No. 50139
Seq. ID seb700651974.h1
Method BLASTX
NCBI GI g3819099
BLAST score 209
E value 3.0e-17

Match length 58
% identity 67
NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]

Seq. No. 50140
Seq. ID seb700651976.h1
Method BLASTX
NCBI GI g3548806
BLAST score 177
E value 2.0e-22
Match length 94
% identity 59
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 50141
Seq. ID seb700651985.h1
Method BLASTN
NCBI GI g169974
BLAST score 215
E value 1.0e-117
Match length 334
% identity 92
NCBI Description Glycine max vspA gene, complete cds

Seq. No. 50142
Seq. ID seb700651986.h1
Method BLASTN
NCBI GI g169344
BLAST score 63
E value 6.0e-27
Match length 304
% identity 80
NCBI Description P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, exon 2

Seq. No. 50143
Seq. ID seb700652166.h1
Method BLASTN
NCBI GI g602605
BLAST score 40
E value 2.0e-13
Match length 68
% identity 45
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 50144
Seq. ID seb700652225.h1
Method BLASTN
NCBI GI g18551
BLAST score 311
E value 1.0e-175
Match length 341
% identity 98
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No. 50145

Seq. ID	seb700652236.h1
Method	BLASTX
NCBI GI	g2244779
BLAST score	146
E value	2.0e-09
Match length	59
% identity	51
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50146
Seq. ID	seb700652242.h1
Method	BLASTN
NCBI GI	g3928141
BLAST score	77
E value	3.0e-35
Match length	161
% identity	87
NCBI Description	Cicer arietinum mRNA for protein phosphatase

Seq. No.	50147
Seq. ID	seb700652290.h1
Method	BLASTX
NCBI GI	g1854445
BLAST score	214
E value	1.0e-18
Match length	68
% identity	68
NCBI Description	(D83971) CPRD14 protein [Vigna unguiculata]

Seq. No.	50148
Seq. ID	seb700652403.h1
Method	BLASTN
NCBI GI	g170065
BLAST score	179
E value	2.0e-96
Match length	223
% identity	13
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	50149
Seq. ID	seb700652405.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	252
E value	1.0e-139
Match length	285
% identity	97
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	50150
Seq. ID	seb700652419.h1
Method	BLASTN
NCBI GI	g1575730
BLAST score	82
E value	1.0e-38
Match length	102

% identity	95
NCBI Description	Glycine max 14-3-3 related protein SGF14D mRNA, complete cds

Seq. No.	50151
Seq. ID	seb700652449.h1
Method	BLASTX
NCBI GI	g3355617
BLAST score	111
E value	2.0e-09
Match length	57
% identity	61
NCBI Description	(AJ000229) unnamed protein product [Hordeum vulgare]

Seq. No.	50152
Seq. ID	seb700652463.h1
Method	BLASTX
NCBI GI	g4218002
BLAST score	235
E value	9.0e-20
Match length	114
% identity	49
NCBI Description	(AC006135) putative UTP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	50153
Seq. ID	seb700652513.h1
Method	BLASTN
NCBI GI	g170089
BLAST score	80
E value	2.0e-37
Match length	99
% identity	96
NCBI Description	G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No.	50154
Seq. ID	seb700652552.h1
Method	BLASTX
NCBI GI	g4220445
BLAST score	147
E value	2.0e-09
Match length	94
% identity	6
NCBI Description	(AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb_AC003673. [Arabidopsis thaliana]

Seq. No.	50155
Seq. ID	seb700652611.h1
Method	BLASTN
NCBI GI	g1431621
BLAST score	51
E value	8.0e-20
Match length	122
% identity	87
NCBI Description	T.repens mRNA for protein kinase

Seq. No.	50156
Seq. ID	seb700652647.h1
Method	BLASTX
NCBI GI	g1762584
BLAST score	184
E value	8.0e-14
Match length	67
% identity	49
NCBI Description	(U63373) polygalacturonase isoenzyme 1 beta subunit homolog [Arabidopsis thaliana]

Seq. No.	50157
Seq. ID	seb700652657.h1
Method	BLASTX
NCBI GI	g4263048
BLAST score	236
E value	7.0e-20
Match length	86
% identity	46
NCBI Description	(AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No.	50158
Seq. ID	seb700652659.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	95
E value	4.0e-46
Match length	104
% identity	25
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	50159
Seq. ID	seb700652732.h1
Method	BLASTX
NCBI GI	g4115379
BLAST score	253
E value	6.0e-22
Match length	106
% identity	47
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	50160
Seq. ID	seb700652738.h1
Method	BLASTX
NCBI GI	g2267567
BLAST score	175
E value	1.0e-12
Match length	43
% identity	77
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	50161
Seq. ID	seb700652741.h1
Method	BLASTX

NCBI GI	g1171979
BLAST score	290
E value	3.0e-26
Match length	90
% identity	27
NCBI Description	POLYADENYLATE-BINDING PROTEIN 5 (POLY(A) BINDING PROTEIN 5) (PABP 5) >gi_166786 (M97657) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	50162
Seq. ID	seb700652746.h1
Method	BLASTN
NCBI GI	g1053215
BLAST score	203
E value	1.0e-110
Match length	260
% identity	96
NCBI Description	Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	50163
Seq. ID	seb700652762.h1
Method	BLASTN
NCBI GI	g170091
BLAST score	244
E value	1.0e-135
Match length	285
% identity	97
NCBI Description	Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No.	50164
Seq. ID	seb700652780.h1
Method	BLASTN
NCBI GI	g2388688
BLAST score	97
E value	3.0e-47
Match length	195
% identity	87
NCBI Description	Glycine max GH1 protein (GH1) mRNA, partial cds

Seq. No.	50165
Seq. ID	seb700652811.h1
Method	BLASTX
NCBI GI	g3687230
BLAST score	614
E value	3.0e-64
Match length	119
% identity	89
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50166
Seq. ID	seb700652816.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	328
E value	0.0e+00

Match length	343
% identity	99
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	50167
Seq. ID	seb700652821.h1
Method	BLASTX
NCBI GI	g1841462
BLAST score	154
E value	3.0e-21
Match length	90
% identity	77
NCBI Description	(Y10991) Elongation factor 2 [Nicotiana tabacum]

Seq. No.	50168
Seq. ID	seb700652868.h1
Method	BLASTX
NCBI GI	g2832241
BLAST score	275
E value	2.0e-24
Match length	112
% identity	39
NCBI Description	(AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana]

Seq. No.	50169
Seq. ID	seb700652920.h1
Method	BLASTN
NCBI GI	g2104680
BLAST score	77
E value	3.0e-35
Match length	276
% identity	82
NCBI Description	V.faba mRNA for putative transciption factor (1556bp)

Seq. No.	50170
Seq. ID	seb700652922.h1
Method	BLASTX
NCBI GI	g4115383
BLAST score	285
E value	1.0e-25
Match length	97
% identity	57
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	50171
Seq. ID	seb700652990.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	308
E value	1.0e-173
Match length	308
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	50172

Seq. ID	seb700652993.h1
Method	BLASTN
NCBI GI	g20732
BLAST score	69
E value	1.0e-30
Match length	129
% identity	88
NCBI Description	Pea chloroplast GAPB mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B (EC 1.2.1.13)

Seq. No.	50173
Seq. ID	seb700653179.h1
Method	BLASTX
NCBI GI	g3482924
BLAST score	142
E value	6.0e-14
Match length	74
% identity	58
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	50174
Seq. ID	seb700653242.h1
Method	BLASTX
NCBI GI	g3372671
BLAST score	163
E value	2.0e-11
Match length	33
% identity	100
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No.	50175
Seq. ID	seb700653254.h1
Method	BLASTX
NCBI GI	g543992
BLAST score	209
E value	4.0e-17
Match length	54
% identity	78
NCBI Description	MITOCHONDRIAL CHAPERONIN CPN60 PRECURSOR >gi_481445_pir__S38634 chaperonin, mitochondrial - rape >gi_415733_emb_CAA81689_ (Z27165) mitochondrial chaperonin [Brassica napus]

Seq. No.	50176
Seq. ID	seb700653284.h1
Method	BLASTX
NCBI GI	g3540180
BLAST score	289
E value	3.0e-26
Match length	100
% identity	61
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	50177
Seq. ID	seb700653302.h1

Method	BLASTX
NCBI GI	g3451071
BLAST score	160
E value	2.0e-11
Match length	51
% identity	73
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	50178
Seq. ID	seb700653358.h1
Method	BLASTX
NCBI GI	g2462756
BLAST score	122
E value	3.0e-10
Match length	90
% identity	43
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	50179
Seq. ID	seb700653418.h1
Method	BLASTX
NCBI GI	g2642435
BLAST score	189
E value	1.0e-14
Match length	46
% identity	70
NCBI Description	(AC002391) MYB-related protein [Arabidopsis thaliana]

Seq. No.	50180
Seq. ID	seb700653424.h1
Method	BLASTX
NCBI GI	g4249413
BLAST score	211
E value	4.0e-17
Match length	45
% identity	84
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	50181
Seq. ID	seb700653455.h1
Method	BLASTX
NCBI GI	g3056595
BLAST score	264
E value	3.0e-23
Match length	109
% identity	53
NCBI Description	(AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No.	50182
Seq. ID	seb700653474.h1
Method	BLASTX
NCBI GI	g2959767
BLAST score	364
E value	6.0e-35
Match length	108
% identity	62

NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	50183
Seq. ID	seb700653494.h1
Method	BLASTX
NCBI GI	g4325342
BLAST score	336
E value	7.0e-32
Match length	84
% identity	80
NCBI Description	(AF128393) No definition line found [Arabidopsis thaliana]

Seq. No.	50184
Seq. ID	seb700653501.h1
Method	BLASTX
NCBI GI	g4406777
BLAST score	254
E value	9.0e-39
Match length	99
% identity	79
NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	50185
Seq. ID	seb700653516.h1
Method	BLASTX
NCBI GI	g4314356
BLAST score	147
E value	7.0e-15
Match length	96
% identity	45
NCBI Description	(AC006340) putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana]

Seq. No.	50186
Seq. ID	seb700653540.h1
Method	BLASTX
NCBI GI	g2117621
BLAST score	186
E value	2.0e-27
Match length	97
% identity	70
NCBI Description	peroxidase (EC 1.11.1.7) 1B - alfalfa >gi_971560_emb_CAA62226_ (X90693) peroxidase1B [Medicago sativa]

Seq. No.	50187
Seq. ID	seb700653553.h1
Method	BLASTN
NCBI GI	g168303
BLAST score	75
E value	3.0e-34
Match length	173
% identity	37
NCBI Description	Linum usitatissimum ubiquitin gene, partial cds

Seq. No.	50188
Seq. ID	seb700653555.h1
Method	BLASTN
NCBI GI	g2264318
BLAST score	49
E value	1.0e-18
Match length	92
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	50189
Seq. ID	seb700653594.h1
Method	BLASTX
NCBI GI	g3522935
BLAST score	119
E value	2.0e-14
Match length	101
% identity	48
NCBI Description	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	50190
Seq. ID	seb700653637.h1
Method	BLASTX
NCBI GI	g4056490
BLAST score	173
E value	1.0e-12
Match length	45
% identity	76
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50191
Seq. ID	seb700653681.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	96
E value	1.0e-46
Match length	201
% identity	88
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	50192
Seq. ID	seb700653712.h1
Method	BLASTX
NCBI GI	g4115377
BLAST score	160
E value	5.0e-11
Match length	59
% identity	63
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	50193
Seq. ID	seb700653721.h1
Method	BLASTN

NCBI GI	g169920
BLAST score	250
E value	1.0e-138
Match length	274
% identity	99
NCBI Description	Soybean auxin-regulated protein (Aux28) mRNA, complete cds

Seq. No.	50194
Seq. ID	seb700653768.h1
Method	BLASTX
NCBI GI	g4220483
BLAST score	222
E value	2.0e-18
Match length	88
% identity	56
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	50195
Seq. ID	seb700653806.h1
Method	BLASTN
NCBI GI	g255407
BLAST score	177
E value	3.0e-95
Match length	205
% identity	14
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	50196
Seq. ID	seb700653852.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	143
E value	6.0e-75
Match length	151
% identity	99
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	50197
Seq. ID	seb700653868.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	67
E value	1.0e-29
Match length	146
% identity	93
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	50198
Seq. ID	seb700653911.h1
Method	BLASTX
NCBI GI	g3057150
BLAST score	287
E value	4.0e-26
Match length	87
% identity	53

NCBI Description	(AF059037) chaperonin 10 [Arabidopsis thaliana]
Seq. No.	50199
Seq. ID	seb700653979.h1
Method	BLASTN
NCBI GI	g886470
BLAST score	46
E value	2.0e-17
Match length	58
% identity	95
NCBI Description	C.roseus MetE mRNA for methionine synthase
Seq. No.	50200
Seq. ID	seb700654122.h1
Method	BLASTN
NCBI GI	g288187
BLAST score	195
E value	1.0e-106
Match length	250
% identity	95
NCBI Description	V.unguiculata cysteine proteinase inhibitor mRNA
Seq. No.	50201
Seq. ID	seb700654142.h1
Method	BLASTN
NCBI GI	g170071
BLAST score	254
E value	1.0e-141
Match length	265
% identity	99
NCBI Description	Soybean calmodulin (SCaM-2) mRNA, complete cds
Seq. No.	50202
Seq. ID	seb700654151.h1
Method	BLASTX
NCBI GI	g2244760
BLAST score	127
E value	2.0e-15
Match length	87
% identity	23
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.	50203
Seq. ID	seb700654155.h1
Method	BLASTX
NCBI GI	g3805964
BLAST score	224
E value	2.0e-37
Match length	87
% identity	89
NCBI Description	(Y13773) laccase [Populus balsamifera subsp. trichocarpa]
Seq. No.	50204
Seq. ID	seb700654162.h1
Method	BLASTN
NCBI GI	g441205
BLAST score	159

E value 2.0e-84
Match length 230
% identity 93
NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4

Seq. No. 50205
Seq. ID seb700654171.h1
Method BLASTN
NCBI GI g296408
BLAST score 212
E value 1.0e-116
Match length 251
% identity 96
NCBI Description G.max ADR12 mRNA

Seq. No. 50206
Seq. ID seb700654252.h1
Method BLASTN
NCBI GI g1575726
BLAST score 109
E value 2.0e-54
Match length 121
% identity 98
NCBI Description Glycine max 14-3-3 related protein SGF14B mRNA, partial cds

Seq. No. 50207
Seq. ID smc700744137.h1
Method BLASTX
NCBI GI g2529370
BLAST score 306
E value 2.0e-28
Match length 79
% identity 80
NCBI Description (L76552) NADP-dependent glyceraldehydephosphate dehydrogenase subunit A [Spinacia oleracea]

Seq. No. 50208
Seq. ID smc700744143.h1
Method BLASTX
NCBI GI g2911048
BLAST score 148
E value 8.0e-10
Match length 41
% identity 66
NCBI Description (AL021961) hypothetical protein [Arabidopsis thaliana]

Seq. No. 50209
Seq. ID smc700744192.h1
Method BLASTX
NCBI GI g4544369
BLAST score 236
E value 3.0e-20
Match length 82
% identity 51
NCBI Description (AC006920) hypothetical protein [Arabidopsis thaliana]

Seq. No. 50210

Seq. ID	smc700744195.h1
Method	BLASTX
NCBI GI	g3860315
BLAST score	283
E value	1.0e-25
Match length	61
% identity	90
NCBI Description	(AJ012684) 40S ribosomal protein S19 [Cicer arietinum]

Seq. No.	50211
Seq. ID	smc700744235.h1
Method	BLASTX
NCBI GI	g4566614
BLAST score	176
E value	4.0e-13
Match length	52
% identity	67
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	50212
Seq. ID	smc700744619.h1
Method	BLASTX
NCBI GI	g3805956
BLAST score	146
E value	1.0e-09
Match length	61
% identity	69
NCBI Description	(Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	50213
Seq. ID	smc700744625.h1
Method	BLASTX
NCBI GI	g1076678
BLAST score	113
E value	6.0e-15
Match length	64
% identity	74
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	50214
Seq. ID	smc700744868.h1
Method	BLASTX
NCBI GI	g3023194
BLAST score	165
E value	8.0e-12
Match length	58
% identity	60
NCBI Description	14-3-3-LIKE PROTEIN A (SGF14A) >gi_1575725 (U70533) SGF14A [Glycine max]

Seq. No.	50215
Seq. ID	smc700745011.h1
Method	BLASTX
NCBI GI	g2982466
BLAST score	189
E value	1.0e-14

Match length	50
% identity	60
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	50216
Seq. ID	smc700745019.h1
Method	BLASTX
NCBI GI	g4512663
BLAST score	162
E value	2.0e-11
Match length	86
% identity	21
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544470_gb_AAD22377.1_AC006580_9 (AC006580) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50217
Seq. ID	smc700745025.h1
Method	BLASTX
NCBI GI	g3046731
BLAST score	275
E value	1.0e-24
Match length	56
% identity	96
NCBI Description	(AJ005373) protein kinase [Craterostigma plantagineum]

Seq. No.	50218
Seq. ID	smc700745093.h1
Method	BLASTX
NCBI GI	g4539400
BLAST score	174
E value	6.0e-13
Match length	63
% identity	57
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	50219
Seq. ID	smc700745105.h1
Method	BLASTX
NCBI GI	g2149955
BLAST score	179
E value	1.0e-13
Match length	47
% identity	72
NCBI Description	(U97023) putative aquaporin-1 [Phaseolus vulgaris]

Seq. No.	50220
Seq. ID	smc700745187.h1
Method	BLASTX
NCBI GI	g4388727
BLAST score	190
E value	6.0e-15
Match length	55
% identity	67
NCBI Description	(AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50221

Seq. ID	smc700745316.h1
Method	BLASTX
NCBI GI	g2245125
BLAST score	139
E value	9.0e-09
Match length	48
% identity	56
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50222
Seq. ID	smc700745405.h1
Method	BLASTX
NCBI GI	g3288594
BLAST score	348
E value	3.0e-33
Match length	68
% identity	99
NCBI Description	(AJ006340) 26S proteasome subunit p112 [Rattus norvegicus]

Seq. No.	50223
Seq. ID	smc700745440.h1
Method	BLASTX
NCBI GI	g3785980
BLAST score	193
E value	3.0e-15
Match length	73
% identity	18
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50224
Seq. ID	smc700745467.h1
Method	BLASTX
NCBI GI	g3702691
BLAST score	216
E value	7.0e-18
Match length	81
% identity	59
NCBI Description	(AB005902) AtPIP5K1 [Arabidopsis thaliana]

Seq. No.	50225
Seq. ID	smc700745651.h1
Method	BLASTX
NCBI GI	g913986
BLAST score	167
E value	3.0e-12
Match length	37
% identity	92
NCBI Description	(S76779) apolipoprotein E, ApoE [rats, Peptide, 312 aa] [Rattus sp.]

Seq. No.	50226
Seq. ID	smc700745654.h1
Method	BLASTX
NCBI GI	g2443875
BLAST score	272
E value	2.0e-24
Match length	83

% identity	61
NCBI Description	(AC002294) amino acid permease [Arabidopsis thaliana]

Seq. No.	50227
Seq. ID	smc700745656.h1
Method	BLASTX
NCBI GI	g3738309
BLAST score	221
E value	1.0e-18
Match length	61
% identity	70
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	50228
Seq. ID	smc700745779.h1
Method	BLASTX
NCBI GI	g3941480
BLAST score	178
E value	1.0e-24
Match length	70
% identity	79
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	50229
Seq. ID	smc700745792.h1
Method	BLASTX
NCBI GI	g1076485
BLAST score	281
E value	2.0e-25
Match length	55
% identity	96
NCBI Description	SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No.	50230
Seq. ID	smc700745964.h1
Method	BLASTX
NCBI GI	g4539305
BLAST score	322
E value	3.0e-30
Match length	91
% identity	62
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	50231
Seq. ID	smc700746023.h1
Method	BLASTX
NCBI GI	g2493895
BLAST score	286
E value	5.0e-26
Match length	70
% identity	81
NCBI Description	CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_1071911_pir__S46438 cysteine synthase (EC 4.2.99.8) -

watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine synthase [Citrullus lanatus]

Seq. No.	50232
Seq. ID	smc700746075.h1
Method	BLASTX
NCBI GI	g1805654
BLAST score	191
E value	7.0e-15
Match length	64
% identity	55
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No.	50233
Seq. ID	smc700746190.h1
Method	BLASTX
NCBI GI	g2924552
BLAST score	203
E value	3.0e-16
Match length	84
% identity	55
NCBI Description	(AL022018) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=165.48; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA264666; 2-match_description=LD08351.5prime LD Drosophila melanogaste

Seq. No.	50234
Seq. ID	smc700746279.h1
Method	BLASTX
NCBI GI	g1076485
BLAST score	274
E value	1.0e-24
Match length	53
% identity	96
NCBI Description	SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No.	50235
Seq. ID	smc700746460.h1
Method	BLASTX
NCBI GI	g1495251
BLAST score	201
E value	5.0e-16
Match length	51
% identity	73
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	50236
Seq. ID	smc700746523.h1
Method	BLASTX
NCBI GI	g3913008
BLAST score	392
E value	2.0e-38

Match length	89
% identity	90
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	50237
Seq. ID	smc700746537.h1
Method	BLASTX
NCBI GI	g4097561
BLAST score	135
E value	2.0e-14
Match length	86
% identity	55
NCBI Description	(U64918) ATGP1 [Arabidopsis thaliana]

Seq. No.	50238
Seq. ID	smc700746570.h1
Method	BLASTX
NCBI GI	g485515
BLAST score	337
E value	2.0e-39
Match length	85
% identity	91
NCBI Description	ADR6 protein - soybean >gi_296445_emb_CAA49340_ (X69639) auxin down regulated [Glycine max] >gi_2304955 (U64866) similar to ADR6 encoded by GenBank Accession Number X69639; aluminum induced [Glycine max]

Seq. No.	50239
Seq. ID	smc700746581.h1
Method	BLASTX
NCBI GI	g2662343
BLAST score	220
E value	5.0e-21
Match length	62
% identity	92
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	50240
Seq. ID	smc700746647.h1
Method	BLASTX
NCBI GI	g3033375
BLAST score	146
E value	1.0e-15
Match length	80
% identity	53
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	50241
Seq. ID	smc700746662.h1
Method	BLASTX
NCBI GI	g121336
BLAST score	234
E value	6.0e-20
Match length	43

% identity	100
NCBI Description	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME (GLUTAMATE--AMMONIA LIGASE) >gi_81774_pir__JQ0937 glutamate--ammonia ligase (EC 6.3.1.2), cytosolic - soybean >gi_256143_bbs_113802 (S46513) cytosolic glutamine synthetase, GS {EC 6.3.1.2} [Glycine max=soybeans, var Prize, Peptide, 355 aa] [Glycine max]

Seq. No.	50242
Seq. ID	smc700746678.h1
Method	BLASTX
NCBI GI	g169900
BLAST score	325
E value	1.0e-30
Match length	68
% identity	91
NCBI Description	(M37529) 31 kDa protein [Glycine max]

Seq. No.	50243
Seq. ID	smc700746788.h1
Method	BLASTX
NCBI GI	g2529665
BLAST score	140
E value	4.0e-09
Match length	52
% identity	54
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	50244
Seq. ID	smc700746833.h1
Method	BLASTX
NCBI GI	g4115922
BLAST score	213
E value	2.0e-29
Match length	91
% identity	72
NCBI Description	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis thaliana]

Seq. No.	50245
Seq. ID	smc700746835.h1
Method	BLASTX
NCBI GI	g629651
BLAST score	366
E value	2.0e-35
Match length	84
% identity	80
NCBI Description	cysteine proteinase - spring vetch >gi_2129904_pir__S51817 cysteine proteinase (EC 3.4.22.-) precursor - spring vetch >gi_535473_emb_CAA53377_ (X75749) cysteine protease [Vicia sativa]

Seq. No.	50246
Seq. ID	smc700746949.h1

Method	BLASTX
NCBI GI	g986969
BLAST score	256
E value	2.0e-22
Match length	49
% identity	100
NCBI Description	(L28005) TGACG-motif-binding protein [Glycine max]

Seq. No.	50247
Seq. ID	smc700746992.h1
Method	BLASTX
NCBI GI	g4490316
BLAST score	152
E value	3.0e-10
Match length	37
% identity	68
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	50248
Seq. ID	smc700747049.h1
Method	BLASTX
NCBI GI	g2160189
BLAST score	183
E value	5.0e-14
Match length	77
% identity	49
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	50249
Seq. ID	smc700747104.h1
Method	BLASTX
NCBI GI	g2661412
BLAST score	150
E value	3.0e-10
Match length	44
% identity	64
NCBI Description	(AJ000728) MAP kinase kinase [Lycopersicon esculentum]

Seq. No.	50250
Seq. ID	smc700747115.h1
Method	BLASTX
NCBI GI	g4191797
BLAST score	172
E value	1.0e-12
Match length	72
% identity	56
NCBI Description	(AC005917) putative receptor protein kinase, 3' partial [Arabidopsis thaliana]

Seq. No.	50251
Seq. ID	smc700747130.h1
Method	BLASTX
NCBI GI	g807698
BLAST score	294
E value	6.0e-27

Match length	91
% identity	58
NCBI Description	(D32206) prepro-cucumisin [Cucumis melo]

Seq. No.	50252
Seq. ID	smc700747164.h1
Method	BLASTX
NCBI GI	g4206209
BLAST score	344
E value	8.0e-33
Match length	83
% identity	80
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	50253
Seq. ID	smc700747186.h1
Method	BLASTX
NCBI GI	g4538935
BLAST score	201
E value	5.0e-16
Match length	61
% identity	65
NCBI Description	(AL049483) putative protein [Arabidopsis thaliana]

Seq. No.	50254
Seq. ID	smc700747188.h1
Method	BLASTX
NCBI GI	g1076274
BLAST score	250
E value	9.0e-22
Match length	84
% identity	56
NCBI Description	cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No.	50255
Seq. ID	smc700747208.h1
Method	BLASTX
NCBI GI	g2252846
BLAST score	209
E value	5.0e-17
Match length	81
% identity	56
NCBI Description	(AF013293) Similar to phospholipase D [Arabidopsis thaliana]

Seq. No.	50256
Seq. ID	smc700747235.h1
Method	BLASTX
NCBI GI	g535428
BLAST score	180
E value	2.0e-14
Match length	62
% identity	36
NCBI Description	(U13736) calmodulin-like protein [Pisum sativum]

Seq. No.	50257
Seq. ID	smc700747284.h1
Method	BLASTX
NCBI GI	g4539390
BLAST score	331
E value	3.0e-31
Match length	63
% identity	95
NCBI Description	(AL035526) shaggy-like protein kinase etha (EC 2.7.1.-) [Arabidopsis thaliana]

Seq. No.	50258
Seq. ID	smc700747305.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	255
E value	2.0e-22
Match length	62
% identity	84
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	50259
Seq. ID	smc700747310.h1
Method	BLASTX
NCBI GI	g136057
BLAST score	187
E value	2.0e-14
Match length	63
% identity	62
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	50260
Seq. ID	smc700747408.h1
Method	BLASTX
NCBI GI	g1944152
BLAST score	169
E value	3.0e-12
Match length	34
% identity	85
NCBI Description	(AB002667) ACC-oxidase [Vigna angularis]

Seq. No.	50261
Seq. ID	smc700747419.h1
Method	BLASTX
NCBI GI	g4467137
BLAST score	222
E value	2.0e-18
Match length	88
% identity	49
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	50262
Seq. ID	smc700747451.h1
Method	BLASTX

NCBI GI	g3894383
BLAST score	175
E value	4.0e-13
Match length	81
% identity	3
NCBI Description	(AF053993) disease resistance protein [Lycopersicon esculentum]

Seq. No.	50263
Seq. ID	smc700747484.h1
Method	BLASTX
NCBI GI	g1076485
BLAST score	283
E value	1.0e-25
Match length	54
% identity	98
NCBI Description	SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No.	50264
Seq. ID	smc700747547.h1
Method	BLASTX
NCBI GI	g1076545
BLAST score	184
E value	3.0e-14
Match length	51
% identity	75
NCBI Description	guanine nucleotide regulatory protein - fava bean >gi_547478_emb_CAA85733_ (Z37503) guanine nucleotide regulatory protein [Vicia faba] >gi_1098297_prf__2115367E small GTP-binding protein [Vicia faba]

Seq. No.	50265
Seq. ID	smc700747550.h1
Method	BLASTX
NCBI GI	g1076485
BLAST score	304
E value	4.0e-28
Match length	58
% identity	98
NCBI Description	SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No.	50266
Seq. ID	smc700747592.h1
Method	BLASTX
NCBI GI	g123617
BLAST score	256
E value	2.0e-22
Match length	61
% identity	80
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_99707_pir__JA0170 heat shock protein 70-2 - Arabidopsis thaliana (fragment) >gi_166766 (M23106) heat shock protein HSP70-2 [Arabidopsis thaliana]

Seq. No.	50267
Seq. ID	smc700747636.h1
Method	BLASTX
NCBI GI	g417148
BLAST score	225
E value	5.0e-19
Match length	63
% identity	68
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) (G2-4) >gi_99912_pir__A33654 heat shock protein 26A - soybean >gi_169981 (M20363) Gmhsp26-A [Glycine max]

Seq. No.	50268
Seq. ID	smc700747645.h1
Method	BLASTX
NCBI GI	g2274862
BLAST score	302
E value	4.0e-28
Match length	60
% identity	87
NCBI Description	(AJ000497) Starch branching enzyme II [Arabidopsis thaliana]

Seq. No.	50269
Seq. ID	smc700747718.h1
Method	BLASTX
NCBI GI	g3913008
BLAST score	415
E value	4.0e-41
Match length	88
% identity	93
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	50270
Seq. ID	smc700747727.h1
Method	BLASTX
NCBI GI	g1146165
BLAST score	272
E value	3.0e-24
Match length	57
% identity	95
NCBI Description	(L47479) urophorphyrin III methylase [Arabidopsis thaliana]

Seq. No.	50271
Seq. ID	smc700747755.h1
Method	BLASTX
NCBI GI	g4206787
BLAST score	368
E value	1.0e-35
Match length	89
% identity	81
NCBI Description	(AF112863) syntaxin-related protein Nt-syr1 [Nicotiana tabacum]

Seq. No.	50272
Seq. ID	smc700747756.h1
Method	BLASTX
NCBI GI	g4538926
BLAST score	325
E value	1.0e-30
Match length	88
% identity	73
NCBI Description	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]

Seq. No.	50273
Seq. ID	smc700747859.h1
Method	BLASTX
NCBI GI	g3702336
BLAST score	388
E value	5.0e-38
Match length	85
% identity	92
NCBI Description	(AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No.	50274
Seq. ID	smc700747878.h1
Method	BLASTX
NCBI GI	g986969
BLAST score	154
E value	2.0e-10
Match length	31
% identity	94
NCBI Description	(L28005) TGACG-motif-binding protein [Glycine max]

Seq. No.	50275
Seq. ID	smc700748001.h1
Method	BLASTX
NCBI GI	g1076485
BLAST score	206
E value	7.0e-17
Match length	39
% identity	100
NCBI Description	SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No.	50276
Seq. ID	smc700748064.h1
Method	BLASTX
NCBI GI	g3157932
BLAST score	136
E value	1.0e-08
Match length	33
% identity	76
NCBI Description	(AC002131) Similar to hypothetical protein HYP1 gb_Z97338 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	50277
Seq. ID	smc700748188.h1

Method	BLASTX
NCBI GI	g3885341
BLAST score	181
E value	9.0e-14
Match length	76
% identity	47
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	50278
Seq. ID	smc700748243.h1
Method	BLASTX
NCBI GI	g2262105
BLAST score	303
E value	6.0e-28
Match length	87
% identity	64
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	50279
Seq. ID	smc700748260.h1
Method	BLASTX
NCBI GI	g1168189
BLAST score	221
E value	3.0e-21
Match length	67
% identity	85
NCBI Description	14-3-3-LIKE PROTEIN A (VFA-1433A) >gi_1076542_pir__S52899 14-3-3 brain protein homolog - fava bean >gi_695765_emb_CAA88415_ (Z48504) 14-3-3 brain protein homolog [Vicia faba]

Seq. No.	50280
Seq. ID	smc700748301.h1
Method	BLASTX
NCBI GI	g2459412
BLAST score	212
E value	3.0e-17
Match length	84
% identity	51
NCBI Description	(AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No.	50281
Seq. ID	smc700748403.h1
Method	BLASTX
NCBI GI	g4531444
BLAST score	164
E value	1.0e-11
Match length	41
% identity	78
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	50282
Seq. ID	smc700748536.h1
Method	BLASTX
NCBI GI	g3850108
BLAST score	250
E value	9.0e-22

Match length	77
% identity	64
NCBI Description	(AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]

Seq. No.	50283
Seq. ID	smc700748565.h1
Method	BLASTX
NCBI GI	g2463577
BLAST score	408
E value	3.0e-40
Match length	82
% identity	95
NCBI Description	(AB007510) PRP8 protein [Homo sapiens]

Seq. No.	50284
Seq. ID	smc700748601.h1
Method	BLASTX
NCBI GI	g4454016
BLAST score	200
E value	7.0e-16
Match length	64
% identity	70
NCBI Description	(AL035396) UMP/CMP kinase like protein [Arabidopsis thaliana]

Seq. No.	50285
Seq. ID	smc700748626.h1
Method	BLASTX
NCBI GI	g3033391
BLAST score	233
E value	9.0e-20
Match length	56
% identity	77
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	50286
Seq. ID	smc700748635.h1
Method	BLASTX
NCBI GI	g3551221
BLAST score	101
E value	8.0e-09
Match length	54
% identity	61
NCBI Description	(AB012628) blue-light photoreceptor [Adiantum capillus-veneris] >gi_3551227_dbj_BAA32812_ (AB012631) blue-light photoreceptor [Adiantum capillus-veneris]

Seq. No.	50287
Seq. ID	smc700748642.h1
Method	BLASTX
NCBI GI	g2979544
BLAST score	206
E value	1.0e-16
Match length	74
% identity	54

NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	50288
Seq. ID	smc700748695.h1
Method	BLASTX
NCBI GI	g3176690
BLAST score	208
E value	7.0e-17
Match length	85
% identity	54
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	50289
Seq. ID	smc700748702.h1
Method	BLASTX
NCBI GI	g111347
BLAST score	251
E value	4.0e-35
Match length	75
% identity	89
NCBI Description	alcohol sulfotransferase (EC 2.8.2.2) - rat >gi_204671 (M31363) hydroxysteroid sulfotransferase [Rattus norvegicus]

Seq. No.	50290
Seq. ID	smc700748756.h1
Method	BLASTX
NCBI GI	g4512654
BLAST score	238
E value	2.0e-20
Match length	65
% identity	66
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	50291
Seq. ID	smc700748769.h1
Method	BLASTX
NCBI GI	g3668083
BLAST score	163
E value	8.0e-12
Match length	49
% identity	65
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50292
Seq. ID	smc700748816.h1
Method	BLASTX
NCBI GI	g4490304
BLAST score	308
E value	1.0e-28
Match length	87
% identity	69
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	50293

Seq. ID	smc700748825.h1
Method	BLASTX
NCBI GI	g1076485
BLAST score	301
E value	1.0e-27
Match length	59
% identity	97
NCBI Description	SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No.	50294
Seq. ID	smc700748867.h1
Method	BLASTX
NCBI GI	g3548802
BLAST score	316
E value	2.0e-29
Match length	88
% identity	67
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	50295
Seq. ID	smc700748902.h1
Method	BLASTX
NCBI GI	g4335967
BLAST score	176
E value	3.0e-13
Match length	43
% identity	79
NCBI Description	(AF062733) cell adhesion molecule [Homo sapiens]

Seq. No.	50296
Seq. ID	smc700748928.h1
Method	BLASTX
NCBI GI	g2500026
BLAST score	201
E value	3.0e-16
Match length	40
% identity	93
NCBI Description	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) >gi_1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana]

Seq. No.	50297
Seq. ID	smc700748979.h1
Method	BLASTX
NCBI GI	g3551742
BLAST score	200
E value	4.0e-16
Match length	38
% identity	100
NCBI Description	(U27112) HT-1080 protein [Homo sapiens]

Seq. No.	50298
Seq. ID	smc700749009.h1

Method	BLASTX
NCBI GI	g1237102
BLAST score	268
E value	7.0e-24
Match length	89
% identity	67
NCBI Description	(L40358) calmodulin-binding protein [Arabidopsis thaliana] >gi_1589171_prf__2210340A calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	50299
Seq. ID	smc700749025.h1
Method	BLASTX
NCBI GI	g2245082
BLAST score	177
E value	5.0e-27
Match length	87
% identity	69
NCBI Description	(Z97343) SCARECROW homolog [Arabidopsis thaliana]

Seq. No.	50300
Seq. ID	smc700749062.h1
Method	BLASTX
NCBI GI	g4240261
BLAST score	196
E value	2.0e-30
Match length	85
% identity	87
NCBI Description	(AB020693) KIAA0886 protein [Homo sapiens]

Seq. No.	50301
Seq. ID	smc700749088.h1
Method	BLASTX
NCBI GI	g267184
BLAST score	352
E value	1.0e-33
Match length	87
% identity	78
NCBI Description	NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 >gi_1360649_pir__TVHUY2 protein-tyrosine kinase (EC 2.7.1.112) tyk2 - human >gi_37504_emb_CAA38449_ (X54637) protein tyrosine kinase [Homo sapiens] >gi_4507749_ref_NP_003322.1_pTYK2_ tyrosine kinase

Seq. No.	50302
Seq. ID	smc700749096.h1
Method	BLASTX
NCBI GI	g3023816
BLAST score	188
E value	2.0e-14
Match length	40
% identity	80
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	50303

Seq. ID	smc700749115.h1
Method	BLASTX
NCBI GI	g3367638
BLAST score	243
E value	1.0e-27
Match length	90
% identity	71
NCBI Description	(AJ000331) monogalactosyldiacylglycerol synthase [Arabidopsis thaliana]

Seq. No.	50304
Seq. ID	smc700749150.h1
Method	BLASTX
NCBI GI	g3093294
BLAST score	170
E value	2.0e-12
Match length	43
% identity	77
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	50305
Seq. ID	smc700749162.h1
Method	BLASTX
NCBI GI	g4580398
BLAST score	119
E value	7.0e-12
Match length	86
% identity	48
NCBI Description	(AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No.	50306
Seq. ID	smc700749192.h1
Method	BLASTX
NCBI GI	g1931638
BLAST score	178
E value	3.0e-13
Match length	81
% identity	47
NCBI Description	(U95973) transcription factor RUSH-1alpha isolog [Arabidopsis thaliana]

Seq. No.	50307
Seq. ID	smc700749230.h1
Method	BLASTX
NCBI GI	g1762935
BLAST score	306
E value	3.0e-28
Match length	72
% identity	88
NCBI Description	(U66264) ubiquitin [Nicotiana tabacum]

Seq. No.	50308
Seq. ID	smc700749238.h1
Method	BLASTX
NCBI GI	g4210948
BLAST score	205

E value	1.0e-16
Match length	53
% identity	77
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	50309
Seq. ID	smc700749260.h1
Method	BLASTX
NCBI GI	g886100
BLAST score	153
E value	1.0e-12
Match length	67
% identity	67
NCBI Description	(U27347) putative water channel protein; plasmalemma intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No.	50310
Seq. ID	smc700749283.h1
Method	BLASTX
NCBI GI	g1346672
BLAST score	111
E value	1.0e-11
Match length	69
% identity	58
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi_421886_pir__S33170 nucleoside-diphosphate kinase (EC 2.7.4.6) - garden pea >gi_1084378_pir__S46513 nucleoside-diphosphate kinase (EC 2.7.4.6) - garden pea >gi_296174_emb_CAA50511_ (X71388) nucleoside-diphosphate kinase [Pisum sativum]

Seq. No.	50311
Seq. ID	smc700749313.h1
Method	BLASTX
NCBI GI	g4185567
BLAST score	170
E value	6.0e-16
Match length	77
% identity	83
NCBI Description	(AF115480) cAMP-dependent Rap1 guanine-nucleotide exchange factor [Mus musculus]

Seq. No.	50312
Seq. ID	smc700749335.h1
Method	BLASTX
NCBI GI	g1491931
BLAST score	145
E value	2.0e-09
Match length	76
% identity	43
NCBI Description	(U52078) kinesin-like protein [Nicotiana tabacum]

Seq. No.	50313
Seq. ID	smc700749407.h1
Method	BLASTX
NCBI GI	g2191144

BLAST score 261
E value 5.0e-23
Match length 90
% identity 61
NCBI Description (AF007269) A_IG002N01.24 gene product [Arabidopsis thaliana]

Seq. No. 50314
Seq. ID smc700749414.h1
Method BLASTX
NCBI GI g2262105
BLAST score 380
E value 5.0e-37
Match length 91
% identity 79
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 50315
Seq. ID smc700749421.h1
Method BLASTX
NCBI GI g418754
BLAST score 385
E value 1.0e-37
Match length 89
% identity 74
NCBI Description catechol oxidase (EC 1.10.3.1) precursor - fava bean

Seq. No. 50316
Seq. ID smc700749547.h1
Method BLASTX
NCBI GI g4455276
BLAST score 298
E value 2.0e-27
Match length 89
% identity 70
NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No. 50317
Seq. ID smc700749567.h1
Method BLASTX
NCBI GI g4335754
BLAST score 394
E value 1.0e-38
Match length 84
% identity 81
NCBI Description (AC006284) putative acid phophatase (contains metallo-phosphoesterase motif, prosite: QDOC50185) [Arabidopsis thaliana]

Seq. No. 50318
Seq. ID smc700749583.h1
Method BLASTX
NCBI GI g2674062
BLAST score 204
E value 1.0e-30
Match length 88

% identity	88
NCBI Description	(AF006043) 3-phosphoglycerate dehydrogenase [Homo sapiens]

Seq. No.	50319
Seq. ID	smc700749609.h1
Method	BLASTX
NCBI GI	g2460318
BLAST score	412
E value	9.0e-41
Match length	83
% identity	96
NCBI Description	(AF021819) RNA-binding protein regulatory subunit [Homo sapiens]

Seq. No.	50320
Seq. ID	smc700749617.h1
Method	BLASTX
NCBI GI	g2739379
BLAST score	181
E value	1.0e-13
Match length	86
% identity	49
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50321
Seq. ID	smc700749619.h1
Method	BLASTX
NCBI GI	g4115341
BLAST score	188
E value	9.0e-15
Match length	64
% identity	53
NCBI Description	(U51100) chromaffin granule ATPase II [Bos taurus]

Seq. No.	50322
Seq. ID	smc700749639.h1
Method	BLASTX
NCBI GI	g1172624
BLAST score	181
E value	1.0e-13
Match length	39
% identity	92
NCBI Description	PROFILIN II >gi_2136802_pir__S65365 profilin II - bovine (fragment)

Seq. No.	50323
Seq. ID	smc700749731.h1
Method	BLASTX
NCBI GI	g3413886
BLAST score	466
E value	5.0e-47
Match length	94
% identity	97
NCBI Description	(AB007931) KIAA0462 protein [Homo sapiens]

Seq. No.	50324
Seq. ID	smc700749747.h1

Method	BLASTX
NCBI GI	g2738998
BLAST score	324
E value	2.0e-30
Match length	89
% identity	70
NCBI Description	(AF022458) CYP98A2p [Glycine max]

Seq. No.	50325
Seq. ID	smc700749759.h1
Method	BLASTX
NCBI GI	g3334413
BLAST score	171
E value	1.0e-12
Match length	49
% identity	71
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_2502087 (AF022926) adenosine triphosphatase; c-subunit of V-ATPase [Vigna radiata]

Seq. No.	50326
Seq. ID	smc700749794.h1
Method	BLASTX
NCBI GI	g3860268
BLAST score	175
E value	6.0e-13
Match length	78
% identity	44
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50327
Seq. ID	smc700749806.h1
Method	BLASTX
NCBI GI	g2829902
BLAST score	246
E value	2.0e-29
Match length	85
% identity	85
NCBI Description	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]

Seq. No.	50328
Seq. ID	smc700749858.h1
Method	BLASTX
NCBI GI	g3451071
BLAST score	266
E value	1.0e-23
Match length	84
% identity	67
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	50329
Seq. ID	smc700749861.h1
Method	BLASTX
NCBI GI	g2982077
BLAST score	453

E value	1.0e-45
Match length	86
% identity	97
NCBI Description	Chain C, Complex Of Gs-Alpha With The Catalytic Domains Of Mammalian Adenylyl Cyclase >gi_2982078_pdb_1AZT_A Chain A, Gs-Alpha Complexed With Gtp-Gamma-S >gi_2982079_pdb_1AZT_B Chain B, Gs-Alpha Complexed With Gtp-Gamma-S

Seq. No.	50330
Seq. ID	smc700749886.h1
Method	BLASTX
NCBI GI	g3080420
BLAST score	365
E value	3.0e-35
Match length	81
% identity	85
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	50331
Seq. ID	smc700749937.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	140
E value	7.0e-09
Match length	55
% identity	47
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	50332
Seq. ID	smc700749963.h1
Method	BLASTX
NCBI GI	g4204304
BLAST score	211
E value	3.0e-17
Match length	87
% identity	51
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	50333
Seq. ID	smc700749981.h1
Method	BLASTX
NCBI GI	g3193284
BLAST score	231
E value	2.0e-19
Match length	77
% identity	57
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	50334
Seq. ID	smc700749986.h1
Method	BLASTX
NCBI GI	g4220474
BLAST score	170
E value	2.0e-21
Match length	83

% identity	67
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	50335
Seq. ID	smc700750165.h1
Method	BLASTX
NCBI GI	g120649
BLAST score	440
E value	4.0e-44
Match length	86
% identity	99
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_182863 (J02642) glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >gi_224880_prf__1203217A dehydrogenase,glyceraldehydephosphate [Homo sapiens]

Seq. No.	50336
Seq. ID	smc700750171.h1
Method	BLASTX
NCBI GI	g688430
BLAST score	228
E value	3.0e-19
Match length	72
% identity	58
NCBI Description	(D26457) tumor-related protein [Nicotiana glauca X Nicotiana langsdorffii]

Seq. No.	50337
Seq. ID	smc700750243.h1
Method	BLASTX
NCBI GI	g121336
BLAST score	262
E value	3.0e-23
Match length	49
% identity	100
NCBI Description	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME (GLUTAMATE--AMMONIA LIGASE) >gi_81774_pir__JQ0937 glutamate--ammonia ligase (EC 6.3.1.2), cytosolic - soybean >gi_256143_bbs_113802 (S46513) cytosolic glutamine synthetase, GS {EC 6.3.1.2} [Glycine max=soybeans, var Prize, Peptide, 355 aa] [Glycine max]

Seq. No.	50338
Seq. ID	smc700750247.h1
Method	BLASTX
NCBI GI	g535454
BLAST score	236
E value	4.0e-20
Match length	55

% identity	75
NCBI Description	(U13940) cysteine proteinase [Alnus glutinosa]

Seq. No.	50339
Seq. ID	smc700750263.h1
Method	BLASTX
NCBI GI	g3746938
BLAST score	137
E value	3.0e-18
Match length	59
% identity	83
NCBI Description	(AF091809) actin 2 [Anemia phyllitidis]

Seq. No.	50340
Seq. ID	smc700750268.h1
Method	BLASTX
NCBI GI	g2851393
BLAST score	413
E value	6.0e-41
Match length	83
% identity	96
NCBI Description	NADPH-CYTOCHROME P450 REDUCTASE (CPR) >gi_482604_pir__A60557 NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - human

Seq. No.	50341
Seq. ID	smc700750269.h1
Method	BLASTX
NCBI GI	g2117899
BLAST score	452
E value	2.0e-45
Match length	84
% identity	99
NCBI Description	creatine kinase-B - human >gi_180555 (M16364) creatine kinase-B [Homo sapiens]

Seq. No.	50342
Seq. ID	smc700750273.h1
Method	BLASTX
NCBI GI	g1688095
BLAST score	268
E value	6.0e-24
Match length	68
% identity	76
NCBI Description	(U68057) frezzled [Homo sapiens]

Seq. No.	50343
Seq. ID	smc700750294.h1
Method	BLASTX
NCBI GI	g3953457
BLAST score	202
E value	3.0e-16
Match length	72
% identity	56
NCBI Description	(AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No.	50344

Seq. ID	smc700750343.h1
Method	BLASTX
NCBI GI	g1066859
BLAST score	239
E value	1.0e-20
Match length	48
% identity	98
NCBI Description	(L49020) acetyl-CoA carboxylase [Glycine max]

Seq. No.	50345
Seq. ID	smc700750369.h1
Method	BLASTX
NCBI GI	g2062176
BLAST score	175
E value	3.0e-13
Match length	40
% identity	80
NCBI Description	(AC001645) Myb-related transcription activator (MybSt1) isolog [Arabidopsis thaliana]

Seq. No.	50346
Seq. ID	smc700750380.h1
Method	BLASTX
NCBI GI	g416914
BLAST score	233
E value	1.0e-38
Match length	89
% identity	97
NCBI Description	DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN DRG (NEDD3 PROTEIN) >gi_220507_dbj_BAA01555_ (D10715) GTP-binding protein [Mus musculus]

Seq. No.	50347
Seq. ID	smw700646115.h1
Method	BLASTX
NCBI GI	g132086
BLAST score	360
E value	1.0e-34
Match length	72
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR (RUBISCO SMALL SUBUNIT 1) >gi_68053_pir__RKSYS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor SRS1 - soybean >gi_18742_emb_CAA23736_ (V00458) rubpcase [Glycine max]

Seq. No.	50348
Seq. ID	smw700646116.h1
Method	BLASTX
NCBI GI	g3738298
BLAST score	146
E value	2.0e-09
Match length	64
% identity	48
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	50349
Seq. ID	smw700646162.h1
Method	BLASTX
NCBI GI	g4263706
BLAST score	236
E value	5.0e-20
Match length	96
% identity	52
NCBI Description	(AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50350
Seq. ID	smw700646176.h1
Method	BLASTX
NCBI GI	g4309723
BLAST score	142
E value	3.0e-09
Match length	30
% identity	93
NCBI Description	(AC006439) putative succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	50351
Seq. ID	smw700646195.h1
Method	BLASTX
NCBI GI	g3850588
BLAST score	288
E value	4.0e-26
Match length	71
% identity	75
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No.	50352
Seq. ID	smw700646213.h1
Method	BLASTX
NCBI GI	g3877205
BLAST score	139
E value	1.0e-08
Match length	60
% identity	48
NCBI Description	(Z70780) similar to lipase [Caenorhabditis elegans]

Seq. No.	50353
Seq. ID	smw700646223.h1
Method	BLASTX
NCBI GI	g20729
BLAST score	276
E value	1.0e-24
Match length	74
% identity	81
NCBI Description	(X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.	50354
Seq. ID	smw700646253.h1

Method	BLASTX
NCBI GI	g140218
BLAST score	148
E value	1.0e-09
Match length	55
% identity	53
NCBI Description	ATP SYNTHASE SUBUNITS REGION ORF

Seq. No.	50355
Seq. ID	ssr700553708.h1
Method	BLASTX
NCBI GI	g3785998
BLAST score	196
E value	9.0e-26
Match length	77
% identity	79
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	50356
Seq. ID	ssr700553725.h1
Method	BLASTX
NCBI GI	g1848212
BLAST score	177
E value	2.0e-18
Match length	70
% identity	50
NCBI Description	(Y11209) protein disulfide-isomerase precursor [Nicotiana tabacum]

Seq. No.	50357
Seq. ID	ssr700553740.h1
Method	BLASTX
NCBI GI	g115765
BLAST score	155
E value	8.0e-11
Match length	33
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A chlorophyll a/b binding protein II [Lycopersicon esculentum]

Seq. No.	50358
Seq. ID	ssr700553770.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	51
E value	7.0e-20
Match length	95
% identity	88
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	50359

Seq. ID	ssr700553779.h1
Method	BLASTX
NCBI GI	g4454031
BLAST score	149
E value	7.0e-10
Match length	35
% identity	80
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	50360
Seq. ID	ssr700553835.h1
Method	BLASTX
NCBI GI	g818849
BLAST score	211
E value	4.0e-17
Match length	56
% identity	70
NCBI Description	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]

Seq. No.	50361
Seq. ID	ssr700553842.h1
Method	BLASTX
NCBI GI	g4455160
BLAST score	282
E value	2.0e-25
Match length	97
% identity	60
NCBI Description	(AL031187) kinesin-related protein katA (fragment) [Arabidopsis thaliana]

Seq. No.	50362
Seq. ID	ssr700554019.h1
Method	BLASTX
NCBI GI	g2827524
BLAST score	195
E value	3.0e-15
Match length	83
% identity	55
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	50363
Seq. ID	ssr700554080.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	93
E value	6.0e-45
Match length	180
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	50364
Seq. ID	ssr700554189.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	124

E value	2.0e-63
Match length	235
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	50365
Seq. ID	ssr700554295.h1
Method	BLASTN
NCBI GI	g2765444
BLAST score	205
E value	1.0e-112
Match length	275
% identity	98
NCBI Description	Glycine max mRNA for ferredoxin thioredoxin reductase

Seq. No.	50366
Seq. ID	ssr700554320.h1
Method	BLASTX
NCBI GI	g4512653
BLAST score	147
E value	7.0e-10
Match length	68
% identity	46
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	50367
Seq. ID	ssr700554475.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	98
E value	6.0e-48
Match length	240
% identity	85
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	50368
Seq. ID	ssr700554528.h1
Method	BLASTX
NCBI GI	g2281090
BLAST score	249
E value	1.0e-21
Match length	92
% identity	58
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50369
Seq. ID	ssr700554582.h1
Method	BLASTX
NCBI GI	g3287695
BLAST score	208
E value	8.0e-17
Match length	90
% identity	51
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No.	50370
Seq. ID	ssr700554603.h1
Method	BLASTN
NCBI GI	g20732
BLAST score	49
E value	4.0e-19
Match length	89
% identity	89
NCBI Description	Pea chloroplast GAPB mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B (EC 1.2.1.13)

Seq. No.	50371
Seq. ID	ssr700554642.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	293
E value	8.0e-27
Match length	69
% identity	77
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	50372
Seq. ID	ssr700554672.h1
Method	BLASTX
NCBI GI	g3420052
BLAST score	168
E value	4.0e-12
Match length	86
% identity	47
NCBI Description	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No.	50373
Seq. ID	ssr700554716.h1
Method	BLASTX
NCBI GI	g4206209
BLAST score	483
E value	5.0e-49
Match length	96
% identity	95
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	50374
Seq. ID	ssr700554813.h1
Method	BLASTX
NCBI GI	g2911077
BLAST score	140
E value	8.0e-09
Match length	49
% identity	47
NCBI Description	(AL021960) gibberellin 20-oxidase - like protein [Arabidopsis thaliana]

Seq. No.	50375
Seq. ID	ssr700554852.h1
Method	BLASTX
NCBI GI	g2961345
BLAST score	186
E value	3.0e-14
Match length	44
% identity	70
NCBI Description	(AL022140) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50376
Seq. ID	ssr700554864.h1
Method	BLASTX
NCBI GI	g2160161
BLAST score	162
E value	2.0e-11
Match length	92
% identity	6
NCBI Description	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]

Seq. No.	50377
Seq. ID	ssr700555020.h1
Method	BLASTX
NCBI GI	g4467117
BLAST score	244
E value	6.0e-21
Match length	80
% identity	65
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50378
Seq. ID	ssr700555083.h1
Method	BLASTX
NCBI GI	g1168609
BLAST score	366
E value	3.0e-35
Match length	91
% identity	75
NCBI Description	AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf__1917337A ubiquitin-activating enzyme E1 [Arabidopsis thaliana]

Seq. No.	50379
Seq. ID	ssr700555141.h1
Method	BLASTX
NCBI GI	g3924596
BLAST score	191
E value	9.0e-15
Match length	48
% identity	77
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	50380
Seq. ID	ssr700555147.h1
Method	BLASTN
NCBI GI	g596077
BLAST score	70
E value	3.0e-31
Match length	138
% identity	88
NCBI Description	Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, complete cds

Seq. No.	50381
Seq. ID	ssr700555265.h1
Method	BLASTX
NCBI GI	g282929
BLAST score	172
E value	1.0e-12
Match length	81
% identity	47
NCBI Description	carbonate dehydratase (EC 4.2.1.1) - garden pea

Seq. No.	50382
Seq. ID	ssr700555282.h1
Method	BLASTX
NCBI GI	g4455367
BLAST score	445
E value	1.0e-44
Match length	88
% identity	51
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	50383
Seq. ID	ssr700555303.h1
Method	BLASTX
NCBI GI	g3367576
BLAST score	126
E value	4.0e-10
Match length	38
% identity	82
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	50384
Seq. ID	ssr700555337.h1
Method	BLASTN
NCBI GI	g170087
BLAST score	258
E value	1.0e-143
Match length	265
% identity	100
NCBI Description	G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No.	50385
Seq. ID	ssr700555386.h1
Method	BLASTX
NCBI GI	g3927835
BLAST score	301

E value	8.0e-28
Match length	80
% identity	66
NCBI Description	(AC005727) similar to Streptomyces PapA [Arabidopsis thaliana]

Seq. No.	50386
Seq. ID	ssr700555394.h1
Method	BLASTX
NCBI GI	g3746568
BLAST score	271
E value	3.0e-24
Match length	57
% identity	88
NCBI Description	(AF061638) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	50387
Seq. ID	ssr700555461.h1
Method	BLASTX
NCBI GI	g3377941
BLAST score	311
E value	7.0e-29
Match length	91
% identity	64
NCBI Description	(AL021960) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	50388
Seq. ID	ssr700555466.h1
Method	BLASTX
NCBI GI	g2213620
BLAST score	374
E value	3.0e-36
Match length	92
% identity	78
NCBI Description	(AC000103) F21J9.13 [Arabidopsis thaliana]

Seq. No.	50389
Seq. ID	ssr700555488.h1
Method	BLASTX
NCBI GI	g4469011
BLAST score	214
E value	8.0e-24
Match length	90
% identity	83
NCBI Description	(AL035602) carbohydrate kinase-like protein [Arabidopsis thaliana]

Seq. No.	50390
Seq. ID	ssr700555515.h1
Method	BLASTX
NCBI GI	g4567197
BLAST score	247
E value	2.0e-27
Match length	94
% identity	59

NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]

Seq. No. 50391
Seq. ID ssr700555545.h1
Method BLASTX
NCBI GI g2708750
BLAST score 236
E value 4.0e-20
Match length 90
% identity 44
NCBI Description (AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No. 50392
Seq. ID ssr700555564.h1
Method BLASTN
NCBI GI g3869075
BLAST score 38
E value 4.0e-12
Match length 54
% identity 93
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 50393
Seq. ID ssr700555640.h1
Method BLASTN
NCBI GI g18764
BLAST score 141
E value 1.0e-73
Match length 239
% identity 91
NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 50394
Seq. ID ssr700555675.h1
Method BLASTX
NCBI GI g4455367
BLAST score 253
E value 4.0e-22
Match length 66
% identity 48
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 50395
Seq. ID ssr700555694.h1
Method BLASTN
NCBI GI g4406529
BLAST score 219
E value 1.0e-120
Match length 267
% identity 96
NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 50396
Seq. ID ssr700555713.h1

Method	BLASTX
NCBI GI	g3643608
BLAST score	220
E value	3.0e-18
Match length	66
% identity	70
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50397
Seq. ID	ssr700555741.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	201
E value	1.0e-109
Match length	229
% identity	97
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	50398
Seq. ID	ssr700555747.h1
Method	BLASTX
NCBI GI	g404688
BLAST score	167
E value	5.0e-12
Match length	58
% identity	52
NCBI Description	(L19074) cytochrome P450 [Catharanthus roseus]

Seq. No.	50399
Seq. ID	ssr700555760.h1
Method	BLASTX
NCBI GI	g1621467
BLAST score	369
E value	1.0e-35
Match length	88
% identity	76
NCBI Description	(U73106) laccase [Liriodendron tulipifera]

Seq. No.	50400
Seq. ID	ssr700555793.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	106
E value	1.0e-52
Match length	194
% identity	89
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	50401
Seq. ID	ssr700555795.h1
Method	BLASTX
NCBI GI	g4138608
BLAST score	178
E value	1.0e-13
Match length	44
% identity	80
NCBI Description	(AJ010455) glutathione peroxidase [Triticum aestivum]

Seq. No.	50402
Seq. ID	ssr700555814.h1
Method	BLASTX
NCBI GI	g3628757
BLAST score	161
E value	9.0e-13
Match length	72
% identity	56
NCBI Description	(AF038007) FIC1 [Homo sapiens]

Seq. No.	50403
Seq. ID	ssr700555943.h1
Method	BLASTN
NCBI GI	g3747088
BLAST score	92
E value	2.0e-44
Match length	150
% identity	91
NCBI Description	Glycine max NADP-dependent isocitrate dehydrogenase (IDH1) mRNA, complete cds

Seq. No.	50404
Seq. ID	ssr700555952.h1
Method	BLASTX
NCBI GI	g82200
BLAST score	157
E value	8.0e-11
Match length	70
% identity	47
NCBI Description	hypothetical protein 1244 - common tobacco chloroplast

Seq. No.	50405
Seq. ID	ssr700555987.h1
Method	BLASTX
NCBI GI	g3176874
BLAST score	148
E value	1.0e-18
Match length	89
% identity	56
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	50406
Seq. ID	ssr700556028.h1
Method	BLASTX
NCBI GI	g2506139
BLAST score	209
E value	4.0e-28
Match length	92
% identity	71
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	50407
Seq. ID	ssr700556037.h1

Method	BLASTN
NCBI GI	g1336081
BLAST score	157
E value	4.0e-83
Match length	284
% identity	100
NCBI Description	Glycine max var. Century ascorbate peroxidase 2 (APx2) mRNA, complete cds

Seq. No.	50408
Seq. ID	ssr700556076.h1
Method	BLASTX
NCBI GI	g3879061
BLAST score	209
E value	6.0e-17
Match length	91
% identity	58
NCBI Description	(Z50874) cDNA EST yk226g5.5 comes from this gene; cDNA EST yk260d5.5 comes from this gene; cDNA EST yk346a10.5 comes from this gene; cDNA EST yk419f10.5 comes from this gene; cDNA EST yk421g3.5 comes from this gene; cDNA EST yk... >gi_3879590_emb_CAA90777_ (Z50875) cDNA EST yk226g5.5 comes from this gene; cDNA EST yk260d5.5 comes from this gene; cDNA EST yk346a10.5 comes from this gene; cDNA EST yk419f10.5 comes from this gene; cDNA EST yk421g3.5 comes from this gene; cDNA EST yk

Seq. No.	50409
Seq. ID	ssr700556117.h1
Method	BLASTX
NCBI GI	g131384
BLAST score	309
E value	1.0e-28
Match length	88
% identity	80
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	50410
Seq. ID	ssr700556205.h1
Method	BLASTN
NCBI GI	g806807
BLAST score	74
E value	1.0e-33
Match length	126
% identity	90
NCBI Description	Pisum sativum chaperonin precursor mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 50411

Seq. ID	ssr700556274.h1
Method	BLASTX
NCBI GI	g2827710
BLAST score	237
E value	4.0e-20
Match length	80
% identity	53
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]

Seq. No.	50412
Seq. ID	ssr700556311.h1
Method	BLASTX
NCBI GI	g4469014
BLAST score	142
E value	5.0e-09
Match length	35
% identity	69
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	50413
Seq. ID	ssr700556360.h1
Method	BLASTN
NCBI GI	g3033512
BLAST score	217
E value	1.0e-119
Match length	264
% identity	96
NCBI Description	Phaseolus vulgaris rubisco activase (Rca1) mRNA, complete cds

Seq. No.	50414
Seq. ID	ssr700556443.h1
Method	BLASTX
NCBI GI	g2129651
BLAST score	357
E value	3.0e-34
Match length	95
% identity	74
NCBI Description	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana]

Seq. No.	50415
Seq. ID	ssr700556453.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	233
E value	1.0e-128
Match length	289
% identity	96
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50416
Seq. ID	ssr700556468.h1
Method	BLASTX
NCBI GI	g4567269

BLAST score	362
E value	7.0e-35
Match length	88
% identity	78
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	50417
Seq. ID	ssr700556518.h1
Method	BLASTN
NCBI GI	g2253383
BLAST score	188
E value	1.0e-101
Match length	188
% identity	100
NCBI Description	Glycine max biotin carboxylase precursor (accC-2) mRNA, complete cds

Seq. No.	50418
Seq. ID	ssr700556550.h1
Method	BLASTX
NCBI GI	g1495802
BLAST score	197
E value	2.0e-15
Match length	82
% identity	45
NCBI Description	(X96405) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	50419
Seq. ID	ssr700556601.h1
Method	BLASTX
NCBI GI	g2392895
BLAST score	186
E value	4.0e-14
Match length	96
% identity	48
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	50420
Seq. ID	ssr700556657.h1
Method	BLASTN
NCBI GI	g857396
BLAST score	76
E value	8.0e-35
Match length	270
% identity	83
NCBI Description	Glycine max mRNA for mitotic cyclin a2-type, complete cds

Seq. No.	50421
Seq. ID	ssr700556665.h1
Method	BLASTX
NCBI GI	g114640
BLAST score	144
E value	3.0e-19
Match length	78
% identity	65
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_282923_pir__S27976 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - garden pea
>gi_20654_emb_CAA45150_ (X63604) ATP synthase (gamma subunit) [Pisum sativum]

Seq. No.	50422
Seq. ID	ssr700556677.h1
Method	BLASTX
NCBI GI	g2190548
BLAST score	254
E value	3.0e-22
Match length	78
% identity	65
NCBI Description	(AC001229) EST gb_ATTS1121 comes from this gene. [Arabidopsis thaliana]

Seq. No.	50423
Seq. ID	ssr700556687.h1
Method	BLASTN
NCBI GI	g2905771
BLAST score	85
E value	4.0e-40
Match length	115
% identity	98
NCBI Description	Glycine max glyceraldehyde-3 phosphate dehydrogenase (GAPDH) mRNA, partial cds

Seq. No.	50424
Seq. ID	ssr700556718.h1
Method	BLASTN
NCBI GI	g4469002
BLAST score	35
E value	3.0e-10
Match length	71
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	50425
Seq. ID	ssr700556771.h1
Method	BLASTX
NCBI GI	g2664200
BLAST score	162
E value	2.0e-11
Match length	86
% identity	41
NCBI Description	(AJ003216) GTL2 [Arabidopsis thaliana]

Seq. No.	50426
Seq. ID	ssr700556784.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	116
E value	1.0e-58
Match length	164
% identity	93
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene

sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana
S-adenosylmethionine synthetase gene, complete cds

Seq. No.	50427
Seq. ID	ssr700556924.h1
Method	BLASTN
NCBI GI	g1808591
BLAST score	122
E value	3.0e-62
Match length	182
% identity	92
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	50428
Seq. ID	ssr700556935.h1
Method	BLASTX
NCBI GI	g2494266
BLAST score	258
E value	1.0e-22
Match length	71
% identity	75
NCBI Description	GTP-BINDING PROTEIN LEPA >gi_1653961_dbj_BAA18871_ (D90917) LepA [Synechocystis sp.]

Seq. No.	50429
Seq. ID	ssr700557088.h1
Method	BLASTX
NCBI GI	g2245030
BLAST score	213
E value	2.0e-17
Match length	79
% identity	57
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	50430
Seq. ID	ssr700557174.h1
Method	BLASTX
NCBI GI	g294668
BLAST score	216
E value	5.0e-18
Match length	50
% identity	86
NCBI Description	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No.	50431
Seq. ID	ssr700557207.h1
Method	BLASTN
NCBI GI	g295447
BLAST score	87
E value	8.0e-42
Match length	107
% identity	95
NCBI Description	Vigna radiata NADPH cytochrome P450 mRNA, complete cds

Seq. No.	50432
Seq. ID	ssr700557285.h1

Method	BLASTN
NCBI GI	g403328
BLAST score	45
E value	3.0e-16
Match length	96
% identity	88
NCBI Description	T.repens TrMT1B mRNA for metallothionein-like protein

Seq. No.	50433
Seq. ID	ssr700557314.h1
Method	BLASTN
NCBI GI	g170073
BLAST score	140
E value	6.0e-73
Match length	193
% identity	94
NCBI Description	Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No.	50434
Seq. ID	ssr700557315.h1
Method	BLASTX
NCBI GI	g2511594
BLAST score	194
E value	6.0e-22
Match length	65
% identity	85
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	50435
Seq. ID	ssr700557324.h1
Method	BLASTX
NCBI GI	g4539459
BLAST score	194
E value	4.0e-15
Match length	40
% identity	82
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	50436
Seq. ID	ssr700557346.h1
Method	BLASTN
NCBI GI	g217902
BLAST score	68
E value	5.0e-30
Match length	231
% identity	83
NCBI Description	Catharanthus roseus cyc07 mRNA, complete cds

Seq. No.	50437
Seq. ID	ssr700557349.h1
Method	BLASTX
NCBI GI	g4415931

BLAST score	201
E value	3.0e-27
Match length	82
% identity	71
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	50438
Seq. ID	ssr700557377.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	120
E value	5.0e-61
Match length	238
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	50439
Seq. ID	ssr700557421.h1
Method	BLASTX
NCBI GI	g2347088
BLAST score	264
E value	3.0e-23
Match length	78
% identity	65
NCBI Description	(U72765) non-specific lipid transfer protein PvLTP-24 [Phaseolus vulgaris]

Seq. No.	50440
Seq. ID	ssr700557455.h1
Method	BLASTN
NCBI GI	g1165321
BLAST score	101
E value	1.0e-49
Match length	159
% identity	95
NCBI Description	Glycine max extensin (SbHRGP3) gene, complete cds

Seq. No.	50441
Seq. ID	ssr700557459.h1
Method	BLASTX
NCBI GI	g1134882
BLAST score	398
E value	5.0e-39
Match length	96
% identity	74
NCBI Description	(Z68291) cysteine protease [Pisum sativum]

Seq. No.	50442
Seq. ID	ssr700557476.h1
Method	BLASTX
NCBI GI	g3935138
BLAST score	162
E value	2.0e-11
Match length	91

% identity	37
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	50443
Seq. ID	ssr700557585.h1
Method	BLASTX
NCBI GI	g3702340
BLAST score	218
E value	5.0e-18
Match length	91
% identity	51
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50444
Seq. ID	ssr700557651.h1
Method	BLASTN
NCBI GI	g170455
BLAST score	50
E value	2.0e-19
Match length	74
% identity	92
NCBI Description	Tomato heat shock cognate protein 80 gene, 3' end

Seq. No.	50445
Seq. ID	ssr700557659.h1
Method	BLASTX
NCBI GI	g1498315
BLAST score	296
E value	4.0e-27
Match length	86
% identity	72
NCBI Description	(U56419) IAP100 [Pisum sativum]

Seq. No.	50446
Seq. ID	ssr700557709.h1
Method	BLASTX
NCBI GI	g2252843
BLAST score	260
E value	7.0e-23
Match length	91
% identity	57
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	50447
Seq. ID	ssr700557732.h1
Method	BLASTX
NCBI GI	g2809257
BLAST score	217
E value	8.0e-18
Match length	84
% identity	51
NCBI Description	(AC002560) F21B7.26 [Arabidopsis thaliana]

Seq. No.	50448
Seq. ID	ssr700557735.h1
Method	BLASTN
NCBI GI	g344003

BLAST score	80
E value	3.0e-37
Match length	272
% identity	83
NCBI Description	Pisum sativum mRNA for precursor for 33-kDa protein of photosystem II, complete cds

Seq. No.	50449
Seq. ID	ssr700557738.h1
Method	BLASTX
NCBI GI	g3335354
BLAST score	212
E value	3.0e-17
Match length	91
% identity	52
NCBI Description	(AC004512) This gene is continued from gene F5I14.1 from BAC sequence gb_AC001229 from A. thaliana. EST gb_AA585814 comes from this gene. [Arabidopsis thaliana]

Seq. No.	50450
Seq. ID	ssr700557746.h1
Method	BLASTX
NCBI GI	g2760830
BLAST score	322
E value	4.0e-30
Match length	92
% identity	63
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	50451
Seq. ID	ssr700557786.h1
Method	BLASTX
NCBI GI	g3288823
BLAST score	163
E value	7.0e-12
Match length	63
% identity	49
NCBI Description	(AF063852) FUS5 [Arabidopsis thaliana]

Seq. No.	50452
Seq. ID	ssr700557893.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	236
E value	1.0e-130
Match length	272
% identity	100
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50453
Seq. ID	ssr700558310.h1
Method	BLASTX
NCBI GI	g1402883
BLAST score	175
E value	6.0e-13
Match length	91

% identity	43
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495263_emb_CAA66119_ (X97487) orf09 [Arabidopsis thaliana]

Seq. No.	50454
Seq. ID	ssr700558318.h1
Method	BLASTX
NCBI GI	g3540184
BLAST score	204
E value	6.0e-21
Match length	84
% identity	25
NCBI Description	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No.	50455
Seq. ID	ssr700558329.h1
Method	BLASTX
NCBI GI	g4325371
BLAST score	133
E value	2.0e-13
Match length	68
% identity	67
NCBI Description	(AF128396) contains similarity to Medicago truncatula N7 protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No.	50456
Seq. ID	ssr700558333.h1
Method	BLASTX
NCBI GI	g1256259
BLAST score	273
E value	2.0e-24
Match length	82
% identity	70
NCBI Description	(U50900) voltage-dependent anion channel protein [Spinacia oleracea]

Seq. No.	50457
Seq. ID	ssr700558352.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	101
E value	1.0e-49
Match length	181
% identity	89
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	50458
Seq. ID	ssr700558479.h1
Method	BLASTX
NCBI GI	g3025189
BLAST score	211
E value	2.0e-17
Match length	68
% identity	60
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]

Seq. No.	50459
Seq. ID	ssr700558483.h1
Method	BLASTX
NCBI GI	g3335060
BLAST score	310
E value	7.0e-29
Match length	75
% identity	77
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	50460
Seq. ID	ssr700558535.h1
Method	BLASTX
NCBI GI	g2443887
BLAST score	166
E value	7.0e-12
Match length	57
% identity	58
NCBI Description	(AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No.	50461
Seq. ID	ssr700558542.h1
Method	BLASTX
NCBI GI	g4218120
BLAST score	181
E value	1.0e-13
Match length	35
% identity	94
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	50462
Seq. ID	ssr700558549.h1
Method	BLASTX
NCBI GI	g1854445
BLAST score	156
E value	5.0e-23
Match length	68
% identity	85
NCBI Description	(D83971) CPRD14 protein [Vigna unguiculata]

Seq. No.	50463
Seq. ID	ssr700558736.h1
Method	BLASTN
NCBI GI	g3868852
BLAST score	44
E value	1.0e-15
Match length	134
% identity	90
NCBI Description	Vigna radiata ARG8 mRNA for GPI-anchored protein, complete cds

Seq. No.	50464
Seq. ID	ssr700558742.h1
Method	BLASTX
NCBI GI	g4539335
BLAST score	175
E value	7.0e-13
Match length	99
% identity	34
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	50465
Seq. ID	ssr700558755.h1
Method	BLASTX
NCBI GI	g4220535
BLAST score	230
E value	2.0e-19
Match length	49
% identity	94
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	50466
Seq. ID	ssr700558793.h1
Method	BLASTX
NCBI GI	g2244970
BLAST score	280
E value	3.0e-25
Match length	72
% identity	72
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	50467
Seq. ID	ssr700558937.h1
Method	BLASTN
NCBI GI	g662929
BLAST score	207
E value	1.0e-113
Match length	230
% identity	98
NCBI Description	G.max mRNA for heat shock transcription factor

Seq. No.	50468
Seq. ID	ssr700559085.h1
Method	BLASTX
NCBI GI	g3757521
BLAST score	162
E value	2.0e-11
Match length	56
% identity	55
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	50469
Seq. ID	ssr700559088.h1
Method	BLASTX

NCBI GI	g2944178
BLAST score	389
E value	5.0e-38
Match length	88
% identity	80
NCBI Description	(AF007778) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	50470
Seq. ID	ssr700559103.h1
Method	BLASTN
NCBI GI	g3377602
BLAST score	33
E value	4.0e-09
Match length	49
% identity	92
NCBI Description	Homo sapiens full length insert cDNA YP07G10

Seq. No.	50471
Seq. ID	ssr700559107.h1
Method	BLASTN
NCBI GI	g520589
BLAST score	170
E value	7.0e-91
Match length	274
% identity	91
NCBI Description	Human scr3 mRNA for RNA binding protein SCR3, complete cds >gi_4506448_ref_NM_002898.1_RBMS2_ Homo sapiens RNA binding motif, single stranded interacting protein 2 (RBMS2) mRNA

Seq. No.	50472
Seq. ID	ssr700559108.h1
Method	BLASTN
NCBI GI	g55538
BLAST score	97
E value	3.0e-47
Match length	150
% identity	100
NCBI Description	Rat mRNA for zinc(2+) binding protein

Seq. No.	50473
Seq. ID	ssr700559114.h1
Method	BLASTN
NCBI GI	g1197179
BLAST score	263
E value	1.0e-146
Match length	278
% identity	99
NCBI Description	Rattus norvegicus mRNA, complete cds, similar to cdc37

Seq. No.	50474
Seq. ID	ssr700559118.h1
Method	BLASTN
NCBI GI	g2769255
BLAST score	223
E value	1.0e-122
Match length	279

% identity	95
NCBI Description	Mus musculus mRNA for NIPSNAP1 protein

Seq. No.	50475
Seq. ID	ssr700559119.h1
Method	BLASTN
NCBI GI	g847784
BLAST score	243
E value	1.0e-134
Match length	263
% identity	98
NCBI Description	Rattus norvegicus kinase substrate HASPP28 mRNA, complete cds

Seq. No.	50476
Seq. ID	ssr700559136.h1
Method	BLASTN
NCBI GI	g204855
BLAST score	212
E value	1.0e-116
Match length	284
% identity	94
NCBI Description	Rat (clone RLV124) Ig productively rearranged lambda chain mRNA V-J region, partial cds

Seq. No.	50477
Seq. ID	ssr700559137.h1
Method	BLASTN
NCBI GI	g57681
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Rat mRNA for ribosomal protein L17

Seq. No.	50478
Seq. ID	ssr700559138.h1
Method	BLASTN
NCBI GI	g4153895
BLAST score	277
E value	1.0e-154
Match length	277
% identity	100
NCBI Description	Rattus norvegicus mRNA for ribonucleoprotein F, complete cds

Seq. No.	50479
Seq. ID	ssr700559147.h1
Method	BLASTN
NCBI GI	g207313
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Rat thymosin beta-10 mRNA, complete cds

Seq. No. 50480

Seq. ID	ssr700559149.h1
Method	BLASTN
NCBI GI	g52737
BLAST score	118
E value	7.0e-60
Match length	194
% identity	90
NCBI Description	Mus musculus mRNA Interferon-induced 15-KDa protein

Seq. No.	50481
Seq. ID	ssr700559151.h1
Method	BLASTN
NCBI GI	g1877415
BLAST score	280
E value	1.0e-156
Match length	280
% identity	100
NCBI Description	Rattus norvegicus MHC class I RT1.Aa alpha-chain precursor mRNA, complete cds

Seq. No.	50482
Seq. ID	ssr700559153.h1
Method	BLASTN
NCBI GI	g710562
BLAST score	276
E value	1.0e-154
Match length	276
% identity	100
NCBI Description	Rattus norvegicus MHC class I protein mRNA, 3'end of cds

Seq. No.	50483
Seq. ID	ssr700559164.h1
Method	BLASTN
NCBI GI	g1395178
BLAST score	235
E value	1.0e-129
Match length	256
% identity	97
NCBI Description	Rattus norvegicus mRNA for proteasomal ATPase (MSS1), complete cds

Seq. No.	50484
Seq. ID	ssr700559168.h1
Method	BLASTN
NCBI GI	g56497
BLAST score	244
E value	1.0e-135
Match length	244
% identity	100
NCBI Description	Rat mRNA for MHC-associated invariant chain gamma

Seq. No.	50485
Seq. ID	ssr700559176.h1
Method	BLASTX
NCBI GI	g4335760
BLAST score	159
E value	4.0e-11

Match length 85
% identity 7
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 50486
Seq. ID ssr700559193.h1
Method BLASTN
NCBI GI g3164099
BLAST score 103
E value 6.0e-51
Match length 267
% identity 85
NCBI Description Mus musculus V kappa 8-19 gene, partial

Seq. No. 50487
Seq. ID ssr700559201.h1
Method BLASTN
NCBI GI g3483552
BLAST score 265
E value 1.0e-147
Match length 297
% identity 98
NCBI Description Homo sapiens full length insert cDNA clone ZC48C05

Seq. No. 50488
Seq. ID ssr700559203.h1
Method BLASTN
NCBI GI g2723485
BLAST score 289
E value 1.0e-162
Match length 289
% identity 100
NCBI Description Rattus norvegicus gene for BAF60b, complete cds

Seq. No. 50489
Seq. ID ssr700559204.h1
Method BLASTX
NCBI GI g3097047
BLAST score 276
E value 1.0e-24
Match length 86
% identity 64
NCBI Description (Y15035) S1R [Cowpox virus]

Seq. No. 50490
Seq. ID ssr700559206.h1
Method BLASTN
NCBI GI g2465726
BLAST score 86
E value 1.0e-40
Match length 226
% identity 85
NCBI Description Mus musculus interferon-inducible protein 203 (Ifi203) mRNA, complete cds

Seq. No. 50491
Seq. ID ssr700559214.h1

Method	BLASTX
NCBI GI	g3451240
BLAST score	261
E value	6.0e-23
Match length	71
% identity	69
NCBI Description	(AJ225089) 2'-5' oligoadenylate synthetase (p59OAS) [Homo sapiens]

Seq. No.	50492
Seq. ID	ssr700559223.h1
Method	BLASTN
NCBI GI	g1490383
BLAST score	224
E value	1.0e-123
Match length	259
% identity	97
NCBI Description	R.norvegicus mRNA for ribosomal protein L6

Seq. No.	50493
Seq. ID	ssr700559230.h1
Method	BLASTN
NCBI GI	g206727
BLAST score	234
E value	1.0e-129
Match length	238
% identity	100
NCBI Description	Rat ribosomal protein L30 mRNA, complete cds

Seq. No.	50494
Seq. ID	ssr700559237.h1
Method	BLASTN
NCBI GI	g453280
BLAST score	272
E value	1.0e-152
Match length	284
% identity	99
NCBI Description	R.norvegicus (Sprague-Dawley) ribosomal protein S23 mRNA

Seq. No.	50495
Seq. ID	ssr700559241.h1
Method	BLASTN
NCBI GI	g206474
BLAST score	226
E value	1.0e-124
Match length	285
% identity	94
NCBI Description	Rat thymosin beta 4 gene (pTB4G),intron

Seq. No.	50496
Seq. ID	ssr700559262.h1
Method	BLASTN
NCBI GI	g433436
BLAST score	211
E value	1.0e-115
Match length	286
% identity	94

NCBI Description M.musculus RNPS1 mRNA for RNA/DNA-binding protein

Seq. No. 50497
Seq. ID ssr700559270.h1
Method BLASTN
NCBI GI g2769543
BLAST score 33
E value 4.0e-09
Match length 73
% identity 88
NCBI Description Mus musculus cosmid CMX137 containing part of Nsdhl

Seq. No. 50498
Seq. ID ssr700559302.h1
Method BLASTN
NCBI GI g2695712
BLAST score 296
E value 1.0e-166
Match length 304
% identity 99
NCBI Description Rattus norvegicus mRNA for MST2 kinase

Seq. No. 50499
Seq. ID ssr700559312.h1
Method BLASTN
NCBI GI g639682
BLAST score 196
E value 1.0e-106
Match length 196
% identity 100
NCBI Description Rat MHC class II gene (RT1.DOa), exon 2, 3, 4 and

Seq. No. 50500
Seq. ID ssr700559315.h1
Method BLASTN
NCBI GI g4426564
BLAST score 295
E value 1.0e-165
Match length 299
% identity 100
NCBI Description Rattus norvegicus hfb2 mRNA, complete cds

Seq. No. 50501
Seq. ID ssr700559320.h1
Method BLASTN
NCBI GI g4426612
BLAST score 149
E value 2.0e-78
Match length 209
% identity 93
NCBI Description Mus musculus SLM-1 (Slm1) mRNA, complete cds

Seq. No. 50502
Seq. ID ssr700559323.h1
Method BLASTN
NCBI GI g1255241
BLAST score 180

E value	8.0e-97
Match length	276
% identity	91
NCBI Description	Mus musculus lysosomal-associated multitransmembrane protein (LAPTm5) mRNA, complete cds

Seq. No.	50503
Seq. ID	ssr700559324.h1
Method	BLASTN
NCBI GI	g202884
BLAST score	280
E value	1.0e-156
Match length	280
% identity	100
NCBI Description	Rat amphoterin mRNA, complete cds

Seq. No.	50504
Seq. ID	ssr700559327.h1
Method	BLASTN
NCBI GI	g452948
BLAST score	58
E value	5.0e-24
Match length	82
% identity	93
NCBI Description	U1 small nuclear ribonucleoprotein 1SNRP homolog [human, thyroid associated ophthalmopathy patient, mRNA Partial, 255 nt]

Seq. No.	50505
Seq. ID	ssr700559330.h1
Method	BLASTN
NCBI GI	g2564746
BLAST score	78
E value	6.0e-36
Match length	78
% identity	100
NCBI Description	Mus musculus X box binding protein-1 (XBP-1) mRNA, complete cds

Seq. No.	50506
Seq. ID	ssr700559331.h1
Method	BLASTN
NCBI GI	g1107695
BLAST score	170
E value	7.0e-91
Match length	290
% identity	90
NCBI Description	H.sapiens mRNA for 218kD Mi-2 protein >gi_4557452_ref_NM_001273.1_CHD4_ Homo sapiens chromodomain helicase DNA binding protein 4 (CHD4) mRNA

Seq. No.	50507
Seq. ID	ssr700559333.h1
Method	BLASTX
NCBI GI	g4559351
BLAST score	241
E value	1.0e-20

Match length	98
% identity	49
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50508
Seq. ID	ssr700559336.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	100
E value	4.0e-49
Match length	252
% identity	85
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	50509
Seq. ID	ssr700559409.h1
Method	BLASTN
NCBI GI	g206731
BLAST score	267
E value	1.0e-148
Match length	278
% identity	99
NCBI Description	Rattus norvegicus large subunit ribosomal protein L36a mRNA, complete cds

Seq. No.	50510
Seq. ID	ssr700559410.h1
Method	BLASTN
NCBI GI	g3492891
BLAST score	70
E value	4.0e-31
Match length	252
% identity	86
NCBI Description	Homo sapiens chromosome 17, clone hRPC.62_O_9, complete sequence [Homo sapiens]

Seq. No.	50511
Seq. ID	ssr700559415.h1
Method	BLASTN
NCBI GI	g57138
BLAST score	256
E value	1.0e-142
Match length	303
% identity	96
NCBI Description	Rat mRNA for ribosomal protein S8

Seq. No.	50512
Seq. ID	ssr700559420.h1
Method	BLASTX
NCBI GI	g2827495
BLAST score	127
E value	3.0e-12
Match length	58
% identity	71
NCBI Description	(AL009196) 1-evidence=predicted by content; 1-method=genefinder;084; 1-evidence_end;

2-evidence=predicted by match; 2-match_accession=AA391048;
2-match_description=LD09991.5prime LD Drosophila
melanogaster embryo BlueScript Dro

Seq. No.	50513
Seq. ID	ssr700559423.h1
Method	BLASTN
NCBI GI	g4454703
BLAST score	182
E value	4.0e-98
Match length	237
% identity	95
NCBI Description	Homo sapiens HSPC008 mRNA, complete cds

Seq. No.	50514
Seq. ID	ssr700559433.h1
Method	BLASTN
NCBI GI	g188564
BLAST score	48
E value	3.0e-18
Match length	80
% identity	90
NCBI Description	Human mitochondrial hinge protein mRNA, complete cds

Seq. No.	50515
Seq. ID	ssr700559436.h1
Method	BLASTN
NCBI GI	g349088
BLAST score	172
E value	3.0e-92
Match length	203
% identity	97
NCBI Description	Rat lysozyme gene exons 1-4, complete cds

Seq. No.	50516
Seq. ID	ssr700559440.h1
Method	BLASTN
NCBI GI	g206723
BLAST score	139
E value	2.0e-72
Match length	225
% identity	91
NCBI Description	Rat ribosomal protein L18 mRNA, complete cds

Seq. No.	50517
Seq. ID	ssr700559449.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	88
E value	5.0e-42
Match length	168
% identity	88
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	50518
Seq. ID	ssr700559456.h1
Method	BLASTN

NCBI GI g57163
BLAST score 176
E value 2.0e-94
Match length 293
% identity 90
NCBI Description Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)

Seq. No. 50519
Seq. ID ssr700559462.h1
Method BLASTX
NCBI GI g2984292
BLAST score 181
E value 1.0e-13
Match length 76
% identity 50
NCBI Description (AE000771) GTP-binding protein [Aquifex aeolicus]

Seq. No. 50520
Seq. ID ssr700559472.h1
Method BLASTN
NCBI GI g53017
BLAST score 37
E value 5.0e-12
Match length 65
% identity 89
NCBI Description M.musculus mbh1 gene for Myc basic motif homologue-1 (mbh1)

Seq. No. 50521
Seq. ID ssr700559473.h1
Method BLASTN
NCBI GI g57134
BLAST score 274
E value 1.0e-153
Match length 288
% identity 99
NCBI Description Rat mRNA for ribosomal protein S4

Seq. No. 50522
Seq. ID ssr700559474.h1
Method BLASTN
NCBI GI g4097872
BLAST score 144
E value 2.0e-75
Match length 200
% identity 93
NCBI Description Mus musculus translation initiation factor eIF3-p44 mRNA, complete cds

Seq. No. 50523
Seq. ID ssr700559485.h1
Method BLASTN
NCBI GI g3779239
BLAST score 60
E value 3.0e-25
Match length 167
% identity 85
NCBI Description Homo sapiens zinc finger protein (MBLL) mRNA, complete cds

Seq. No.	50524
Seq. ID	ssr700559492.h1
Method	BLASTN
NCBI GI	g57120
BLAST score	272
E value	1.0e-152
Match length	286
% identity	99
NCBI Description	R.norvegicus mRNA for ribosomal protein L37 >gi_1839336_gb_S79981_S79981 ribosomal protein L37 [rats, myoblast L6 cells, mRNA Partial, 366 nt]

Seq. No.	50525
Seq. ID	ssr700559493.h1
Method	BLASTN
NCBI GI	g53017
BLAST score	120
E value	4.0e-61
Match length	220
% identity	88
NCBI Description	M.musculus mbh1 gene for Myc basic motif homologue-1 (mbh1)

Seq. No.	50526
Seq. ID	ssr700559517.h1
Method	BLASTN
NCBI GI	g1277163
BLAST score	226
E value	1.0e-124
Match length	262
% identity	97
NCBI Description	Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No.	50527
Seq. ID	ssr700559523.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	236
E value	1.0e-130
Match length	284
% identity	96
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	50528
Seq. ID	ssr700559571.h1
Method	BLASTX
NCBI GI	g3367519
BLAST score	272
E value	3.0e-24
Match length	90
% identity	61
NCBI Description	(AC004392) Contains similarity to gb_U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	50529

Seq. ID	ssr700559574.h1
Method	BLASTN
NCBI GI	g632721
BLAST score	54
E value	1.0e-21
Match length	142
% identity	85
NCBI Description	psaEa=photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, mRNA, 648 nt]

Seq. No.	50530
Seq. ID	ssr700559613.h1
Method	BLASTX
NCBI GI	g2829871
BLAST score	208
E value	8.0e-17
Match length	65
% identity	71
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	50531
Seq. ID	ssr700559625.h1
Method	BLASTN
NCBI GI	g170043
BLAST score	223
E value	1.0e-122
Match length	290
% identity	100
NCBI Description	Soybean phytoene desaturase mRNA, complete cds

Seq. No.	50532
Seq. ID	ssr700559642.h1
Method	BLASTN
NCBI GI	g2463568
BLAST score	45
E value	2.0e-16
Match length	52
% identity	98
NCBI Description	Glycine max mRNA for squalene synthase, complete cds

Seq. No.	50533
Seq. ID	ssr700559687.h1
Method	BLASTX
NCBI GI	g2894612
BLAST score	204
E value	2.0e-16
Match length	65
% identity	55
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	50534
Seq. ID	ssr700559705.h1
Method	BLASTX
NCBI GI	g2244804
BLAST score	197
E value	2.0e-15
Match length	60

% identity	60
NCBI Description	(Z97336) Ste20-like kinase homolog [Arabidopsis thaliana]

Seq. No.	50535
Seq. ID	ssr700559716.h1
Method	BLASTX
NCBI GI	g3643090
BLAST score	245
E value	4.0e-21
Match length	83
% identity	57
NCBI Description	(AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	50536
Seq. ID	ssr700559721.h1
Method	BLASTX
NCBI GI	g124429
BLAST score	253
E value	5.0e-22
Match length	85
% identity	66
NCBI Description	37 KD CHLOROPLAST INNER ENVELOPE MEMBRANE PROTEIN PRECURSOR (E37) >gi_99543_pir__S14409 membrane protein, 37K, precursor, chloroplast inner envelope - spinach >gi_21228_emb_CAA40283_ (X56963) 37 kD inner envelope membrane polypeptide [Spinacia oleracea]

Seq. No.	50537
Seq. ID	ssr700559755.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	236
E value	4.0e-20
Match length	60
% identity	73
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	50538
Seq. ID	ssr700559776.h1
Method	BLASTN
NCBI GI	g975632
BLAST score	63
E value	5.0e-27
Match length	147
% identity	86
NCBI Description	Pumpkin mRNA for glyoxysomal citrate synthase, complete cds

Seq. No.	50539
Seq. ID	ssr700559787.h1
Method	BLASTX
NCBI GI	g133447
BLAST score	153
E value	3.0e-10
Match length	52
% identity	62
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN

>gi_81957_pir__S07137 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - garden pea chloroplast (fragment)
>gi_829325_emb_CAA27545_ (X03912) ORF with large areas of homology to RNA polymerase subunit beta [Pisum sativum]

Seq. No.	50540
Seq. ID	ssr700559859.h1
Method	BLASTN
NCBI GI	g3378649
BLAST score	93
E value	6.0e-45
Match length	193
% identity	87
NCBI Description	M.sativa mRNA translated from abscisic activated gene

Seq. No.	50541
Seq. ID	ssr700559888.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	282
E value	1.0e-157
Match length	282
% identity	100
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50542
Seq. ID	ssr700559905.h1
Method	BLASTX
NCBI GI	g2618698
BLAST score	189
E value	6.0e-16
Match length	58
% identity	84
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	50543
Seq. ID	ssr700559952.h1
Method	BLASTX
NCBI GI	g4406530
BLAST score	138
E value	7.0e-09
Match length	46
% identity	63
NCBI Description	(AF126870) rubisco activase [Vigna radiata]

Seq. No.	50544
Seq. ID	ssr700559987.h1
Method	BLASTX
NCBI GI	g4454467
BLAST score	308
E value	4.0e-34
Match length	95
% identity	73
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	50545
Seq. ID	ssr700559988.h1

Method	BLASTX
NCBI GI	g2213586
BLAST score	296
E value	4.0e-27
Match length	80
% identity	70
NCBI Description	(AC000348) T7N9.6 [Arabidopsis thaliana]

Seq. No.	50546
Seq. ID	ssr700560001.h1
Method	BLASTX
NCBI GI	g4263787
BLAST score	205
E value	1.0e-16
Match length	49
% identity	78
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	50547
Seq. ID	ssr700560034.h1
Method	BLASTX
NCBI GI	g2289003
BLAST score	129
E value	2.0e-09
Match length	52
% identity	53
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	50548
Seq. ID	ssr700560114.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	169
E value	3.0e-90
Match length	256
% identity	93
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50549
Seq. ID	ssr700560135.h1
Method	BLASTX
NCBI GI	g3096949
BLAST score	229
E value	2.0e-26
Match length	74
% identity	79
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	50550
Seq. ID	ssr700560157.h1
Method	BLASTX
NCBI GI	g4218011
BLAST score	191
E value	9.0e-15

Match length	45
% identity	78
NCBI Description	(AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	50551
Seq. ID	ssr700560213.h1
Method	BLASTX
NCBI GI	g2961357
BLAST score	350
E value	2.0e-33
Match length	94
% identity	69
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	50552
Seq. ID	ssr700560242.h1
Method	BLASTN
NCBI GI	g4101472
BLAST score	70
E value	3.0e-31
Match length	154
% identity	88
NCBI Description	Arabidopsis thaliana K efflux antiporter KEA1 mRNA, complete cds

Seq. No.	50553
Seq. ID	ssr700560258.h1
Method	BLASTX
NCBI GI	g3510258
BLAST score	149
E value	7.0e-10
Match length	87
% identity	41
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50554
Seq. ID	ssr700560260.h1
Method	BLASTX
NCBI GI	g2160692
BLAST score	361
E value	1.0e-34
Match length	92
% identity	75
NCBI Description	(U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	50555
Seq. ID	ssr700560274.h1
Method	BLASTX
NCBI GI	g131384
BLAST score	321
E value	5.0e-30
Match length	93
% identity	78
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132 photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving complex 33kD protein [Arachis hypogaea]

Seq. No.	50556
Seq. ID	ssr700560292.h1
Method	BLASTN
NCBI GI	g344003
BLAST score	83
E value	6.0e-39
Match length	279
% identity	83
NCBI Description	Pisum sativum mRNA for precursor for 33-kDa protein of photosystem II, complete cds

Seq. No.	50557
Seq. ID	ssr700560301.h1
Method	BLASTX
NCBI GI	g1117793
BLAST score	340
E value	3.0e-32
Match length	96
% identity	64
NCBI Description	(U24232) lipoxygenase [Solanum tuberosum]

Seq. No.	50558
Seq. ID	ssr700560305.h1
Method	BLASTX
NCBI GI	g2496789
BLAST score	199
E value	1.0e-15
Match length	77
% identity	51
NCBI Description	1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE) >gi_1001556_dbj_BAA10183_ (D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	50559
Seq. ID	ssr700560437.h1
Method	BLASTX
NCBI GI	g4454042
BLAST score	365
E value	4.0e-35
Match length	97
% identity	71
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	50560
Seq. ID	ssr700560454.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	267

E value	1.0e-149
Match length	283
% identity	99
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	50561
Seq. ID	ssr700560484.h1
Method	BLASTX
NCBI GI	g22491
BLAST score	151
E value	4.0e-10
Match length	91
% identity	30
NCBI Description	(X01380) ORF2 [Zea mays]

Seq. No.	50562
Seq. ID	ssr700560513.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	178
E value	1.0e-95
Match length	240
% identity	94
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	50563
Seq. ID	ssr700560541.h1
Method	BLASTX
NCBI GI	g3643085
BLAST score	148
E value	1.0e-09
Match length	64
% identity	47
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	50564
Seq. ID	ssr700560550.h1
Method	BLASTN
NCBI GI	g12178
BLAST score	153
E value	1.0e-80
Match length	295
% identity	90
NCBI Description	Pea chloroplast rpl36 (partial), rps11, rpoA, and petD (partial) genes for ribosomal proteins L36 and S11, RNA polymerase alpha subunit, and cytochrome bf complex subunit IV

Seq. No.	50565
Seq. ID	ssr700560615.h1
Method	BLASTN
NCBI GI	g19280
BLAST score	76
E value	9.0e-35
Match length	147

% identity	89
NCBI Description	L.esculentum mRNA for enolase

Seq. No.	50566
Seq. ID	ssr700560664.h1
Method	BLASTN
NCBI GI	g169974
BLAST score	138
E value	9.0e-72
Match length	280
% identity	89
NCBI Description	Glycine max vspA gene, complete cds

Seq. No.	50567
Seq. ID	ssr700560684.h1
Method	BLASTN
NCBI GI	g1518539
BLAST score	223
E value	1.0e-122
Match length	231
% identity	99
NCBI Description	Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No.	50568
Seq. ID	ssr700560690.h1
Method	BLASTN
NCBI GI	g344003
BLAST score	45
E value	3.0e-16
Match length	139
% identity	86
NCBI Description	Pisum sativum mRNA for precursor for 33-kDa protein of photosystem II, complete cds

Seq. No.	50569
Seq. ID	ssr700560704.h1
Method	BLASTX
NCBI GI	g2809237
BLAST score	179
E value	3.0e-13
Match length	63
% identity	59
NCBI Description	(AC002560) F21B7.6 [Arabidopsis thaliana]

Seq. No.	50570
Seq. ID	ssr700560716.h1
Method	BLASTX
NCBI GI	g3298539
BLAST score	164
E value	2.0e-14
Match length	88
% identity	52
NCBI Description	(AC004681) NPK1-related protein kinase [Arabidopsis thaliana]

Seq. No.	50571
Seq. ID	ssr700560825.h1

Method	BLASTX
NCBI GI	g3860319
BLAST score	142
E value	5.0e-09
Match length	50
% identity	62
NCBI Description	(AJ012686) nucleolar protein [Cicer arietinum]

Seq. No.	50572
Seq. ID	ssr700560828.h1
Method	BLASTX
NCBI GI	g2565010
BLAST score	167
E value	6.0e-12
Match length	37
% identity	78
NCBI Description	(AC002983) putative microfibril-associated protein [Arabidopsis thaliana] >gi_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm, score: 11.71) [Arabidopsis thaliana]

Seq. No.	50573
Seq. ID	ssr700560911.h1
Method	BLASTX
NCBI GI	g3935183
BLAST score	286
E value	5.0e-26
Match length	94
% identity	62
NCBI Description	(AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No.	50574
Seq. ID	ssr700560950.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	178
E value	1.0e-95
Match length	254
% identity	93
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	50575
Seq. ID	ssr700561004.h1
Method	BLASTX
NCBI GI	g2444176
BLAST score	202
E value	4.0e-16
Match length	87
% identity	52
NCBI Description	(U94782) unconventional myosin [Helianthus annuus]

Seq. No.	50576
Seq. ID	taw700654356.h1
Method	BLASTX
NCBI GI	g2500354
BLAST score	284

E value	9.0e-26
Match length	61
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No.	50577
Seq. ID	taw700654388.h1
Method	BLASTX
NCBI GI	g2864609
BLAST score	191
E value	7.0e-15
Match length	70
% identity	59
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	50578
Seq. ID	taw700654438.h1
Method	BLASTX
NCBI GI	g2160188
BLAST score	209
E value	5.0e-17
Match length	84
% identity	49
NCBI Description	(AC000132) Similar to Vicia sucrose transport protein (gb_Z93774). [Arabidopsis thaliana]

Seq. No.	50579
Seq. ID	taw700654466.h1
Method	BLASTX
NCBI GI	g4455246
BLAST score	158
E value	5.0e-11
Match length	79
% identity	46
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	50580
Seq. ID	taw700654727.h1
Method	BLASTX
NCBI GI	g3337367
BLAST score	149
E value	5.0e-10
Match length	50
% identity	54
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50581
Seq. ID	taw700654861.h1
Method	BLASTX
NCBI GI	g4468804
BLAST score	122
E value	5.0e-14
Match length	80
% identity	51

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 50582
Seq. ID taw700654869.h1
Method BLASTX
NCBI GI g166410
BLAST score 122
E value 8.0e-16
Match length 50
% identity 86
NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 50583
Seq. ID taw700654923.h1
Method BLASTN
NCBI GI g16508
BLAST score 66
E value 7.0e-29
Match length 158
% identity 85
NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No. 50584
Seq. ID taw700654976.h1
Method BLASTX
NCBI GI g2129752
BLAST score 156
E value 1.0e-10
Match length 50
% identity 46
NCBI Description thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_ (Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No. 50585
Seq. ID taw700655052.h1
Method BLASTX
NCBI GI g2911059
BLAST score 416
E value 3.0e-41
Match length 87
% identity 87
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 50586
Seq. ID taw700655091.h1
Method BLASTX
NCBI GI g4467128
BLAST score 312
E value 4.0e-29
Match length 82
% identity 68
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 50587
Seq. ID taw700655136.h1

Method	BLASTX
NCBI GI	g3334349
BLAST score	142
E value	2.0e-09
Match length	52
% identity	58
NCBI Description	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS) >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	50588
Seq. ID	taw700655188.h1
Method	BLASTX
NCBI GI	g1709990
BLAST score	144
E value	1.0e-09
Match length	40
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L35A

Seq. No.	50589
Seq. ID	taw700655215.h1
Method	BLASTN
NCBI GI	g1304226
BLAST score	108
E value	5.0e-54
Match length	196
% identity	89
NCBI Description	Soybean mRNA for epoxide hydrolase, complete cds

Seq. No.	50590
Seq. ID	taw700655263.h1
Method	BLASTN
NCBI GI	g170025
BLAST score	111
E value	1.0e-55
Match length	247
% identity	91
NCBI Description	Soybean malate synthase (MS) mRNA, 3' end

Seq. No.	50591
Seq. ID	taw700655287.h1
Method	BLASTN
NCBI GI	g2970050
BLAST score	35
E value	2.0e-10
Match length	95
% identity	84
NCBI Description	Vigna radiata mRNA for ARG10, complete cds

Seq. No.	50592
Seq. ID	taw700655306.h1
Method	BLASTX
NCBI GI	g3128177
BLAST score	177
E value	4.0e-22
Match length	78

% identity	73
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	50593
Seq. ID	taw700655319.h1
Method	BLASTX
NCBI GI	g2982432
BLAST score	178
E value	2.0e-13
Match length	56
% identity	64
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	50594
Seq. ID	taw700655349.h1
Method	BLASTX
NCBI GI	g2854153
BLAST score	150
E value	3.0e-10
Match length	68
% identity	46
NCBI Description	(AF045640) No definition line found [Caenorhabditis elegans]

Seq. No.	50595
Seq. ID	taw700655351.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	135
E value	4.0e-70
Match length	239
% identity	89
NCBI Description	G.max ADR6 mRNA

Seq. No.	50596
Seq. ID	taw700655495.h1
Method	BLASTX
NCBI GI	g3402749
BLAST score	197
E value	1.0e-15
Match length	67
% identity	49
NCBI Description	(AL031187) putative protein [Arabidopsis thaliana]

Seq. No.	50597
Seq. ID	taw700655516.h1
Method	BLASTX
NCBI GI	g3123209
BLAST score	311
E value	5.0e-29
Match length	82
% identity	74
NCBI Description	ELONGATION FACTOR G, MITOCHONDRIAL 1 PRECURSOR (MEF-G-1) >gi_2119928_pir__S61642 translation elongation factor G, mitochondrial - yeast (Saccharomyces cerevisiae) >gi_1181289_emb_CAA64315_ (X94607) Mef1 protein [Saccharomyces cerevisiae] >gi_1360422_emb_CAA97626_

(Z73241) ORF YLR069c [Saccharomyces cerevisiae]

Seq. No.	50598
Seq. ID	taw700655557.h1
Method	BLASTN
NCBI GI	g2970653
BLAST score	123
E value	6.0e-63
Match length	199
% identity	90
NCBI Description	Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	50599
Seq. ID	taw700655630.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	168
E value	7.0e-90
Match length	183
% identity	98
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	50600
Seq. ID	taw700655668.h1
Method	BLASTX
NCBI GI	g2500354
BLAST score	327
E value	8.0e-31
Match length	81
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No.	50601
Seq. ID	taw700655773.h1
Method	BLASTX
NCBI GI	g4468812
BLAST score	197
E value	1.0e-15
Match length	50
% identity	68
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	50602
Seq. ID	taw700655783.h1
Method	BLASTX
NCBI GI	g3176669
BLAST score	134
E value	5.0e-16
Match length	64
% identity	70
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.	50603
Seq. ID	taw700655801.h1

Method	BLASTX
NCBI GI	g4105798
BLAST score	353
E value	8.0e-34
Match length	87
% identity	59
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	50604
Seq. ID	taw700655806.h1
Method	BLASTN
NCBI GI	g560790
BLAST score	240
E value	1.0e-132
Match length	263
% identity	98
NCBI Description	Human mRNA for calgizzarin, complete cds

Seq. No.	50605
Seq. ID	taw700655828.h1
Method	BLASTN
NCBI GI	g498907
BLAST score	32
E value	1.0e-08
Match length	74
% identity	88
NCBI Description	Pisum sativum ribosomal protein L34 homolog (RPL34) mRNA, complete cds

Seq. No.	50606
Seq. ID	taw700655882.h1
Method	BLASTX
NCBI GI	g3201680
BLAST score	138
E value	1.0e-08
Match length	69
% identity	46
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	50607
Seq. ID	taw700655993.h1
Method	BLASTX
NCBI GI	g1903034
BLAST score	288
E value	3.0e-26
Match length	81
% identity	68
NCBI Description	(X94625) amp-binding protein [Brassica napus]

Seq. No.	50608
Seq. ID	taw700656031.h1
Method	BLASTX
NCBI GI	g3914472
BLAST score	250
E value	9.0e-22
Match length	60
% identity	80

NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]
Seq. No.	50609
Seq. ID	taw700656084.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	74
E value	9.0e-34
Match length	129
% identity	91
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds
Seq. No.	50610
Seq. ID	taw700656322.h1
Method	BLASTX
NCBI GI	g560150
BLAST score	128
E value	3.0e-11
Match length	74
% identity	54
NCBI Description	(X74772) SF16 protein [Helianthus annuus]
Seq. No.	50611
Seq. ID	taw700656402.h1
Method	BLASTX
NCBI GI	g322750
BLAST score	199
E value	1.0e-19
Match length	81
% identity	77
NCBI Description	ubiquitin / ribosomal protein CEP52 - wood tobacco >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris]
Seq. No.	50612
Seq. ID	taw700656422.h1
Method	BLASTN
NCBI GI	g303900
BLAST score	236
E value	1.0e-130
Match length	264
% identity	25
NCBI Description	Soybean gene for ubiquitin, complete cds
Seq. No.	50613
Seq. ID	taw700656559.h1
Method	BLASTN
NCBI GI	g2815245
BLAST score	53
E value	4.0e-21
Match length	101
% identity	88
NCBI Description	C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)

Seq. No.	50614
Seq. ID	taw700656574.h1
Method	BLASTX
NCBI GI	g1117778
BLAST score	119
E value	1.0e-12
Match length	83
% identity	51
NCBI Description	(D49366) 4-coumarate:CoA ligase [Lithospermum erythrorhizon]

Seq. No.	50615
Seq. ID	taw700656578.h1
Method	BLASTN
NCBI GI	g2055227
BLAST score	199
E value	1.0e-108
Match length	259
% identity	94
NCBI Description	Glycine max mRNA for SRC1, complete cds

Seq. No.	50616
Seq. ID	taw700656810.h1
Method	BLASTN
NCBI GI	g3319339
BLAST score	41
E value	6.0e-14
Match length	100
% identity	90
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	50617
Seq. ID	taw700656855.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	158
E value	1.0e-83
Match length	280
% identity	90
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	50618
Seq. ID	taw700656940.h1
Method	BLASTN
NCBI GI	g2735036
BLAST score	201
E value	1.0e-109
Match length	257
% identity	95
NCBI Description	Homo sapiens cosmid LM1937 from Xq28

Seq. No.	50619
Seq. ID	taw700657072.h1
Method	BLASTX
NCBI GI	g3559816

BLAST score	251
E value	6.0e-22
Match length	81
% identity	65
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	50620
Seq. ID	taw700657119.h1
Method	BLASTN
NCBI GI	g1236948
BLAST score	228
E value	1.0e-125
Match length	260
% identity	97
NCBI Description	Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No.	50621
Seq. ID	taw700657154.h1
Method	BLASTN
NCBI GI	g559854
BLAST score	214
E value	1.0e-117
Match length	238
% identity	98
NCBI Description	Human transcription factor IL-4 Stat mRNA, complete cds. >gi_4507258_ref_NM_003153.1_STAT6_ Homo sapiens signal transducer and activator of transcription 6, interleukin-4 induced (STAT6) mRNA >gi_1824256_gb_I33465_I33465 Sequence 1 from patent US 5591825 >gi_3209783_gb_I81486_I81486 Sequence 1 from patent US

Seq. No.	50622
Seq. ID	taw700657170.h1
Method	BLASTN
NCBI GI	g2076716
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	Human glutathione S-transferase (P1b) mRNA, complete cds

Seq. No.	50623
Seq. ID	taw700657216.h1
Method	BLASTN
NCBI GI	g170091
BLAST score	241
E value	1.0e-133
Match length	266
% identity	99
NCBI Description	Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No.	50624
Seq. ID	taw700657234.h1
Method	BLASTX
NCBI GI	g4335773
BLAST score	228

E value	2.0e-19
Match length	64
% identity	75
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	50625
Seq. ID	taw700657243.h1
Method	BLASTX
NCBI GI	g4006887
BLAST score	316
E value	2.0e-29
Match length	77
% identity	73
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	50626
Seq. ID	taw700657310.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	62
E value	1.0e-26
Match length	118
% identity	88
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	50627
Seq. ID	taw700657326.h1
Method	BLASTX
NCBI GI	g2305222
BLAST score	183
E value	4.0e-14
Match length	46
% identity	72
NCBI Description	(AF012089) phenylalanyl tRNA synthetase [Drosophila melanogaster]

Seq. No.	50628
Seq. ID	taw700657347.h1
Method	BLASTX
NCBI GI	g3600032
BLAST score	192
E value	4.0e-15
Match length	49
% identity	78
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	50629
Seq. ID	taw700657366.h1
Method	BLASTX
NCBI GI	g2651316
BLAST score	203
E value	2.0e-16
Match length	51
% identity	73
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	50630
Seq. ID	taw700657388.h1
Method	BLASTN
NCBI GI	g18551
BLAST score	114
E value	1.0e-57
Match length	182
% identity	92
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	50631
Seq. ID	taw700657412.h1
Method	BLASTN
NCBI GI	g3212846
BLAST score	50
E value	2.0e-19
Match length	184
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	50632
Seq. ID	taw700657418.h1
Method	BLASTX
NCBI GI	g2832357
BLAST score	155
E value	1.0e-10
Match length	45
% identity	67
NCBI Description	(Y14071) HMG protein [Arabidopsis thaliana] >gi_3068715 (AF049236) unknown [Arabidopsis thaliana]

Seq. No.	50633
Seq. ID	taw700657448.h1
Method	BLASTN
NCBI GI	g1304226
BLAST score	85
E value	3.0e-40
Match length	129
% identity	92
NCBI Description	Soybean mRNA for epoxide hydrolase, complete cds

Seq. No.	50634
Seq. ID	taw700657487.h1
Method	BLASTX
NCBI GI	g4558462
BLAST score	230
E value	1.0e-19
Match length	53
% identity	87
NCBI Description	(AF079404) cell cycle switch protein [Medicago sativa subsp. X varia]

Seq. No.	50635
Seq. ID	taw700657519.h1

Method	BLASTX
NCBI GI	g3193315
BLAST score	238
E value	2.0e-20
Match length	83
% identity	59
NCBI Description	(AF069299) contains similarity to transcriptional activator Ra [Arabidopsis thaliana]

Seq. No.	50636
Seq. ID	taw700657564.h1
Method	BLASTN
NCBI GI	g21004
BLAST score	57
E value	1.0e-23
Match length	109
% identity	91
NCBI Description	French Bean mRNA for plastid-located glutamine synthetase (EC 6.3.1.2)

Seq. No.	50637
Seq. ID	taw700657664.h1
Method	BLASTX
NCBI GI	g1710546
BLAST score	306
E value	2.0e-28
Match length	65
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative ribosomal protein [Daucus carota]

Seq. No.	50638
Seq. ID	taw700657667.h1
Method	BLASTX
NCBI GI	g3582328
BLAST score	209
E value	5.0e-17
Match length	79
% identity	47
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50639
Seq. ID	taw700657720.h1
Method	BLASTX
NCBI GI	g4049401
BLAST score	331
E value	3.0e-31
Match length	84
% identity	74
NCBI Description	(AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No.	50640
Seq. ID	taw700657753.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	249

E value	1.0e-138
Match length	249
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	50641
Seq. ID	taw700657794.h1
Method	BLASTN
NCBI GI	g439856
BLAST score	142
E value	3.0e-74
Match length	222
% identity	91
NCBI Description	Glycine max Williams 82 lipoxygenase mRNA, complete cds

Seq. No.	50642
Seq. ID	taw700657806.h1
Method	BLASTX
NCBI GI	g3335378
BLAST score	162
E value	2.0e-11
Match length	43
% identity	70
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	50643
Seq. ID	taw700657811.h1
Method	BLASTN
NCBI GI	g3449331
BLAST score	47
E value	1.0e-17
Match length	115
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	50644
Seq. ID	taw700657947.h1
Method	BLASTN
NCBI GI	g1277163
BLAST score	240
E value	1.0e-132
Match length	240
% identity	100
NCBI Description	Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No.	50645
Seq. ID	taw700658012.h1
Method	BLASTX
NCBI GI	g1076942
BLAST score	216
E value	9.0e-18
Match length	82
% identity	51
NCBI Description	mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase (EC 3.2.1.96) precursor - yeast (Candida albicans) >gi_432354

(L26488) hexosaminidase [Candida albicans]

Seq. No.	50646
Seq. ID	taw700658019.h1
Method	BLASTN
NCBI GI	g3832527
BLAST score	62
E value	2.0e-26
Match length	138
% identity	93
NCBI Description	Glycine max unknown mRNA

Seq. No.	50647
Seq. ID	taw700658119.h1
Method	BLASTX
NCBI GI	g2809246
BLAST score	205
E value	2.0e-16
Match length	83
% identity	47
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	50648
Seq. ID	taw700658184.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	100
E value	4.0e-49
Match length	224
% identity	93
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	50649
Seq. ID	taw700658267.h1
Method	BLASTX
NCBI GI	g3600049
BLAST score	160
E value	3.0e-11
Match length	55
% identity	64
NCBI Description	(AF080120) similar to initiation factor IF2-beta (Pfam: GTP_EFTU.hmm, score: 226.67) [Arabidopsis thaliana]

Seq. No.	50650
Seq. ID	taw700658278.h1
Method	BLASTN
NCBI GI	g3021337
BLAST score	81
E value	8.0e-38
Match length	187
% identity	86
NCBI Description	Cicer arietinum mRNA for cytosolic fructose-1,6-bisphosphate aldolase

Seq. No.	50651
Seq. ID	taw700658314.h1
Method	BLASTN

NCBI GI	g3287367
BLAST score	48
E value	4.0e-18
Match length	215
% identity	86
NCBI Description	Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence [Mus musculus]

Seq. No.	50652
Seq. ID	taw700658316.h1
Method	BLASTN
NCBI GI	g1150555
BLAST score	284
E value	1.0e-159
Match length	293
% identity	99
NCBI Description	R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein

Seq. No.	50653
Seq. ID	taw700658318.h1
Method	BLASTN
NCBI GI	g2361032
BLAST score	285
E value	1.0e-159
Match length	285
% identity	100
NCBI Description	Rattus sp. mRNA for CDP-diacylglycerol synthase, complete cds

Seq. No.	50654
Seq. ID	taw700658319.h1
Method	BLASTN
NCBI GI	g1754509
BLAST score	260
E value	1.0e-144
Match length	284
% identity	97
NCBI Description	Rattus norvegicus DNA for cysteine dioxygenase, complete cds

Seq. No.	50655
Seq. ID	taw700658329.h1
Method	BLASTX
NCBI GI	g2633977
BLAST score	193
E value	5.0e-15
Match length	73
% identity	48
NCBI Description	(Z99112) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	50656
Seq. ID	taw700658331.h1
Method	BLASTN
NCBI GI	g57122
BLAST score	273

E value	1.0e-152
Match length	273
% identity	100
NCBI Description	Rat mRNA for ribosomal protein L37a

Seq. No.	50657
Seq. ID	taw700658332.h1
Method	BLASTX
NCBI GI	g4493522
BLAST score	234
E value	8.0e-20
Match length	83
% identity	54
NCBI Description	(AL022476) dJ323M22.2.1 (novel protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase) (isoform 1) [Homo sapiens]

Seq. No.	50658
Seq. ID	taw700658337.h1
Method	BLASTN
NCBI GI	g199585
BLAST score	199
E value	1.0e-108
Match length	274
% identity	93
NCBI Description	Mouse MHC class I tum- transplantation antigen mRNA P35B, complete cds

Seq. No.	50659
Seq. ID	taw700658340.h1
Method	BLASTN
NCBI GI	g57687
BLAST score	278
E value	1.0e-155
Match length	278
% identity	100
NCBI Description	Rat mRNA for ribosomal protein L23

Seq. No.	50660
Seq. ID	taw700658343.h1
Method	BLASTN
NCBI GI	g1019367
BLAST score	131
E value	1.0e-67
Match length	231
% identity	89
NCBI Description	Human SSR2 mRNA for beta-signal sequence receptor, complete cds

Seq. No.	50661
Seq. ID	taw700658348.h1
Method	BLASTN
NCBI GI	g189396
BLAST score	92
E value	2.0e-44
Match length	264
% identity	86

NCBI Description	Human ORF mRNA, complete cds
Seq. No.	50662
Seq. ID	taw700658360.h1
Method	BLASTN
NCBI GI	g4508150
BLAST score	57
E value	2.0e-23
Match length	96
% identity	91
NCBI Description	Homo sapiens clone DJ0726N20, complete sequence
Seq. No.	50663
Seq. ID	taw700658362.h1
Method	BLASTN
NCBI GI	g3327063
BLAST score	39
E value	1.0e-12
Match length	149
% identity	86
NCBI Description	Homo sapiens mRNA for KIAA0625 protein, partial cds
Seq. No.	50664
Seq. ID	taw700658369.h1
Method	BLASTN
NCBI GI	g310084
BLAST score	261
E value	1.0e-145
Match length	273
% identity	99
NCBI Description	Rattus rattus calnexin mRNA, complete cds
Seq. No.	50665
Seq. ID	taw700658370.h1
Method	BLASTN
NCBI GI	g3249127
BLAST score	35
E value	2.0e-10
Match length	176
% identity	81
NCBI Description	Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence [Homo sapiens]
Seq. No.	50666
Seq. ID	taw700658374.h1
Method	BLASTX
NCBI GI	g3913065
BLAST score	219
E value	4.0e-18
Match length	45
% identity	96
NCBI Description	PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 2D-0014IV)
Seq. No.	50667
Seq. ID	taw700658376.h1
Method	BLASTN

NCBI GI	g555751
BLAST score	275
E value	1.0e-153
Match length	275
% identity	100
NCBI Description	Rattus norvegicus orphan receptor RLD-1 (rld-1) mRNA, complete cds

Seq. No.	50668
Seq. ID	taw700658377.h1
Method	BLASTN
NCBI GI	g998519
BLAST score	253
E value	1.0e-140
Match length	257
% identity	100
NCBI Description	non-muscle myosin alkali light chain [rats, Sprague-Dawley, new-born, heart ventricle, mRNA, 613 nt]

Seq. No.	50669
Seq. ID	taw700658387.h1
Method	BLASTN
NCBI GI	g3483674
BLAST score	39
E value	1.0e-12
Match length	47
% identity	96
NCBI Description	Homo sapiens full length insert cDNA clone ZD54C08

Seq. No.	50670
Seq. ID	taw700658402.h1
Method	BLASTN
NCBI GI	g506600
BLAST score	102
E value	8.0e-51
Match length	102
% identity	100
NCBI Description	R.norvegicus mRNA for factor X

Seq. No.	50671
Seq. ID	taw700658406.h1
Method	BLASTN
NCBI GI	g57713
BLAST score	205
E value	1.0e-112
Match length	212
% identity	100
NCBI Description	Rat mRNA for ribosomal protein S16

Seq. No.	50672
Seq. ID	taw700658408.h1
Method	BLASTN
NCBI GI	g535011
BLAST score	40
E value	2.0e-13
Match length	76
% identity	88

NCBI Description	H.sapiens mRNA for NADP+-dependent malic enzyme
Seq. No.	50673
Seq. ID	taw700658414.h1
Method	BLASTN
NCBI GI	g57179
BLAST score	225
E value	1.0e-123
Match length	246
% identity	98
NCBI Description	R.norvegicus mRNA for serum amyloid P (SAP)
Seq. No.	50674
Seq. ID	taw700658424.h1
Method	BLASTN
NCBI GI	g204534
BLAST score	103
E value	6.0e-51
Match length	136
% identity	92
NCBI Description	Rat glucose transporter mRNA, complete cds
Seq. No.	50675
Seq. ID	taw700658426.h1
Method	BLASTN
NCBI GI	g203920
BLAST score	97
E value	2.0e-47
Match length	109
% identity	97
NCBI Description	Sprague-Dawley D-beta-hydroxybutyrate dehydrogenase mRNA, complete cds
Seq. No.	50676
Seq. ID	taw700658447.h1
Method	BLASTN
NCBI GI	g163131
BLAST score	130
E value	5.0e-67
Match length	205
% identity	91
NCBI Description	Bovine vacuolar H+ ATPase 31kDa subunit mRNA, complete cds
Seq. No.	50677
Seq. ID	taw700658453.h1
Method	BLASTN
NCBI GI	g286222
BLAST score	96
E value	3.0e-47
Match length	100
% identity	99
NCBI Description	Rat gene for L-gulono-gamma-lactone oxidase, exon
Seq. No.	50678
Seq. ID	taw700658460.h1
Method	BLASTN
NCBI GI	g3776070

BLAST score	51
E value	6.0e-20
Match length	67
% identity	94
NCBI Description	Homo sapiens mRNA for histone deacetylase-like protein (JM21)

Seq. No.	50679
Seq. ID	taw700658468.h1
Method	BLASTN
NCBI GI	g2645207
BLAST score	99
E value	1.0e-48
Match length	122
% identity	96
NCBI Description	Rattus norvegicus apolipoprotein B mRNA editing enzyme complex-1 (apobec-1) gene, exon 1 and partial cds

Seq. No.	50680
Seq. ID	taw700658470.h1
Method	BLASTN
NCBI GI	g2738914
BLAST score	122
E value	3.0e-62
Match length	209
% identity	90
NCBI Description	Homo sapiens serine protease (Omi) mRNA, complete cds

Seq. No.	50681
Seq. ID	taw700658479.h1
Method	BLASTN
NCBI GI	g296442
BLAST score	45
E value	2.0e-16
Match length	93
% identity	95
NCBI Description	G.max ADR11 mRNA

Seq. No.	50682
Seq. ID	taw700658490.h1
Method	BLASTN
NCBI GI	g1036804
BLAST score	181
E value	2.0e-97
Match length	252
% identity	93
NCBI Description	Human TGF-beta receptor interacting protein 1 mRNA, complete cds

Seq. No.	50683
Seq. ID	taw700658509.h1
Method	BLASTN
NCBI GI	g3510373
BLAST score	222
E value	1.0e-122
Match length	250
% identity	97

NCBI Description	Rattus norvegicus mRNA for antisecretory factor, complete cds

Seq. No.	50684
Seq. ID	taw700658510.h1
Method	BLASTN
NCBI GI	g1905893
BLAST score	47
E value	2.0e-17
Match length	147
% identity	89
NCBI Description	Homo sapiens DNA from chromosome 19-cosmid f24109 containing HRX2, genomic sequence

Seq. No.	50685
Seq. ID	taw700658512.h1
Method	BLASTN
NCBI GI	g1794204
BLAST score	222
E value	1.0e-122
Match length	242
% identity	98
NCBI Description	Rattus norvegicus calpain small subunit (css1) mRNA, partial cds

Seq. No.	50686
Seq. ID	taw700658513.h1
Method	BLASTN
NCBI GI	g405555
BLAST score	200
E value	1.0e-109
Match length	233
% identity	96
NCBI Description	Rat marker SCAMP 37 mRNA

Seq. No.	50687
Seq. ID	taw700658532.h1
Method	BLASTN
NCBI GI	g456281
BLAST score	172
E value	4.0e-92
Match length	250
% identity	91
NCBI Description	Rattus norvegicus clone par-4 induced by effectors of apoptosis mRNA, complete cds

Seq. No.	50688
Seq. ID	taw700658535.h1
Method	BLASTN
NCBI GI	g495127
BLAST score	117
E value	1.0e-59
Match length	129
% identity	98
NCBI Description	M.musculus mCBP mRNA

Seq. No.	50689

Seq. ID	taw700658536.h1
Method	BLASTN
NCBI GI	g1498195
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	Rat mRNA for Sky, complete cds

Seq. No.	50690
Seq. ID	taw700658541.h1
Method	BLASTX
NCBI GI	g730536
BLAST score	218
E value	5.0e-18
Match length	74
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal protein subunit L17 [Nicotiana tabacum]

Seq. No.	50691
Seq. ID	taw700658542.h1
Method	BLASTN
NCBI GI	g57003
BLAST score	195
E value	1.0e-106
Match length	252
% identity	94
NCBI Description	Rat PYBP2 mRNA for pyrimidine binding protein

Seq. No.	50692
Seq. ID	taw700658544.h1
Method	BLASTN
NCBI GI	g4164453
BLAST score	51
E value	6.0e-20
Match length	227
% identity	81
NCBI Description	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	50693
Seq. ID	taw700658547.h1
Method	BLASTN
NCBI GI	g398594
BLAST score	220
E value	1.0e-121
Match length	228
% identity	100
NCBI Description	Rat mRNA for mitochondrial adenine nuleotide translocator

Seq. No.	50694
Seq. ID	taw700658549.h1
Method	BLASTX
NCBI GI	g3688090
BLAST score	251

E value	9.0e-26
Match length	75
% identity	84
NCBI Description	(AC005757) R32611_2 [Homo sapiens]

Seq. No.	50695
Seq. ID	taw700658555.h1
Method	BLASTN
NCBI GI	g3882182
BLAST score	43
E value	4.0e-15
Match length	179
% identity	84
NCBI Description	Homo sapiens mRNA for KIAA0731 protein, partial cds

Seq. No.	50696
Seq. ID	taw700658557.h1
Method	BLASTN
NCBI GI	g3523147
BLAST score	230
E value	1.0e-127
Match length	230
% identity	100
NCBI Description	Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds

Seq. No.	50697
Seq. ID	taw700658561.h1
Method	BLASTN
NCBI GI	g4165024
BLAST score	79
E value	1.0e-36
Match length	127
% identity	91
NCBI Description	Homo sapiens zinc-finger protein MCG4 mRNA, complete cds

Seq. No.	50698
Seq. ID	taw700658563.h1
Method	BLASTN
NCBI GI	g35517
BLAST score	94
E value	1.0e-45
Match length	250
% identity	84
NCBI Description	Human mRNA for pleckstrin (P47) >gi_4505878_ref_NM_002664.1_PLEK_ Homo sapiens pleckstrin (PLEK) mRNA

Seq. No.	50699
Seq. ID	taw700658567.h1
Method	BLASTN
NCBI GI	g2358084
BLAST score	35
E value	1.0e-10
Match length	71
% identity	24
NCBI Description	Mus musculus TCR beta locus from bases 250554 to 501917

(section 2 of 3) of the complete sequence

Seq. No.	50700
Seq. ID	taw700658568.h1
Method	BLASTN
NCBI GI	g1432168
BLAST score	149
E value	1.0e-78
Match length	149
% identity	100
NCBI Description	Rattus norvegicus macrophage migration inhibitory factor (Mif) mRNA, complete cds

Seq. No.	50701
Seq. ID	taw700658570.h1
Method	BLASTN
NCBI GI	g4519620
BLAST score	134
E value	2.0e-69
Match length	204
% identity	92
NCBI Description	Mus musculus mRNA for OASIS protein, complete cds

Seq. No.	50702
Seq. ID	taw700658573.h1
Method	BLASTN
NCBI GI	g4097696
BLAST score	196
E value	1.0e-106
Match length	196
% identity	100
NCBI Description	Rattus norvegicus purine-selective sodium/nucleoside cotransporter (rCNT2) mRNA, complete cds

Seq. No.	50703
Seq. ID	taw700658579.h1
Method	BLASTN
NCBI GI	g258002
BLAST score	249
E value	1.0e-138
Match length	249
% identity	100
NCBI Description	insulin-like growth factor binding protein complex acid-labile subunit [rats, liver, mRNA, 2190 nt]

Seq. No.	50704
Seq. ID	taw700658583.h1
Method	BLASTN
NCBI GI	g957211
BLAST score	131
E value	1.0e-67
Match length	175
% identity	94
NCBI Description	Murine Glvr-1 mRNA, complete cds

Seq. No.	50705
Seq. ID	taw700658587.h1

Method	BLASTX
NCBI GI	g2501599
BLAST score	142
E value	4.0e-09
Match length	50
% identity	58
NCBI Description	HYPOTHETICAL 29.1 KD PROTEIN W06E11.4 IN CHROMOSOME III >gi_669022 (U20862) W06E11.4 gene product [Caenorhabditis elegans]

Seq. No.	50706
Seq. ID	taw700658590.h1
Method	BLASTN
NCBI GI	g732917
BLAST score	143
E value	8.0e-75
Match length	244
% identity	93
NCBI Description	R.norvegicus RPL19 gene

Seq. No.	50707
Seq. ID	taw700658591.h1
Method	BLASTN
NCBI GI	g57807
BLAST score	39
E value	9.0e-13
Match length	107
% identity	84
NCBI Description	Rat mRNA for histone H2A.Z

Seq. No.	50708
Seq. ID	taw700658606.h1
Method	BLASTN
NCBI GI	g56299
BLAST score	62
E value	1.0e-26
Match length	77
% identity	96
NCBI Description	R.norvegicus mRNA for gamma subunit of sodium potassium ATPase

Seq. No.	50709
Seq. ID	taw700658607.h1
Method	BLASTN
NCBI GI	g473932
BLAST score	148
E value	8.0e-78
Match length	248
% identity	90
NCBI Description	Human mRNA for KIAA0052 gene, partial cds

Seq. No.	50710
Seq. ID	taw700658614.h1
Method	BLASTN
NCBI GI	g207693
BLAST score	166
E value	9.0e-89

Match length	166
% identity	100
NCBI Description	Rat sperm membrane protein (YWK-II) mRNA, 3' end

Seq. No.	50711
Seq. ID	taw700658629.h1
Method	BLASTN
NCBI GI	g1621616
BLAST score	158
E value	6.0e-84
Match length	182
% identity	97
NCBI Description	Mus musculus KRAB-A interacting protein mRNA, complete cds

Seq. No.	50712
Seq. ID	taw700658644.h1
Method	BLASTN
NCBI GI	g50488
BLAST score	77
E value	9.0e-36
Match length	125
% identity	90
NCBI Description	Mouse COL1A2 mRNA for pro-alpha-2(I) collagen

Seq. No.	50713
Seq. ID	taw700658650.h1
Method	BLASTN
NCBI GI	g286199
BLAST score	232
E value	1.0e-128
Match length	236
% identity	100
NCBI Description	Rattus norvegicus P1 mRNA for ATP synthase subunit c, complete cds

Seq. No.	50714
Seq. ID	taw700658654.h1
Method	BLASTN
NCBI GI	g4544348
BLAST score	57
E value	2.0e-23
Match length	133
% identity	92
NCBI Description	Homo sapiens PAC RPCI4-613B23 (Roswell Park Cancer Institute Human PAC Library) complete sequence

Seq. No.	50715
Seq. ID	taw700658657.h1
Method	BLASTN
NCBI GI	g50838
BLAST score	75
E value	2.0e-34
Match length	139
% identity	88
NCBI Description	Mouse mRNA for entactin

Seq. No.	50716

Seq. ID	taw700658660.h1
Method	BLASTN
NCBI GI	g2897074
BLAST score	144
E value	1.0e-75
Match length	160
% identity	97
NCBI Description	Rattus norvegicus electrogenic Na+ bicarbonate cotransporter (NBC) mRNA, complete cds

Seq. No.	50717
Seq. ID	taw700658663.h1
Method	BLASTN
NCBI GI	g310169
BLAST score	77
E value	9.0e-36
Match length	125
% identity	90
NCBI Description	Rattus norvegicus NGF-binding Ig rearranged L-chain mRNA, V-region, partial cds

Seq. No.	50718
Seq. ID	taw700658678.h1
Method	BLASTN
NCBI GI	g468549
BLAST score	129
E value	1.0e-66
Match length	161
% identity	95
NCBI Description	M.musculus (129/Sv) Ccte mRNA for CCT (chaperonin containing TCP-1) epsilon subunit

Seq. No.	50719
Seq. ID	taw700658679.h1
Method	BLASTN
NCBI GI	g4138415
BLAST score	128
E value	4.0e-66
Match length	144
% identity	97
NCBI Description	Rattus norvegicus mRNA for SMC-protein Molecular characterization of a rat heterochromatin associated SMC-protein

Seq. No.	50720
Seq. ID	taw700658685.h1
Method	BLASTN
NCBI GI	g1199601
BLAST score	125
E value	4.0e-64
Match length	237
% identity	88
NCBI Description	Human cyclophilin-like protein mRNA, partial cds

Seq. No.	50721
Seq. ID	taw700658688.h1
Method	BLASTN

NCBI GI	g1296990
BLAST score	125
E value	2.0e-64
Match length	149
% identity	96
NCBI Description	R.norvegicus mRNA for RT1.Mb

Seq. No.	50722
Seq. ID	taw700658693.h1
Method	BLASTN
NCBI GI	g204490
BLAST score	156
E value	8.0e-83
Match length	156
% identity	100
NCBI Description	Rat glutathione S-transferase mRNA, complete cds

Seq. No.	50723
Seq. ID	taw700658748.h1
Method	BLASTN
NCBI GI	g609224
BLAST score	42
E value	9.0e-15
Match length	54
% identity	94
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	50724
Seq. ID	taw700658828.h1
Method	BLASTN
NCBI GI	g725331
BLAST score	116
E value	1.0e-58
Match length	116
% identity	100
NCBI Description	Glycine max mitochondrion polymorphic marker DNA sequence

Seq. No.	50725
Seq. ID	taw700658941.h1
Method	BLASTN
NCBI GI	g914956
BLAST score	109
E value	1.0e-54
Match length	109
% identity	100
NCBI Description	Rat mRNA for Ash-m, complete cds

Seq. No.	50726
Seq. ID	taw700658984.h1
Method	BLASTX
NCBI GI	g1173198
BLAST score	169
E value	1.0e-18
Match length	55
% identity	83

NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	50727
Seq. ID	taw700659104.h1
Method	BLASTX
NCBI GI	g4530585
BLAST score	166
E value	5.0e-12
Match length	50
% identity	66
NCBI Description	(AF130978) B12D protein [Ipomoea batatas]

Seq. No.	50728
Seq. ID	taw700659196.h1
Method	BLASTN
NCBI GI	g11576
BLAST score	60
E value	2.0e-25
Match length	124
% identity	87
NCBI Description	Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NADH dehydrogenase and ORF

Seq. No.	50729
Seq. ID	taw700659302.h1
Method	BLASTX
NCBI GI	g4490321
BLAST score	232
E value	1.0e-19
Match length	71
% identity	72
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	50730
Seq. ID	taw700659335.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	108
E value	3.0e-54
Match length	120
% identity	97
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	50731
Seq. ID	taw700659535.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	188
E value	1.0e-101
Match length	259
% identity	93
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	50732

Seq. ID	taw700659653.h1
Method	BLASTX
NCBI GI	g4218014
BLAST score	269
E value	5.0e-24
Match length	68
% identity	79
NCBI Description	(AC006135) putative spliceosomal protein (RNA binding protein) [Arabidopsis thaliana]

Seq. No.	50733
Seq. ID	taw700659665.h1
Method	BLASTN
NCBI GI	g3184523
BLAST score	45
E value	2.0e-16
Match length	49
% identity	98
NCBI Description	Allium cepa tRNA-Leu (trnL) and tRNA-Thr (trnT) genes, chloroplast genes for chloroplast RNAs, partial sequence

Seq. No.	50734
Seq. ID	taw700659821.h1
Method	BLASTX
NCBI GI	g4455331
BLAST score	243
E value	6.0e-21
Match length	63
% identity	68
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	50735
Seq. ID	taw700659825.h1
Method	BLASTX
NCBI GI	g2244996
BLAST score	178
E value	2.0e-13
Match length	63
% identity	26
NCBI Description	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]

Seq. No.	50736
Seq. ID	taw700659833.h1
Method	BLASTN
NCBI GI	g2905771
BLAST score	129
E value	2.0e-66
Match length	156
% identity	97
NCBI Description	Glycine max glyceraldehyde-3 phosphate dehydrogenase (GAPDH) mRNA, partial cds

Seq. No.	50737
Seq. ID	taw700659918.h1
Method	BLASTX
NCBI GI	g1498064

BLAST score	211
E value	4.0e-17
Match length	69
% identity	55
NCBI Description	(U64825) AtE1 [Arabidopsis thaliana]

Seq. No.	50738
Seq. ID	taw700659941.h1
Method	BLASTX
NCBI GI	g549060
BLAST score	235
E value	4.0e-20
Match length	80
% identity	56
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	50739
Seq. ID	taw700659949.h1
Method	BLASTN
NCBI GI	g18551
BLAST score	191
E value	1.0e-103
Match length	219
% identity	97
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	50740
Seq. ID	taw700660002.h1
Method	BLASTX
NCBI GI	g2130052
BLAST score	214
E value	2.0e-17
Match length	61
% identity	68
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase [Hordeum vulgare]

Seq. No.	50741
Seq. ID	taw700660021.h1
Method	BLASTN
NCBI GI	g1370195
BLAST score	115
E value	5.0e-58
Match length	150
% identity	95
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAB8D

Seq. No.	50742
Seq. ID	taw700660224.h1
Method	BLASTX
NCBI GI	g1871185
BLAST score	225

E value	5.0e-19
Match length	50
% identity	78
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	50743
Seq. ID	taw700660474.h1
Method	BLASTX
NCBI GI	g4559339
BLAST score	361
E value	8.0e-35
Match length	83
% identity	84
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	50744
Seq. ID	taw700660494.h1
Method	BLASTX
NCBI GI	g3395439
BLAST score	266
E value	1.0e-23
Match length	71
% identity	69
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50745
Seq. ID	taw700660554.h1
Method	BLASTX
NCBI GI	g541943
BLAST score	190
E value	9.0e-15
Match length	38
% identity	87
NCBI Description	metallothionein - soybean >gi_228682_prf__1808316A metallothionein-like protein [Glycine max]

Seq. No.	50746
Seq. ID	taw700660584.h1
Method	BLASTN
NCBI GI	g2934695
BLAST score	80
E value	2.0e-37
Match length	91
% identity	98
NCBI Description	Glycine max mRNA for class III acidic endochitinase, complete cds

Seq. No.	50747
Seq. ID	taw700660587.h1
Method	BLASTN
NCBI GI	g2852444
BLAST score	33
E value	4.0e-09
Match length	89
% identity	84
NCBI Description	Salix bakko mRNA for SUI1 homolog, complete cds

Seq. No.	50748
Seq. ID	taw700660603.h1
Method	BLASTN
NCBI GI	g347458
BLAST score	96
E value	3.0e-47
Match length	100
% identity	99
NCBI Description	Glycine max brassinosteroid-regulated protein mRNA, complete cds

Seq. No.	50749
Seq. ID	taw700660622.h1
Method	BLASTN
NCBI GI	g18741
BLAST score	131
E value	1.0e-67
Match length	199
% identity	91
NCBI Description	Glycine max gene encoding ribulose-1,5-bisphosphate carboxylase small subunit

Seq. No.	50750
Seq. ID	tku700646326.h1
Method	BLASTX
NCBI GI	g4115926
BLAST score	179
E value	2.0e-13
Match length	79
% identity	48
NCBI Description	(AF118222) similar to the subtilase family of serine proteases (Pfam: PF00082, Score=50.7, E=4.7e-13, n=3) [Arabidopsis thaliana] >gi_4539413_emb_CAB40046.1_ (AL049524) putative subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	50751
Seq. ID	tku700646328.h1
Method	BLASTX
NCBI GI	g4455299
BLAST score	196
E value	2.0e-15
Match length	73
% identity	53
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	50752
Seq. ID	tku700646345.h1
Method	BLASTX
NCBI GI	g4249412
BLAST score	291
E value	2.0e-26
Match length	91
% identity	63
NCBI Description	(AC006072) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50753
Seq. ID	tku700646361.h1
Method	BLASTX
NCBI GI	g2335097
BLAST score	277
E value	7.0e-25
Match length	91
% identity	29
NCBI Description	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	50754
Seq. ID	tku700646403.h1
Method	BLASTX
NCBI GI	g531389
BLAST score	202
E value	4.0e-16
Match length	78
% identity	55
NCBI Description	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No.	50755
Seq. ID	tku700646428.h1
Method	BLASTX
NCBI GI	g1778370
BLAST score	163
E value	2.0e-11
Match length	32
% identity	100
NCBI Description	(U77678) asparagine synthetase 2 [Glycine max]

Seq. No.	50756
Seq. ID	tku700646437.h1
Method	BLASTX
NCBI GI	g3982596
BLAST score	231
E value	1.0e-19
Match length	81
% identity	67
NCBI Description	(AF039027) cationic peroxidase 2 [Glycine max]

Seq. No.	50757
Seq. ID	tku700646476.h1
Method	BLASTX
NCBI GI	g100440
BLAST score	140
E value	8.0e-09
Match length	64
% identity	53
NCBI Description	heat shock protein 70 (clone D7) - potato (fragment) >gi_100441_pir__S21363 heat shock protein 70 (clone D3) - potato (fragment) >gi_21477_emb_CAA78036_ (Z11984) 70-kD heat shock protein [Solanum tuberosum]

Seq. No.	50758
Seq. ID	trc700561124.h1

Method	BLASTX
NCBI GI	g4151068
BLAST score	250
E value	5.0e-22
Match length	62
% identity	74
NCBI Description	(Y10862) ribonucleotide reductase [Nicotiana tabacum]

Seq. No.	50759
Seq. ID	trc700561144.h1
Method	BLASTX
NCBI GI	g2920654
BLAST score	302
E value	9.0e-28
Match length	94
% identity	59
NCBI Description	(AF047697) putative high-pI laccase [Oryza sativa]

Seq. No.	50760
Seq. ID	trc700561171.h1
Method	BLASTX
NCBI GI	g2459412
BLAST score	250
E value	9.0e-22
Match length	92
% identity	54
NCBI Description	(AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No.	50761
Seq. ID	trc700561176.h1
Method	BLASTX
NCBI GI	g3152616
BLAST score	169
E value	3.0e-12
Match length	90
% identity	47
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana] >gi_3242726 (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50762
Seq. ID	trc700561234.h1
Method	BLASTN
NCBI GI	g2388688
BLAST score	40
E value	8.0e-14
Match length	76
% identity	88
NCBI Description	Glycine max GH1 protein (GH1) mRNA, partial cds

Seq. No.	50763
Seq. ID	trc700561250.h1
Method	BLASTX
NCBI GI	g3075392
BLAST score	287
E value	2.0e-26
Match length	72

% identity	76
NCBI Description	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]

Seq. No.	50764
Seq. ID	trc700561285.h1
Method	BLASTX
NCBI GI	g1236961
BLAST score	136
E value	1.0e-08
Match length	39
% identity	59
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	50765
Seq. ID	trc700561314.h1
Method	BLASTN
NCBI GI	g1673513
BLAST score	246
E value	1.0e-136
Match length	305
% identity	95
NCBI Description	Human B-cell receptor associated protein (hBAP) mRNA, partial cds

Seq. No.	50766
Seq. ID	trc700561320.h1
Method	BLASTX
NCBI GI	g585876
BLAST score	163
E value	2.0e-11
Match length	48
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026 ribosomal protein L25 - common tobacco >gi_310935 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No.	50767
Seq. ID	trc700561329.h1
Method	BLASTX
NCBI GI	g4455275
BLAST score	158
E value	3.0e-11
Match length	43
% identity	72
NCBI Description	(AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	50768
Seq. ID	trc700561336.h1
Method	BLASTX
NCBI GI	g2493318
BLAST score	138
E value	8.0e-10
Match length	41
% identity	88
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum]

>gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	50769
Seq. ID	trc700561363.h1
Method	BLASTX
NCBI GI	g3929339
BLAST score	291
E value	2.0e-26
Match length	95
% identity	59
NCBI Description	BYSTIN >gi_1160619 (L36720) bystin [Homo sapiens]

Seq. No.	50770
Seq. ID	trc700561377.h1
Method	BLASTX
NCBI GI	g2289012
BLAST score	318
E value	1.0e-29
Match length	97
% identity	63
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50771
Seq. ID	trc700561450.h1
Method	BLASTX
NCBI GI	g544437
BLAST score	212
E value	3.0e-17
Match length	66
% identity	64
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No.	50772
Seq. ID	trc700561461.h1
Method	BLASTX
NCBI GI	g2827143
BLAST score	345
E value	7.0e-33
Match length	87
% identity	80
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	50773
Seq. ID	trc700561479.h1
Method	BLASTX
NCBI GI	g3033381
BLAST score	308
E value	1.0e-28
Match length	68
% identity	88
NCBI Description	(AC004238) putative UDP-galactose-4-epimerase [Arabidopsis thaliana]

Seq. No.	50774
Seq. ID	trc700561495.h1

Method	BLASTX
NCBI GI	g2827141
BLAST score	424
E value	4.0e-42
Match length	88
% identity	88
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	50775
Seq. ID	trc700561557.h1
Method	BLASTN
NCBI GI	g170061
BLAST score	90
E value	3.0e-43
Match length	157
% identity	90
NCBI Description	Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete cds

Seq. No.	50776
Seq. ID	trc700561601.h1
Method	BLASTN
NCBI GI	g3021372
BLAST score	133
E value	4.0e-69
Match length	153
% identity	97
NCBI Description	Glycine max mRNA for profilin, PRO2

Seq. No.	50777
Seq. ID	trc700561604.h1
Method	BLASTN
NCBI GI	g31972
BLAST score	175
E value	5.0e-94
Match length	183
% identity	99
NCBI Description	Human H2A.X mRNA encoding histone H2A.X >gi_4504252_ref_NM_002105.1_H2AFX_ Homo sapiens H2A histone family, member X (H2AFX) mRNA

Seq. No.	50778
Seq. ID	trc700561638.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	58
E value	3.0e-24
Match length	126
% identity	87
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	50779
Seq. ID	trc700561664.h1
Method	BLASTN
NCBI GI	g21981

BLAST score	33
E value	1.0e-09
Match length	101
% identity	84
NCBI Description	V.angustifolia 25S/18S rRNA intergenic spacer DNA

Seq. No.	50780
Seq. ID	trc700561742.h1
Method	BLASTN
NCBI GI	g1150931
BLAST score	34
E value	8.0e-10
Match length	50
% identity	92
NCBI Description	M.sativa mRNA for cyclin protein

Seq. No.	50781
Seq. ID	trc700561804.h1
Method	BLASTX
NCBI GI	g2809251
BLAST score	304
E value	5.0e-28
Match length	93
% identity	57
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No.	50782
Seq. ID	trc700561808.h1
Method	BLASTX
NCBI GI	g3913379
BLAST score	122
E value	2.0e-16
Match length	91
% identity	51
NCBI Description	CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana]

Seq. No.	50783
Seq. ID	trc700561928.h1
Method	BLASTX
NCBI GI	g114290
BLAST score	142
E value	3.0e-12
Match length	64
% identity	64
NCBI Description	ARGININOSUCCINATE SYNTHASE (CITRULLINE--ASPARTATE LIGASE) >gi_68638_pir__AJMSRS argininosuccinate synthase (EC 6.3.4.5) - mouse >gi_309111 (M31690) argininosuccinate synthetase (EC 6.3.4.5) [Mus musculus]

Seq. No.	50784
Seq. ID	trc700561972.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	274
E value	1.0e-153

Match length	274
% identity	100
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	50785
Seq. ID	trc700562036.h1
Method	BLASTX
NCBI GI	g4454470
BLAST score	192
E value	3.0e-15
Match length	50
% identity	72
NCBI Description	(AC006234) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	50786
Seq. ID	trc700562077.h1
Method	BLASTX
NCBI GI	g3882355
BLAST score	232
E value	1.0e-19
Match length	64
% identity	67
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana]

Seq. No.	50787
Seq. ID	trc700562165.h1
Method	BLASTX
NCBI GI	g1087073
BLAST score	210
E value	3.0e-17
Match length	44
% identity	91
NCBI Description	(S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa] [Nicotiana tabacum]

Seq. No.	50788
Seq. ID	trc700562166.h1
Method	BLASTX
NCBI GI	g2827546
BLAST score	140
E value	4.0e-09
Match length	43
% identity	56
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	50789
Seq. ID	trc700562204.h1
Method	BLASTX
NCBI GI	g4559353
BLAST score	455
E value	1.0e-45
Match length	100
% identity	86

NCBI Description	(AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]

Seq. No.	50790
Seq. ID	trc700562245.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	244
E value	1.0e-135
Match length	271
% identity	98
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	50791
Seq. ID	trc700562276.h1
Method	BLASTX
NCBI GI	g728906
BLAST score	259
E value	9.0e-23
Match length	84
% identity	57
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 5 >gi_1077722_pir__S50669 hypothetical protein YER166w - yeast (Saccharomyces cerevisiae) >gi_603407 (U18922) Yer166wp [Saccharomyces cerevisiae]

Seq. No.	50792
Seq. ID	trc700562289.h1
Method	BLASTN
NCBI GI	g170087
BLAST score	118
E value	7.0e-60
Match length	251
% identity	89
NCBI Description	G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No.	50793
Seq. ID	trc700562326.h1
Method	BLASTN
NCBI GI	g166873
BLAST score	95
E value	4.0e-46
Match length	203
% identity	87
NCBI Description	A.thaliana S-adenosylmethionine synthetase 2 (sam-2) gene, complete cds

Seq. No.	50794
Seq. ID	trc700562332.h1
Method	BLASTX
NCBI GI	g2245108
BLAST score	174
E value	8.0e-13
Match length	40
% identity	78
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	50795
Seq. ID	trc700562339.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	59
E value	6.0e-25
Match length	127
% identity	87
NCBI Description	G.max ADR6 mRNA

Seq. No.	50796
Seq. ID	trc700562358.h1
Method	BLASTN
NCBI GI	g297877
BLAST score	108
E value	7.0e-54
Match length	200
% identity	89
NCBI Description	A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana ubiquitin conjugating enzyme mRNA, complete cds

Seq. No.	50797
Seq. ID	trc700562423.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	254
E value	1.0e-141
Match length	273
% identity	99
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	50798
Seq. ID	trc700562506.h1
Method	BLASTX
NCBI GI	g2833311
BLAST score	253
E value	5.0e-22
Match length	68
% identity	65
NCBI Description	HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III >gi_630728_pir__S43605 R07E5.13 protein (clone R07E5) - Caenorhabditis elegans >gi_3878946_emb_CAA83622_ (Z32683) R07E5.13 [Caenorhabditis elegans]

Seq. No.	50799
Seq. ID	trc700562520.h1
Method	BLASTX
NCBI GI	g3426048
BLAST score	205
E value	4.0e-34
Match length	86
% identity	85
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No. 50800

Seq. ID	trc700562565.h1
Method	BLASTX
NCBI GI	g1143511
BLAST score	204
E value	2.0e-21
Match length	58
% identity	90
NCBI Description	(Z47076) Ser/Thr protein phosphatase homologous to PPX [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein phosphatase [Malus domestica]

Seq. No.	50801
Seq. ID	trc700562579.h1
Method	BLASTX
NCBI GI	g3201680
BLAST score	186
E value	3.0e-14
Match length	60
% identity	57
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	50802
Seq. ID	trc700562593.h1
Method	BLASTX
NCBI GI	g1351018
BLAST score	196
E value	2.0e-15
Match length	47
% identity	74
NCBI Description	RSI-1 PROTEIN PRECURSOR (TR132) >gi_1076597_pir__S43909 RSI-1 protein - tomato >gi_405585 (L22188) RSI-1 protein [Lycopersicon esculentum] >gi_405587 (L22189) RSI-1 protein [Lycopersicon esculentum]

Seq. No.	50803
Seq. ID	trc700562675.h1
Method	BLASTX
NCBI GI	g3386611
BLAST score	228
E value	4.0e-19
Match length	77
% identity	52
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	50804
Seq. ID	trc700562694.h1
Method	BLASTX
NCBI GI	g4006878
BLAST score	208
E value	9.0e-17
Match length	54
% identity	67
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	50805
Seq. ID	trc700562764.h1
Method	BLASTN

NCBI GI	g4220624
BLAST score	85
E value	4.0e-40
Match length	157
% identity	89
NCBI Description	Vicia faba VHA2 mRNA for p-type H+-ATPase, complete cds

Seq. No.	50806
Seq. ID	trc700562766.h1
Method	BLASTX
NCBI GI	g1149569
BLAST score	177
E value	2.0e-13
Match length	36
% identity	86
NCBI Description	(Z50851) HD-zip [Arabidopsis thaliana]

Seq. No.	50807
Seq. ID	trc700562787.h1
Method	BLASTX
NCBI GI	g4314388
BLAST score	438
E value	1.0e-43
Match length	96
% identity	83
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50808
Seq. ID	trc700562801.h1
Method	BLASTN
NCBI GI	g1326160
BLAST score	58
E value	5.0e-24
Match length	176
% identity	93
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	50809
Seq. ID	trc700562813.h1
Method	BLASTX
NCBI GI	g3172538
BLAST score	162
E value	1.0e-11
Match length	77
% identity	47
NCBI Description	(AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]

Seq. No.	50810
Seq. ID	trc700562851.h1
Method	BLASTX
NCBI GI	g2914703
BLAST score	241
E value	1.0e-20
Match length	96
% identity	51
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	50811
Seq. ID	trc700562951.h1
Method	BLASTN
NCBI GI	g170073
BLAST score	166
E value	2.0e-88
Match length	227
% identity	94
NCBI Description	Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No.	50812
Seq. ID	trc700563012.h1
Method	BLASTN
NCBI GI	g667048
BLAST score	48
E value	4.0e-18
Match length	148
% identity	83
NCBI Description	P.vulgaris mRNA for protein phosphatase 1 (PP1)

Seq. No.	50813
Seq. ID	trc700563020.h1
Method	BLASTN
NCBI GI	g3721539
BLAST score	53
E value	2.0e-21
Match length	109
% identity	87
NCBI Description	Nicotiana tabacum mRNA for Sulfite Reductase, complete cds

Seq. No.	50814
Seq. ID	trc700563058.h1
Method	BLASTX
NCBI GI	g2760325
BLAST score	336
E value	8.0e-32
Match length	89
% identity	74
NCBI Description	(AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No.	50815
Seq. ID	trc700563087.h1
Method	BLASTX
NCBI GI	g3421102
BLAST score	232
E value	1.0e-19
Match length	90
% identity	54
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	50816
Seq. ID	trc700563096.h1
Method	BLASTX
NCBI GI	g4522003
BLAST score	228
E value	2.0e-22

Match length 87
% identity 67
NCBI Description (AC007069) putative protein kinase [Arabidopsis thaliana]

Seq. No. 50817
Seq. ID trc700563110.h1
Method BLASTX
NCBI GI g4566505
BLAST score 395
E value 1.0e-38
Match length 93
% identity 75
NCBI Description (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No. 50818
Seq. ID trc700563111.h1
Method BLASTN
NCBI GI g871507
BLAST score 60
E value 3.0e-25
Match length 109
% identity 97
NCBI Description P.sativum mRNA for small GTP-binding protein (clone pGTP13)

Seq. No. 50819
Seq. ID trc700563113.h1
Method BLASTN
NCBI GI g2317899
BLAST score 260
E value 1.0e-144
Match length 284
% identity 98
NCBI Description Glycine max Sali3-2 mRNA, complete cds

Seq. No. 50820
Seq. ID trc700563147.h1
Method BLASTX
NCBI GI g3036807
BLAST score 204
E value 5.0e-20
Match length 89
% identity 53
NCBI Description (AL022373) putative protein [Arabidopsis thaliana]

Seq. No. 50821
Seq. ID trc700563183.h1
Method BLASTX
NCBI GI g4314356
BLAST score 147
E value 6.0e-10
Match length 57
% identity 53
NCBI Description (AC006340) putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana]

Seq. No. 50822

Seq. ID	trc700563211.h1
Method	BLASTN
NCBI GI	g4454703
BLAST score	267
E value	1.0e-149
Match length	271
% identity	100
NCBI Description	Homo sapiens HSPC008 mRNA, complete cds

Seq. No.	50823
Seq. ID	trc700563229.h1
Method	BLASTX
NCBI GI	g4432854
BLAST score	147
E value	4.0e-11
Match length	83
% identity	45
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50824
Seq. ID	trc700563289.h1
Method	BLASTN
NCBI GI	g3158473
BLAST score	34
E value	4.0e-10
Match length	86
% identity	85
NCBI Description	Samanea saman aquaporin 1 (Aqp1) mRNA, complete cds

Seq. No.	50825
Seq. ID	trc700563378.h1
Method	BLASTX
NCBI GI	g2832642
BLAST score	219
E value	1.0e-26
Match length	94
% identity	66
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	50826
Seq. ID	trc700563388.h1
Method	BLASTX
NCBI GI	g282946
BLAST score	340
E value	3.0e-32
Match length	93
% identity	62
NCBI Description	Ca2+-transporting ATPase (EC 3.6.1.38) - tomato >gi_423783_pir__A46284 Ca(2+)-ATPase, LCA1 - Lycopersicon=tomatoes >gi_170378 (M96324) Ca2+-ATPase [Lycopersicon esculentum] >gi_4206311 (AF050495) Ca2+ ATP synthase [Lycopersicon esculentum] >gi_4206313 (AF050496) Ca2+ ATP synthase [Lycopersicon esculentum]

Seq. No.	50827
Seq. ID	trc700563417.h1
Method	BLASTX

NCBI GI	g3176669
BLAST score	153
E value	3.0e-10
Match length	83
% identity	43
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.	50828
Seq. ID	trc700563458.h1
Method	BLASTN
NCBI GI	g1044867
BLAST score	197
E value	1.0e-107
Match length	197
% identity	100
NCBI Description	Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73)

Seq. No.	50829
Seq. ID	trc700563506.h1
Method	BLASTN
NCBI GI	g1370197
BLAST score	147
E value	4.0e-77
Match length	211
% identity	92
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAB8E

Seq. No.	50830
Seq. ID	trc700563522.h1
Method	BLASTX
NCBI GI	g3983665
BLAST score	357
E value	3.0e-34
Match length	99
% identity	71
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No.	50831
Seq. ID	trc700563550.h1
Method	BLASTN
NCBI GI	g438216
BLAST score	34
E value	1.0e-09
Match length	67
% identity	85
NCBI Description	P.sativum mRNA for T subunit of glycine decarboxylase multi-enzyme complex

Seq. No.	50832
Seq. ID	trc700563609.h1
Method	BLASTX
NCBI GI	g399213
BLAST score	408
E value	3.0e-40
Match length	94
% identity	87
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum]

Seq. No.	50833
Seq. ID	trc700563628.h1
Method	BLASTN
NCBI GI	g4165487
BLAST score	46
E value	7.0e-17
Match length	90
% identity	88
NCBI Description	Hordeum vulgare mRNA for alpha-tubulin

Seq. No.	50834
Seq. ID	trc700563687.h1
Method	BLASTX
NCBI GI	g3901012
BLAST score	346
E value	5.0e-33
Match length	73
% identity	81
NCBI Description	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]

Seq. No.	50835
Seq. ID	trc700563711.h1
Method	BLASTX
NCBI GI	g4309738
BLAST score	152
E value	3.0e-10
Match length	46
% identity	61
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	50836
Seq. ID	trc700563759.h1
Method	BLASTN
NCBI GI	g1813330
BLAST score	123
E value	7.0e-63
Match length	267
% identity	87
NCBI Description	Vigna radiata mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds

Seq. No.	50837
Seq. ID	trc700563820.h1
Method	BLASTX
NCBI GI	g3695389
BLAST score	217
E value	9.0e-18
Match length	76
% identity	28
NCBI Description	(AF096371) contains similarity to D-isomer specific 2-hydroxyacid dehydrogenases (Pfam: 2-Hacid_DH.hmm, score: 19.11) [Arabidopsis thaliana]

Seq. No.	50838
Seq. ID	trc700563871.h1
Method	BLASTX
NCBI GI	g1408296
BLAST score	200
E value	8.0e-16
Match length	96
% identity	48
NCBI Description	(U61984) phosphoglucomutase A [Dictyostelium discoideum]

Seq. No.	50839
Seq. ID	trc700563905.h1
Method	BLASTN
NCBI GI	g218255
BLAST score	74
E value	1.0e-33
Match length	95
% identity	93
NCBI Description	Soybean mRNA for early nodulin

Seq. No.	50840
Seq. ID	trc700563954.h1
Method	BLASTN
NCBI GI	g974700
BLAST score	46
E value	7.0e-17
Match length	46
% identity	100
NCBI Description	Glycine max 28S ribosomal RNA (28S rRNA) gene

Seq. No.	50841
Seq. ID	trc700564003.h1
Method	BLASTX
NCBI GI	g3834314
BLAST score	321
E value	6.0e-30
Match length	100
% identity	63
NCBI Description	(AC005679) Similar to gene pi010 glycosyltransferase gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis thaliana]

Seq. No.	50842
Seq. ID	trc700564066.h1
Method	BLASTX
NCBI GI	g3193302
BLAST score	291
E value	2.0e-26
Match length	98
% identity	54
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) [Arabidopsis thaliana]

Seq. No.	50843
Seq. ID	trc700564208.h1
Method	BLASTN
NCBI GI	g1906001
BLAST score	60
E value	3.0e-25
Match length	142
% identity	92
NCBI Description	Glycine max nitrite reductase gene, complete cds

Seq. No.	50844
Seq. ID	trc700564271.h1
Method	BLASTX
NCBI GI	g1514643
BLAST score	226
E value	3.0e-30
Match length	90
% identity	76
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	50845
Seq. ID	trc700564312.h1
Method	BLASTX
NCBI GI	g3805962
BLAST score	186
E value	2.0e-14
Match length	56
% identity	61
NCBI Description	(Y13772) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	50846
Seq. ID	trc700564374.h1
Method	BLASTX
NCBI GI	g136057
BLAST score	120
E value	2.0e-11
Match length	61
% identity	67
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	50847
Seq. ID	trc700564384.h1
Method	BLASTX
NCBI GI	g2832680
BLAST score	119
E value	1.0e-14
Match length	79
% identity	30
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	50848
Seq. ID	trc700564423.h1
Method	BLASTX
NCBI GI	g3269291

BLAST score	320
E value	7.0e-30
Match length	95
% identity	67
NCBI Description	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	50849
Seq. ID	trc700564685.h1
Method	BLASTN
NCBI GI	g1806145
BLAST score	101
E value	1.0e-49
Match length	229
% identity	89
NCBI Description	M.sativa mRNA for cdc2 kinase homologue, cdc2MsF

Seq. No.	50850
Seq. ID	trc700564695.h1
Method	BLASTX
NCBI GI	g3650037
BLAST score	142
E value	5.0e-09
Match length	29
% identity	100
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	50851
Seq. ID	trc700564776.h1
Method	BLASTN
NCBI GI	g2606080
BLAST score	52
E value	6.0e-21
Match length	60
% identity	97
NCBI Description	Glycine max sucrose synthase (SS) mRNA, complete cds

Seq. No.	50852
Seq. ID	trc700564777.h1
Method	BLASTN
NCBI GI	g4240302
BLAST score	54
E value	4.0e-22
Match length	86
% identity	91
NCBI Description	Homo sapiens mRNA for KIAA0907 protein, complete cds

Seq. No.	50853
Seq. ID	trc700564889.h1
Method	BLASTN
NCBI GI	g1155239
BLAST score	33
E value	1.0e-09
Match length	49
% identity	92
NCBI Description	Dianthus caryophyllus S-adenosylmethionine decarboxylase 1

mRNA, complete cds

Seq. No.	50854
Seq. ID	trc700564972.h1
Method	BLASTX
NCBI GI	g3128228
BLAST score	151
E value	4.0e-17
Match length	66
% identity	66
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	50855
Seq. ID	trc700565009.h1
Method	BLASTX
NCBI GI	g585452
BLAST score	178
E value	2.0e-13
Match length	51
% identity	67
NCBI Description	MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076666_pir__A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002) precursor of the 59kDa subunit of the mitochondrial NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No.	50856
Seq. ID	trc700565013.h1
Method	BLASTN
NCBI GI	g904153
BLAST score	35
E value	1.0e-10
Match length	116
% identity	88
NCBI Description	Glycine max FAD2-2 microsomal omega-6 desaturase mRNA, complete cds

Seq. No.	50857
Seq. ID	trc700565017.h1
Method	BLASTX
NCBI GI	g2316016
BLAST score	368
E value	2.0e-35
Match length	89
% identity	80
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	50858
Seq. ID	trc700565019.h1
Method	BLASTX
NCBI GI	g3426064
BLAST score	301
E value	1.0e-27

Match length	92
% identity	60
NCBI Description	(AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]

Seq. No.	50859
Seq. ID	trc700565022.h1
Method	BLASTX
NCBI GI	g2661840
BLAST score	227
E value	5.0e-19
Match length	64
% identity	72
NCBI Description	(Y15430) adenosine kinase [Physcomitrella patens]

Seq. No.	50860
Seq. ID	trc700565062.h1
Method	BLASTX
NCBI GI	g2462754
BLAST score	263
E value	3.0e-23
Match length	87
% identity	56
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	50861
Seq. ID	trc700565074.h1
Method	BLASTN
NCBI GI	g310560
BLAST score	141
E value	1.0e-73
Match length	253
% identity	89
NCBI Description	Soybean ascorbate peroxidase mRNA, complete cds

Seq. No.	50862
Seq. ID	trc700565156.h1
Method	BLASTX
NCBI GI	g4567265
BLAST score	244
E value	3.0e-21
Match length	54
% identity	85
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	50863
Seq. ID	trc700565158.h1
Method	BLASTX
NCBI GI	g3212869
BLAST score	107
E value	3.0e-09
Match length	57
% identity	49
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	50864

Seq. ID	trc700565166.h1
Method	BLASTN
NCBI GI	g2668743
BLAST score	66
E value	8.0e-29
Match length	154
% identity	86
NCBI Description	Zea mays ubiquitin conjugating enzyme (UBC) mRNA, complete cds

Seq. No.	50865
Seq. ID	trc700565220.h1
Method	BLASTX
NCBI GI	g2982462
BLAST score	157
E value	7.0e-11
Match length	83
% identity	55
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	50866
Seq. ID	trc700565223.h1
Method	BLASTX
NCBI GI	g2558654
BLAST score	261
E value	5.0e-23
Match length	71
% identity	72
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	50867
Seq. ID	trc700565227.h1
Method	BLASTX
NCBI GI	g2281100
BLAST score	140
E value	4.0e-09
Match length	62
% identity	45
NCBI Description	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	50868
Seq. ID	trc700565253.h1
Method	BLASTX
NCBI GI	g3913008
BLAST score	100
E value	9.0e-10
Match length	59
% identity	55
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	50869
Seq. ID	trc700565295.h1
Method	BLASTN
NCBI GI	g395078

BLAST score	90
E value	3.0e-43
Match length	134
% identity	92
NCBI Description	B.rapa ubiquitin and ribosomal protein mRNA, complete CDS's

Seq. No.	50870
Seq. ID	trc700565345.h1
Method	BLASTX
NCBI GI	g1931655
BLAST score	268
E value	8.0e-24
Match length	94
% identity	54
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	50871
Seq. ID	trc700565387.h1
Method	BLASTX
NCBI GI	g2660674
BLAST score	154
E value	2.0e-10
Match length	30
% identity	87
NCBI Description	(AC002342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50872
Seq. ID	trc700565433.h1
Method	BLASTX
NCBI GI	g2501148
BLAST score	127
E value	3.0e-15
Match length	75
% identity	58
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_3876335_emb_CAB02099_ (Z79754) similar to TCTP protein; cDNA EST EMBL:D71034 comes from this gene; cDNA EST EMBL:D71224 comes from this gene; cDNA EST EMBL:D71479 comes from this gene; cDNA EST EMBL:D71692 comes from this gene; cDNA EST EMBL:D72340

Seq. No.	50873
Seq. ID	trc700565440.h1
Method	BLASTX
NCBI GI	g2708745
BLAST score	187
E value	2.0e-14
Match length	43
% identity	81
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	50874
Seq. ID	trc700565442.h1
Method	BLASTN
NCBI GI	g2598656
BLAST score	51

E value	4.0e-20
Match length	90
% identity	90
NCBI Description	Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.	50875
Seq. ID	trc700565466.h1
Method	BLASTX
NCBI GI	g4262154
BLAST score	151
E value	5.0e-22
Match length	83
% identity	72
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No.	50876
Seq. ID	trc700565486.h1
Method	BLASTX
NCBI GI	g3461846
BLAST score	171
E value	2.0e-23
Match length	87
% identity	32
NCBI Description	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	50877
Seq. ID	trc700565493.h1
Method	BLASTX
NCBI GI	g3834310
BLAST score	231
E value	9.0e-20
Match length	47
% identity	89
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	50878
Seq. ID	trc700565495.h1
Method	BLASTX
NCBI GI	g423988
BLAST score	136
E value	1.0e-08
Match length	46
% identity	57
NCBI Description	serine/threonine kinase homolog PRO25 - Arabidopsis thaliana >gi_166813 (L04999) serine threonine kinase [Arabidopsis thaliana]

Seq. No.	50879
Seq. ID	trc700565540.h1
Method	BLASTX
NCBI GI	g3075397
BLAST score	287

E value	5.0e-26
Match length	79
% identity	70
NCBI Description	(AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50880
Seq. ID	trc700565618.h1
Method	BLASTX
NCBI GI	g3885334
BLAST score	198
E value	2.0e-26
Match length	93
% identity	71
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	50881
Seq. ID	trc700565652.h1
Method	BLASTX
NCBI GI	g2651308
BLAST score	141
E value	6.0e-09
Match length	35
% identity	83
NCBI Description	(AC002336) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	50882
Seq. ID	trc700565663.h1
Method	BLASTX
NCBI GI	g2829912
BLAST score	184
E value	3.0e-14
Match length	47
% identity	74
NCBI Description	(AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]

Seq. No.	50883
Seq. ID	trc700565670.h1
Method	BLASTX
NCBI GI	g4510400
BLAST score	198
E value	2.0e-29
Match length	89
% identity	80
NCBI Description	(AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis thaliana]

Seq. No.	50884
Seq. ID	trc700565706.h1
Method	BLASTX
NCBI GI	g1871187
BLAST score	250
E value	5.0e-22
Match length	64
% identity	70

NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	50885
Seq. ID	trc700565743.h1
Method	BLASTX
NCBI GI	g4006884
BLAST score	255
E value	3.0e-25
Match length	86
% identity	73
NCBI Description	(Z99707) BEL1-like homeodomain protein [Arabidopsis thaliana]

Seq. No.	50886
Seq. ID	trc700565793.h1
Method	BLASTX
NCBI GI	g3080420
BLAST score	291
E value	2.0e-26
Match length	92
% identity	64
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	50887
Seq. ID	trc700565837.h1
Method	BLASTX
NCBI GI	g4263507
BLAST score	176
E value	6.0e-13
Match length	84
% identity	38
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	50888
Seq. ID	trc700565874.h1
Method	BLASTX
NCBI GI	g3928084
BLAST score	267
E value	1.0e-23
Match length	58
% identity	76
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]

Seq. No.	50889
Seq. ID	trc700565889.h1
Method	BLASTX
NCBI GI	g2827631
BLAST score	317
E value	2.0e-32
Match length	99
% identity	47
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	50890
Seq. ID	trc700565970.h1

Method	BLASTX
NCBI GI	g3925277
BLAST score	215
E value	1.0e-17
Match length	93
% identity	46
NCBI Description	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	50891
Seq. ID	trc700566022.h1
Method	BLASTX
NCBI GI	g4220534
BLAST score	322
E value	4.0e-30
Match length	91
% identity	63
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	50892
Seq. ID	trc700566084.h1
Method	BLASTN
NCBI GI	g4324966
BLAST score	171
E value	2.0e-91
Match length	188
% identity	98
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No.	50893
Seq. ID	trc700566276.h1
Method	BLASTX
NCBI GI	g2829927
BLAST score	178
E value	2.0e-13
Match length	59
% identity	63
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	50894
Seq. ID	trc700566309.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	87
E value	2.0e-41
Match length	181
% identity	87
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	50895
Seq. ID	trc700566342.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	257
E value	1.0e-143

Match length	277
% identity	98
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	50896
Seq. ID	trc700566362.h1
Method	BLASTN
NCBI GI	g1665818
BLAST score	70
E value	3.0e-31
Match length	201
% identity	85
NCBI Description	Human mRNA for KIAA0277 gene, complete cds

Seq. No.	50897
Seq. ID	trc700566412.h1
Method	BLASTN
NCBI GI	g169988
BLAST score	243
E value	1.0e-134
Match length	276
% identity	100
NCBI Description	Glycine max NADP-specific isocitrate dehydrogenase (idh1) mRNA, 3' end

Seq. No.	50898
Seq. ID	trc700566431.h1
Method	BLASTX
NCBI GI	g1083069
BLAST score	258
E value	6.0e-23
Match length	65
% identity	68
NCBI Description	triacylglycerol lipase (EC 3.1.1.3) PGE precursor - bovine >gi_600757 (L26319) pregastric esterase [Bos taurus]

Seq. No.	50899
Seq. ID	trc700566543.h1
Method	BLASTX
NCBI GI	g1946366
BLAST score	183
E value	8.0e-14
Match length	95
% identity	41
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	50900
Seq. ID	trc700566572.h1
Method	BLASTX
NCBI GI	g3892045
BLAST score	253
E value	5.0e-22
Match length	54
% identity	81
NCBI Description	(AC002330) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	50901
Seq. ID	trc700566655.h1
Method	BLASTN
NCBI GI	g206451
BLAST score	198
E value	1.0e-107
Match length	251
% identity	95
NCBI Description	rat prostatein subunit c3, mrna

Seq. No.	50902
Seq. ID	trc700566662.h1
Method	BLASTX
NCBI GI	g4006867
BLAST score	240
E value	8.0e-21
Match length	52
% identity	88
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	50903
Seq. ID	trc700566676.h1
Method	BLASTX
NCBI GI	g2497541
BLAST score	123
E value	4.0e-13
Match length	69
% identity	59
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_482936_emb_CAA82222_ (Z28373) pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	50904
Seq. ID	trc700566725.h1
Method	BLASTN
NCBI GI	g1279232
BLAST score	38
E value	4.0e-12
Match length	217
% identity	16
NCBI Description	C.arietinum mRNA for proline rich protein

Seq. No.	50905
Seq. ID	trc700566785.h1
Method	BLASTX
NCBI GI	g3176711
BLAST score	264
E value	2.0e-23
Match length	86
% identity	59
NCBI Description	(AC002392) bZIP-like protein [Arabidopsis thaliana]

Seq. No.	50906
Seq. ID	trc700566822.h1
Method	BLASTN
NCBI GI	g644492
BLAST score	125

E value	5.0e-64
Match length	200
% identity	91
NCBI Description	Corn elongation factor 1alpha gene, complete cds

Seq. No.	50907
Seq. ID	trc700566867.h1
Method	BLASTX
NCBI GI	g2529686
BLAST score	246
E value	3.0e-21
Match length	49
% identity	90
NCBI Description	(AC002535) putative G-beta-repeat containing protein, 5' partial [Arabidopsis thaliana]

Seq. No.	50908
Seq. ID	trc700567008.h1
Method	BLASTX
NCBI GI	g3128187
BLAST score	290
E value	2.0e-26
Match length	97
% identity	58
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	50909
Seq. ID	trc700567131.h1
Method	BLASTX
NCBI GI	g3046815
BLAST score	134
E value	6.0e-18
Match length	61
% identity	75
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	50910
Seq. ID	trc700567137.h1
Method	BLASTX
NCBI GI	g3281868
BLAST score	237
E value	2.0e-20
Match length	50
% identity	84
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	50911
Seq. ID	trc700567177.h1
Method	BLASTX
NCBI GI	g2129953
BLAST score	173
E value	6.0e-13
Match length	42
% identity	71
NCBI Description	laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542) diphenol oxidase [Nicotiana tabacum]

Seq. No.	50912
Seq. ID	trc700567193.h1
Method	BLASTX
NCBI GI	g4539324
BLAST score	195
E value	3.0e-15
Match length	74
% identity	62
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	50913
Seq. ID	trc700567372.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	252
E value	1.0e-140
Match length	292
% identity	97
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	50914
Seq. ID	trc700567378.h1
Method	BLASTX
NCBI GI	g4220537
BLAST score	287
E value	5.0e-26
Match length	65
% identity	77
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	50915
Seq. ID	trc700567515.h1
Method	BLASTX
NCBI GI	g4467147
BLAST score	227
E value	4.0e-19
Match length	59
% identity	76
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	50916
Seq. ID	trc700567529.h1
Method	BLASTN
NCBI GI	g440856
BLAST score	37
E value	2.0e-11
Match length	53
% identity	92
NCBI Description	Rice mitochondrion DNA for ATPase subunit 6 and ORFs, complete cds

Seq. No.	50917
Seq. ID	trc700567711.h1
Method	BLASTN
NCBI GI	g4406805
BLAST score	45
E value	3.0e-16

Match length	85
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	50918
Seq. ID	trc700567730.h1
Method	BLASTX
NCBI GI	g2842493
BLAST score	356
E value	3.0e-40
Match length	96
% identity	85
NCBI Description	(AL021749) predicted protein [Arabidopsis thaliana]

Seq. No.	50919
Seq. ID	trc700567764.h1
Method	BLASTN
NCBI GI	g1220521
BLAST score	84
E value	5.0e-40
Match length	108
% identity	94
NCBI Description	Glycine max TATA-box binding protein (STBP1) mRNA, complete cds

Seq. No.	50920
Seq. ID	trc700567812.h1
Method	BLASTX
NCBI GI	g4220523
BLAST score	246
E value	3.0e-21
Match length	93
% identity	54
NCBI Description	(AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No.	50921
Seq. ID	trc700567825.h1
Method	BLASTX
NCBI GI	g2642648
BLAST score	233
E value	1.0e-36
Match length	87
% identity	94
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	50922
Seq. ID	trc700567840.h1
Method	BLASTN
NCBI GI	g2924653
BLAST score	71
E value	8.0e-32
Match length	188
% identity	34

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.	50923
Seq. ID	trc700567895.h1
Method	BLASTX
NCBI GI	g3426064
BLAST score	193
E value	4.0e-15
Match length	81
% identity	47
NCBI Description	(AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
Seq. No.	50924
Seq. ID	trc700567951.h1
Method	BLASTN
NCBI GI	g169936
BLAST score	36
E value	2.0e-11
Match length	72
% identity	88
NCBI Description	Glycine max chalcone synthase (chs7) gene, complete cds
Seq. No.	50925
Seq. ID	trc700567963.h1
Method	BLASTX
NCBI GI	g1922242
BLAST score	161
E value	3.0e-11
Match length	58
% identity	55
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.	50926
Seq. ID	trc700568325.h1
Method	BLASTX
NCBI GI	g3935167
BLAST score	208
E value	5.0e-17
Match length	45
% identity	87
NCBI Description	(AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.	50927
Seq. ID	trc700568333.h1
Method	BLASTX
NCBI GI	g2239085
BLAST score	242
E value	1.0e-20
Match length	89
% identity	56
NCBI Description	(Z84384) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]
Seq. No.	50928

09654.9.0.0.0

Seq. ID	trc700568356.h1
Method	BLASTX
NCBI GI	g2494034
BLAST score	212
E value	1.0e-17
Match length	63
% identity	62
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	50929
Seq. ID	trc700568422.h1
Method	BLASTX
NCBI GI	g2462748
BLAST score	234
E value	2.0e-24
Match length	70
% identity	89
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	50930
Seq. ID	trc700568659.h1
Method	BLASTN
NCBI GI	g829118
BLAST score	85
E value	2.0e-40
Match length	144
% identity	90
NCBI Description	P.vulgaris gene for cyclophilin

Seq. No.	50931
Seq. ID	txt700731392.h1
Method	BLASTX
NCBI GI	g2459435
BLAST score	185
E value	3.0e-14
Match length	63
% identity	59
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	50932
Seq. ID	txt700731443.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	248
E value	1.0e-137
Match length	248
% identity	100
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	50933
Seq. ID	txt700731520.h1
Method	BLASTN

NCBI GI	g256428
BLAST score	202
E value	1.0e-110
Match length	250
% identity	97
NCBI Description	KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and Forrest, mRNA, 1259 nt]

Seq. No.	50934
Seq. ID	txt700731528.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	245
E value	1.0e-135
Match length	249
% identity	100
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	50935
Seq. ID	txt700731604.h1
Method	BLASTN
NCBI GI	g4097895
BLAST score	122
E value	3.0e-62
Match length	134
% identity	98
NCBI Description	Glycine max napin-type 2S albumin 3 mRNA, complete cds

Seq. No.	50936
Seq. ID	txt700731616.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	263
E value	1.0e-146
Match length	263
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	50937
Seq. ID	txt700731617.h1
Method	BLASTN
NCBI GI	g736001
BLAST score	82
E value	2.0e-38
Match length	134
% identity	99
NCBI Description	G.soja (SH1) Gy5 mRNA for glycinin

Seq. No.	50938
Seq. ID	txt700731674.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	201
E value	1.0e-109
Match length	209
% identity	99

NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin
Seq. No.	50939
Seq. ID	txt700731703.h1
Method	BLASTN
NCBI GI	g2108433
BLAST score	138
E value	8.0e-72
Match length	277
% identity	88
NCBI Description	Phaseolus vulgaris gibberellin 20-oxidase mRNA, complete cds
Seq. No.	50940
Seq. ID	txt700731786.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	117
E value	3.0e-59
Match length	243
% identity	88
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds
Seq. No.	50941
Seq. ID	txt700731804.h1
Method	BLASTN
NCBI GI	g1946328
BLAST score	62
E value	2.0e-26
Match length	110
% identity	89
NCBI Description	Nicotiana tabacum prohibitin mRNA, complete cds
Seq. No.	50942
Seq. ID	txt700731830.h1
Method	BLASTX
NCBI GI	g2244826
BLAST score	158
E value	3.0e-14
Match length	80
% identity	56
NCBI Description	(Z97336) replication control protein homolog [Arabidopsis thaliana]
Seq. No.	50943
Seq. ID	txt700731843.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	147
E value	3.0e-77
Match length	240
% identity	91
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	50944
Seq. ID	txt700731845.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	257
E value	1.0e-143
Match length	257
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	50945
Seq. ID	txt700731864.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	240
E value	1.0e-132
Match length	274
% identity	100
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	50946
Seq. ID	txt700731961.h1
Method	BLASTN
NCBI GI	g18638
BLAST score	76
E value	3.0e-35
Match length	96
% identity	95
NCBI Description	Soybean Gy3 gene for glycinin subunit G3

Seq. No.	50947
Seq. ID	txt700732027.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	208
E value	1.0e-113
Match length	219
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	50948
Seq. ID	txt700732039.h1
Method	BLASTX
NCBI GI	g122007
BLAST score	189
E value	1.0e-14
Match length	38
% identity	97
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	50949
Seq. ID	txt700732134.h1
Method	BLASTX
NCBI GI	g1076685
BLAST score	220

E value	2.0e-18
Match length	56
% identity	36
NCBI Description	SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ (D30038) SPF1 protein [Ipomoea batatas]

Seq. No.	50950
Seq. ID	txt700732139.h1
Method	BLASTN
NCBI GI	g4249567
BLAST score	235
E value	1.0e-129
Match length	259
% identity	98
NCBI Description	Glycine max A5A4B3 glycinin gene, complete cds

Seq. No.	50951
Seq. ID	txt700732183.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	213
E value	1.0e-116
Match length	241
% identity	97
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	50952
Seq. ID	txt700732190.h1
Method	BLASTX
NCBI GI	g2281115
BLAST score	321
E value	4.0e-30
Match length	81
% identity	75
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	50953
Seq. ID	txt700732219.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	191
E value	1.0e-103
Match length	257
% identity	98
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	50954
Seq. ID	txt700732312.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	243
E value	1.0e-134
Match length	251
% identity	99

NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds
Seq. No.	50955
Seq. ID	txt700732326.h1
Method	BLASTX
NCBI GI	g3738332
BLAST score	233
E value	8.0e-20
Match length	82
% identity	52
NCBI Description	(AC005170) putative eukaryotic initiation factor [Arabidopsis thaliana]
Seq. No.	50956
Seq. ID	txt700732346.h1
Method	BLASTX
NCBI GI	g1495251
BLAST score	309
E value	1.0e-28
Match length	72
% identity	78
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.	50957
Seq. ID	txt700732358.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	237
E value	1.0e-131
Match length	245
% identity	99
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]
Seq. No.	50958
Seq. ID	txt700732428.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	157
E value	3.0e-83
Match length	157
% identity	100
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds
Seq. No.	50959
Seq. ID	txt700732448.h1
Method	BLASTN
NCBI GI	g4056476
BLAST score	50
E value	2.0e-19
Match length	90
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	50960

Seq. ID	txt700732519.h1
Method	BLASTX
NCBI GI	g3046696
BLAST score	399
E value	3.0e-39
Match length	86
% identity	86
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	50961
Seq. ID	txt700732602.h1
Method	BLASTX
NCBI GI	g3395938
BLAST score	260
E value	4.0e-23
Match length	56
% identity	45
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	50962
Seq. ID	txt700732603.h1
Method	BLASTN
NCBI GI	g736001
BLAST score	197
E value	1.0e-107
Match length	201
% identity	100
NCBI Description	G.soja (SH1) Gy5 mRNA for glycinin

Seq. No.	50963
Seq. ID	txt700732890.h1
Method	BLASTN
NCBI GI	g4249567
BLAST score	213
E value	1.0e-116
Match length	237
% identity	97
NCBI Description	Glycine max A5A4B3 glycinin gene, complete cds

Seq. No.	50964
Seq. ID	txt700732904.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	251
E value	1.0e-139
Match length	251
% identity	100
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	50965
Seq. ID	txt700732906.h1
Method	BLASTN
NCBI GI	g2924257
BLAST score	54
E value	1.0e-21
Match length	141

% identity	84
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	50966
Seq. ID	txt700732945.h1
Method	BLASTN
NCBI GI	g167227
BLAST score	158
E value	9.0e-84
Match length	242
% identity	91
NCBI Description	Canavalia ensiformis urease (ure) mRNA, complete cds

Seq. No.	50967
Seq. ID	txt700732965.h1
Method	BLASTN
NCBI GI	g18608
BLAST score	252
E value	1.0e-140
Match length	252
% identity	100
NCBI Description	Glycine max mRNA for glycinin >gi_2170693_dbj_E02462_E02462 cDNA encoding glycinine subunit A2B1a precursor

Seq. No.	50968
Seq. ID	txt700732982.h1
Method	BLASTX
NCBI GI	g3063710
BLAST score	294
E value	5.0e-27
Match length	67
% identity	76
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	50969
Seq. ID	txt700732983.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	239
E value	1.0e-132
Match length	247
% identity	99
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	50970
Seq. ID	txt700732991.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	241
E value	1.0e-133
Match length	241
% identity	100
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	50971
Seq. ID	txt700733025.h1

Method	BLASTN
NCBI GI	g256634
BLAST score	201
E value	1.0e-109
Match length	228
% identity	49
NCBI Description	KTi1=Kunitz trypsin inhibitor KTi1, KTi2=Kunitz trypsin inhibitor KTi2 [soybeans, Genomic, 3269 nt]

Seq. No.	50972
Seq. ID	txt700733027.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	196
E value	1.0e-106
Match length	211
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	50973
Seq. ID	txt700733049.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	229
E value	1.0e-126
Match length	244
% identity	99
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	50974
Seq. ID	txt700733055.h1
Method	BLASTX
NCBI GI	g4432846
BLAST score	194
E value	5.0e-16
Match length	51
% identity	90
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	50975
Seq. ID	txt700733065.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	193
E value	1.0e-104
Match length	204
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	50976
Seq. ID	txt700733071.h1
Method	BLASTN
NCBI GI	g18634
BLAST score	186
E value	1.0e-100
Match length	241
% identity	95

NCBI Description	Soybean Gy1 gene for glycinin subunit G1
Seq. No.	50977
Seq. ID	txt700733106.h1
Method	BLASTN
NCBI GI	g736001
BLAST score	270
E value	1.0e-150
Match length	270
% identity	100
NCBI Description	G.soja (SH1) Gy5 mRNA for glycinin
Seq. No.	50978
Seq. ID	txt700733146.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	223
E value	1.0e-122
Match length	247
% identity	98
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase
Seq. No.	50979
Seq. ID	txt700733165.h1
Method	BLASTN
NCBI GI	g1046277
BLAST score	95
E value	4.0e-46
Match length	193
% identity	87
NCBI Description	Phaseolus vulgaris embryo-specific acidic transcriptional activator PvAlf mRNA, complete cds
Seq. No.	50980
Seq. ID	txt700733184.h1
Method	BLASTN
NCBI GI	g1008880
BLAST score	43
E value	4.0e-15
Match length	55
% identity	95
NCBI Description	Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5) gene, complete cds
Seq. No.	50981
Seq. ID	txt700733187.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	175
E value	6.0e-94
Match length	247
% identity	93
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor
Seq. No.	50982

Seq. ID	txt700733235.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	130
E value	4.0e-67
Match length	206
% identity	91
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	50983
Seq. ID	txt700733257.h1
Method	BLASTN
NCBI GI	g2305019
BLAST score	245
E value	1.0e-135
Match length	245
% identity	100
NCBI Description	Glycine max 2S albumin pre-propeptide mRNA, complete cds

Seq. No.	50984
Seq. ID	txt700733264.h1
Method	BLASTX
NCBI GI	g4455276
BLAST score	144
E value	2.0e-09
Match length	45
% identity	56
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	50985
Seq. ID	txt700733269.h1
Method	BLASTN
NCBI GI	g18636
BLAST score	123
E value	4.0e-63
Match length	163
% identity	94
NCBI Description	Soybean Gy2 gene for glycinin subunit G2

Seq. No.	50986
Seq. ID	txt700733290.h1
Method	BLASTN
NCBI GI	g288618
BLAST score	100
E value	3.0e-49
Match length	120
% identity	96
NCBI Description	G.max GB-D-II gene for proteinase inhibitor D-II

Seq. No.	50987
Seq. ID	txt700733371.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	236
E value	1.0e-130
Match length	244

% identity	99
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	50988
Seq. ID	txt700733377.h1
Method	BLASTN
NCBI GI	g747967
BLAST score	128
E value	7.0e-66
Match length	215
% identity	93
NCBI Description	Glycine max glutamate 1-semialdehyde aminotransferase (Gsa1) gene, complete cds

Seq. No.	50989
Seq. ID	txt700733382.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	168
E value	9.0e-90
Match length	248
% identity	100
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	50990
Seq. ID	txt700733405.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	164
E value	2.0e-87
Match length	188
% identity	97
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	50991
Seq. ID	txt700733461.h1
Method	BLASTX
NCBI GI	g3334280
BLAST score	201
E value	5.0e-16
Match length	68
% identity	56
NCBI Description	OLEOSIN 16 KD (OSE701) >gi_1171352 (U43930) 16 kDa oleosin [Oryza sativa]

Seq. No.	50992
Seq. ID	txt700733463.h1
Method	BLASTN
NCBI GI	g3241923
BLAST score	54
E value	1.0e-21
Match length	131
% identity	46
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	50993
Seq. ID	txt700733472.h1
Method	BLASTX
NCBI GI	g4468990
BLAST score	277
E value	2.0e-25
Match length	83
% identity	75
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	50994
Seq. ID	txt700733488.h1
Method	BLASTN
NCBI GI	g18640
BLAST score	257
E value	1.0e-143
Match length	257
% identity	83
NCBI Description	G.max Gy4 gene for glycinin

Seq. No.	50995
Seq. ID	txt700733503.h1
Method	BLASTN
NCBI GI	g18676
BLAST score	137
E value	3.0e-71
Match length	248
% identity	92
NCBI Description	Soybean lox-3 gene for seed lipoxygenase-3 gene (EC 1.13.11.12)

Seq. No.	50996
Seq. ID	txt700733554.h1
Method	BLASTN
NCBI GI	g18542
BLAST score	137
E value	3.0e-71
Match length	198
% identity	100
NCBI Description	Soybean Bg gene for basic 7S globulin

Seq. No.	50997
Seq. ID	txt700733621.h1
Method	BLASTX
NCBI GI	g4185599
BLAST score	142
E value	4.0e-09
Match length	71
% identity	45
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	50998
Seq. ID	txt700733647.h1
Method	BLASTN
NCBI GI	g169928
BLAST score	249

E value	1.0e-138
Match length	253
% identity	100
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A

Seq. No.	50999
Seq. ID	txt700733682.h1
Method	BLASTN
NCBI GI	g555890
BLAST score	259
E value	1.0e-144
Match length	259
% identity	100
NCBI Description	Glycine max 7S storage protein alpha subunit mRNA, complete cds

Seq. No.	51000
Seq. ID	txt700733713.h1
Method	BLASTX
NCBI GI	g585973
BLAST score	218
E value	5.0e-18
Match length	70
% identity	81
NCBI Description	FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A fructokinase [Solanum tuberosum]

Seq. No.	51001
Seq. ID	txt700733781.h1
Method	BLASTX
NCBI GI	g4455232
BLAST score	163
E value	9.0e-12
Match length	42
% identity	76
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	51002
Seq. ID	txt700733804.h1
Method	BLASTN
NCBI GI	g4097895
BLAST score	240
E value	1.0e-132
Match length	252
% identity	99
NCBI Description	Glycine max napin-type 2S albumin 3 mRNA, complete cds

Seq. No.	51003
Seq. ID	txt700733810.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	229
E value	1.0e-126
Match length	255

% identity	98
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	51004
Seq. ID	txt700733848.h1
Method	BLASTX
NCBI GI	g1663648
BLAST score	147
E value	1.0e-09
Match length	73
% identity	45
NCBI Description	(U75321) chromaffin granule ATPase II homolog [Mus musculus]

Seq. No.	51005
Seq. ID	txt700733889.h1
Method	BLASTN
NCBI GI	g944829
BLAST score	143
E value	8.0e-75
Match length	240
% identity	97
NCBI Description	G.max mRNA for 24 kDa oleosin isoform (clone P24/91)

Seq. No.	51006
Seq. ID	txt700733961.h1
Method	BLASTN
NCBI GI	g11576
BLAST score	253
E value	1.0e-140
Match length	257
% identity	100
NCBI Description	Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NADH dehydrogenase and ORF

Seq. No.	51007
Seq. ID	txt700734056.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	238
E value	1.0e-131
Match length	258
% identity	98
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	51008
Seq. ID	txt700734061.h1
Method	BLASTX
NCBI GI	g4204095
BLAST score	275
E value	1.0e-24
Match length	73
% identity	68
NCBI Description	(AF030260) CYP94A1 [Vicia sativa]

Seq. No. 51009

Seq. ID	txt700734135.h1
Method	BLASTN
NCBI GI	g1732555
BLAST score	39
E value	4.0e-13
Match length	67
% identity	99
NCBI Description	Glycine max desiccation protective protein LEA5 (Lea5) mRNA, complete cds

Seq. No.	51010
Seq. ID	txt700734181.h1
Method	BLASTN
NCBI GI	g1431744
BLAST score	76
E value	4.0e-35
Match length	100
% identity	94
NCBI Description	Glycine max sucrose binding protein (sbp) mRNA, complete cds

Seq. No.	51011
Seq. ID	txt700734243.h1
Method	BLASTN
NCBI GI	g806555
BLAST score	160
E value	5.0e-85
Match length	224
% identity	93
NCBI Description	G.soja mRNA for glycinin

Seq. No.	51012
Seq. ID	txt700734306.h1
Method	BLASTX
NCBI GI	g3738332
BLAST score	196
E value	1.0e-15
Match length	72
% identity	54
NCBI Description	(AC005170) putative eukaryotic initiation factor [Arabidopsis thaliana]

Seq. No.	51013
Seq. ID	txt700734320.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	127
E value	2.0e-65
Match length	127
% identity	100
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	51014
Seq. ID	txt700734338.h1
Method	BLASTN
NCBI GI	g1199562
BLAST score	69

E value	5.0e-31
Match length	118
% identity	95
NCBI Description	Glycine max 34 kDa maturing seed vacuolar thiol protease mRNA, complete cds

Seq. No.	51015
Seq. ID	txt700734350.h1
Method	BLASTN
NCBI GI	g18614
BLAST score	152
E value	3.0e-80
Match length	198
% identity	95
NCBI Description	Soybean mRNA for glycinin A1aBx precursor >gi_2170694_dbj_E02463_E02463 cDNA encoding glycinine subunit A1aB1b precursor

Seq. No.	51016
Seq. ID	txt700734354.h1
Method	BLASTN
NCBI GI	g18640
BLAST score	149
E value	1.0e-78
Match length	168
% identity	97
NCBI Description	G.max Gy4 gene for glycinin

Seq. No.	51017
Seq. ID	txt700734365.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	146
E value	1.0e-76
Match length	157
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	51018
Seq. ID	txt700734371.h1
Method	BLASTN
NCBI GI	g169928
BLAST score	94
E value	1.0e-45
Match length	203
% identity	88
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A

Seq. No.	51019
Seq. ID	txt700734373.h1
Method	BLASTN
NCBI GI	g170005
BLAST score	169
E value	2.0e-90
Match length	241
% identity	93

NCBI Description	Soybean lectin (Le1) gene, complete cds
Seq. No.	51020
Seq. ID	txt700734381.h1
Method	BLASTX
NCBI GI	g3451074
BLAST score	269
E value	3.0e-24
Match length	56
% identity	86
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]
Seq. No.	51021
Seq. ID	txt700734423.h1
Method	BLASTN
NCBI GI	g887572
BLAST score	66
E value	7.0e-29
Match length	227
% identity	86
NCBI Description	P.sativum mRNA for starch synthase (2988 bp)
Seq. No.	51022
Seq. ID	txt700734455.h1
Method	BLASTX
NCBI GI	g2507455
BLAST score	218
E value	4.0e-18
Match length	52
% identity	79
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]
Seq. No.	51023
Seq. ID	txt700734555.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	215
E value	1.0e-118
Match length	247
% identity	97
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds
Seq. No.	51024
Seq. ID	txt700734571.h1
Method	BLASTN
NCBI GI	g2598656
BLAST score	163
E value	9.0e-87
Match length	247
% identity	91
NCBI Description	Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
Seq. No.	51025

Seq. ID	txt700734574.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	229
E value	1.0e-126
Match length	249
% identity	27
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	51026
Seq. ID	txt700734647.h1
Method	BLASTN
NCBI GI	g2598656
BLAST score	152
E value	3.0e-80
Match length	239
% identity	91
NCBI Description	Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.	51027
Seq. ID	txt700734728.h1
Method	BLASTX
NCBI GI	g515616
BLAST score	377
E value	1.0e-36
Match length	77
% identity	92
NCBI Description	(X61608) LHC II Type III chlorophyll a /b binding protein [Brassica napus]

Seq. No.	51028
Seq. ID	txt700734744.h1
Method	BLASTX
NCBI GI	g2462753
BLAST score	182
E value	9.0e-14
Match length	66
% identity	49
NCBI Description	(AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	51029
Seq. ID	txt700734747.h1
Method	BLASTX
NCBI GI	g2558664
BLAST score	331
E value	3.0e-31
Match length	85
% identity	75
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51030
Seq. ID	txt700734756.h1
Method	BLASTX
NCBI GI	g2459448
BLAST score	139
E value	9.0e-12

Match length	66
% identity	64
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	51031
Seq. ID	txt700734774.h1
Method	BLASTX
NCBI GI	g4204308
BLAST score	433
E value	3.0e-43
Match length	89
% identity	84
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	51032
Seq. ID	txt700734788.h1
Method	BLASTX
NCBI GI	g3413719
BLAST score	227
E value	5.0e-19
Match length	65
% identity	69
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643592 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	51033
Seq. ID	txt700734849.h1
Method	BLASTX
NCBI GI	g3935173
BLAST score	252
E value	5.0e-22
Match length	61
% identity	64
NCBI Description	(AC004557) F17L21.16 [Arabidopsis thaliana]

Seq. No.	51034
Seq. ID	txt700734874.h1
Method	BLASTN
NCBI GI	g256428
BLAST score	124
E value	2.0e-63
Match length	145
% identity	97
NCBI Description	KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and Forrest, mRNA, 1259 nt]

Seq. No.	51035
Seq. ID	txt700734890.h1
Method	BLASTN
NCBI GI	g1173643
BLAST score	98
E value	5.0e-48
Match length	98
% identity	100

NCBI Description	Glycine max lipoxygenase (lox8) mRNA, partial cds
Seq. No.	51036
Seq. ID	txt700734907.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	143
E value	7.0e-75
Match length	231
% identity	63
NCBI Description	Glycine max gene for ubiquitin, complete cds
Seq. No.	51037
Seq. ID	txt700734952.h1
Method	BLASTN
NCBI GI	g4097895
BLAST score	229
E value	1.0e-126
Match length	229
% identity	100
NCBI Description	Glycine max napin-type 2S albumin 3 mRNA, complete cds
Seq. No.	51038
Seq. ID	txt700734967.h1
Method	BLASTN
NCBI GI	g169928
BLAST score	143
E value	7.0e-75
Match length	219
% identity	91
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A
Seq. No.	51039
Seq. ID	txt700734987.h1
Method	BLASTN
NCBI GI	g1772307
BLAST score	212
E value	1.0e-116
Match length	228
% identity	98
NCBI Description	Glycine max mRNA for glycinin, complete cds
Seq. No.	51040
Seq. ID	txt700735047.h1
Method	BLASTX
NCBI GI	g3928084
BLAST score	156
E value	8.0e-11
Match length	81
% identity	47
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]
Seq. No.	51041
Seq. ID	txt700735070.h1
Method	BLASTN

NCBI GI	g4097893
BLAST score	74
E value	1.0e-33
Match length	133
% identity	100
NCBI Description	Glycine max napin-type 2S albumin 1 precursor, mRNA, complete cds

Seq. No.	51042
Seq. ID	txt700735081.h1
Method	BLASTN
NCBI GI	g170013
BLAST score	54
E value	9.0e-22
Match length	102
% identity	89
NCBI Description	Soybean lipoxygenase-2 mRNA, complete cds

Seq. No.	51043
Seq. ID	txt700735095.h1
Method	BLASTX
NCBI GI	g4335715
BLAST score	304
E value	4.0e-28
Match length	69
% identity	70
NCBI Description	(AC006248) putative immediate-early salicylate-induced glucosyltransferase [Arabidopsis thaliana]

Seq. No.	51044
Seq. ID	txt700735163.h1
Method	BLASTX
NCBI GI	g2702268
BLAST score	357
E value	2.0e-34
Match length	74
% identity	85
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	51045
Seq. ID	txt700735371.h1
Method	BLASTN
NCBI GI	g476213
BLAST score	72
E value	2.0e-32
Match length	194
% identity	91
NCBI Description	Glycine max Century 84 p24 oleosin isoform A gene, complete cds

Seq. No.	51046
Seq. ID	txt700735374.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	87
E value	2.0e-41
Match length	175

% identity	87
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	51047
Seq. ID	txt700735386.h1
Method	BLASTX
NCBI GI	g2895510
BLAST score	215
E value	1.0e-17
Match length	84
% identity	48
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	51048
Seq. ID	txt700735465.h1
Method	BLASTX
NCBI GI	g4544372
BLAST score	223
E value	1.0e-18
Match length	79
% identity	47
NCBI Description	(AC006920) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	51049
Seq. ID	txt700735481.h1
Method	BLASTX
NCBI GI	g4539420
BLAST score	162
E value	1.0e-11
Match length	66
% identity	58
NCBI Description	(AL049171) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	51050
Seq. ID	txt700735525.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	229
E value	1.0e-126
Match length	249
% identity	98
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	51051
Seq. ID	txt700735543.h1
Method	BLASTX
NCBI GI	g4567227
BLAST score	260
E value	5.0e-23
Match length	82
% identity	59
NCBI Description	(AC007119) putative transport protein [Arabidopsis thaliana]

Seq. No.	51052
Seq. ID	txt700735604.h1
Method	BLASTN
NCBI GI	g1199562
BLAST score	165
E value	6.0e-88
Match length	266
% identity	98
NCBI Description	Glycine max 34 kDa maturing seed vacuolar thiol protease mRNA, complete cds

Seq. No.	51053
Seq. ID	txt700735616.h1
Method	BLASTN
NCBI GI	g4191813
BLAST score	257
E value	1.0e-143
Match length	257
% identity	100
NCBI Description	Glycine max mRNA for alpha' subunit of beta-conglycinin, complete cds

Seq. No.	51054
Seq. ID	txt700735636.h1
Method	BLASTX
NCBI GI	g3451075
BLAST score	190
E value	9.0e-15
Match length	80
% identity	42
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	51055
Seq. ID	txt700735746.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	192
E value	1.0e-104
Match length	192
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	51056
Seq. ID	txt700735748.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	189
E value	1.0e-102
Match length	193
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	51057
Seq. ID	txt700735794.h1
Method	BLASTN
NCBI GI	g18614
BLAST score	191

E value	1.0e-103
Match length	231
% identity	96
NCBI Description	Soybean mRNA for glycinin A1aBx precursor >gi_2170694_dbj_E02463_E02463 cDNA encoding glycinine subunit A1aB1b precursor

Seq. No.	51058
Seq. ID	txt700735796.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	51
E value	6.0e-20
Match length	191
% identity	82
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	51059
Seq. ID	txt700735848.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	232
E value	1.0e-128
Match length	255
% identity	98
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	51060
Seq. ID	txt700735873.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	235
E value	1.0e-129
Match length	250
% identity	99
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	51061
Seq. ID	txt700735889.h1
Method	BLASTX
NCBI GI	g3063448
BLAST score	186
E value	6.0e-18
Match length	82
% identity	60
NCBI Description	(AC003981) F22O13.10 [Arabidopsis thaliana]

Seq. No.	51062
Seq. ID	txt700735923.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	254
E value	1.0e-141
Match length	254
% identity	100

NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase
Seq. No.	51063
Seq. ID	txt700735931.h1
Method	BLASTX
NCBI GI	g3935138
BLAST score	209
E value	5.0e-17
Match length	83
% identity	29
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]
Seq. No.	51064
Seq. ID	txt700735934.h1
Method	BLASTN
NCBI GI	g21981
BLAST score	63
E value	4.0e-27
Match length	181
% identity	88
NCBI Description	V.angustifolia 25S/18S rRNA intergenic spacer DNA
Seq. No.	51065
Seq. ID	txt700736030.h1
Method	BLASTX
NCBI GI	g1743412
BLAST score	223
E value	1.0e-18
Match length	81
% identity	44
NCBI Description	(Y09826) amino acid transporter [Solanum tuberosum]
Seq. No.	51066
Seq. ID	txt700736118.h1
Method	BLASTX
NCBI GI	g3080412
BLAST score	203
E value	2.0e-16
Match length	75
% identity	51
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]
Seq. No.	51067
Seq. ID	txt700736123.h1
Method	BLASTN
NCBI GI	g18542
BLAST score	136
E value	1.0e-70
Match length	196
% identity	100
NCBI Description	Soybean Bg gene for basic 7S globulin
Seq. No.	51068
Seq. ID	txt700736209.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	248

E value	1.0e-137
Match length	256
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	51069
Seq. ID	txt700736227.h1
Method	BLASTN
NCBI GI	g170013
BLAST score	51
E value	3.0e-20
Match length	130
% identity	96
NCBI Description	Soybean lipoxygenase-2 mRNA, complete cds

Seq. No.	51070
Seq. ID	txt700736230.h1
Method	BLASTX
NCBI GI	g2213615
BLAST score	216
E value	8.0e-18
Match length	85
% identity	45
NCBI Description	(AC000103) F21J9.9 [Arabidopsis thaliana]

Seq. No.	51071
Seq. ID	txt700736277.h1
Method	BLASTX
NCBI GI	g229707
BLAST score	303
E value	5.0e-28
Match length	79
% identity	70
NCBI Description	Bean pod mottle virus

Seq. No.	51072
Seq. ID	txt700736290.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	185
E value	1.0e-100
Match length	249
% identity	94
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	51073
Seq. ID	txt700736331.h1
Method	BLASTN
NCBI GI	g4432829
BLAST score	36
E value	5.0e-11
Match length	119
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	51074
Seq. ID	txt700736421.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	186
E value	1.0e-100
Match length	230
% identity	96
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	51075
Seq. ID	txt700736431.h1
Method	BLASTX
NCBI GI	g3329366
BLAST score	141
E value	5.0e-09
Match length	68
% identity	38
NCBI Description	(AF031243) nodule-specific protein Nlj70 [Lotus japonicus]

Seq. No.	51076
Seq. ID	txt700736434.h1
Method	BLASTX
NCBI GI	g1842111
BLAST score	173
E value	1.0e-12
Match length	53
% identity	66
NCBI Description	(U87586) decoy [Arabidopsis thaliana] >gi_1931612 (U93308) decoy [Arabidopsis thaliana]

Seq. No.	51077
Seq. ID	txt700736453.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	182
E value	4.0e-98
Match length	242
% identity	94
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	51078
Seq. ID	txt700736460.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	249
E value	1.0e-138
Match length	249
% identity	100
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	51079
Seq. ID	txt700736495.h1
Method	BLASTN
NCBI GI	g1772307
BLAST score	169

E value	2.0e-90
Match length	221
% identity	94
NCBI Description	Glycine max mRNA for glycinin, complete cds

Seq. No.	51080
Seq. ID	txt700736503.h1
Method	BLASTN
NCBI GI	g1772305
BLAST score	225
E value	1.0e-124
Match length	245
% identity	98
NCBI Description	Glycine max mRNA for glycinin, complete cds

Seq. No.	51081
Seq. ID	txt700736566.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	230
E value	1.0e-127
Match length	238
% identity	99
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	51082
Seq. ID	txt700736570.h1
Method	BLASTN
NCBI GI	g169903
BLAST score	235
E value	1.0e-130
Match length	235
% identity	100
NCBI Description	soybean 7s seed storage protein alpha subunit mrna (c), from gmc-alpha'-alpha 21

Seq. No.	51083
Seq. ID	txt700736572.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	192
E value	1.0e-104
Match length	192
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	51084
Seq. ID	txt700736615.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	181
E value	2.0e-97
Match length	185
% identity	99
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No. 51085

Seq. ID	txt700736655.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	92
E value	2.0e-44
Match length	160
% identity	89
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	51086
Seq. ID	txt700736690.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	192
E value	1.0e-104
Match length	196
% identity	99
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	51087
Seq. ID	txt700736807.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	231
E value	1.0e-127
Match length	251
% identity	98
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	51088
Seq. ID	txt700736822.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	227
E value	1.0e-125
Match length	247
% identity	98
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	51089
Seq. ID	txt700736845.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	396
E value	6.0e-39
Match length	83
% identity	92
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	51090
Seq. ID	txt700736908.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	208
E value	1.0e-113
Match length	223
% identity	98

NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin
Seq. No.	51091
Seq. ID	txt700736909.h1
Method	BLASTN
NCBI GI	g14311
BLAST score	153
E value	5.0e-81
Match length	160
% identity	99
NCBI Description	G.max chloroplast gene rps19 and flanking regions
Seq. No.	51092
Seq. ID	txt700736929.h1
Method	BLASTX
NCBI GI	g1809127
BLAST score	187
E value	2.0e-14
Match length	64
% identity	56
NCBI Description	(U77674) terminal flower 1 [Arabidopsis thaliana] >gi_2208929_dbj_BAA20483_ (D86932) terminal flower1 [Arabidopsis thaliana] >gi_2208931_dbj_BAA20484_ (D87130) terminal flower1 [Arabidopsis thaliana] >gi_2208933_dbj_BAA20485_ (D87519) terminal flower1 [Arabidopsis thaliana]
Seq. No.	51093
Seq. ID	txt700736931.h1
Method	BLASTX
NCBI GI	g3980380
BLAST score	189
E value	5.0e-30
Match length	88
% identity	77
NCBI Description	(AC004561) putative enolase [Arabidopsis thaliana]
Seq. No.	51094
Seq. ID	txt700736943.h1
Method	BLASTN
NCBI GI	g456567
BLAST score	35
E value	2.0e-10
Match length	39
% identity	97
NCBI Description	Pisum sativum ubiquitin conjugating enzyme (UBC4), complete cds
Seq. No.	51095
Seq. ID	txt700736992.h1
Method	BLASTN
NCBI GI	g3126853
BLAST score	54
E value	1.0e-21
Match length	86
% identity	91
NCBI Description	Oryza sativa chlorophyll a/b binding protein (RCABP89)

	mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	51096
Seq. ID	txt700737005.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	219
E value	1.0e-120
Match length	258
% identity	96
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds
Seq. No.	51097
Seq. ID	txt700737010.h1
Method	BLASTN
NCBI GI	g256428
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and Forrest, mRNA, 1259 nt]
Seq. No.	51098
Seq. ID	txt700737016.h1
Method	BLASTX
NCBI GI	g1169286
BLAST score	142
E value	3.0e-09
Match length	33
% identity	76
NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi_1085671_pir__S49205 betaine-aldehyde dehydrogenase (EC 1.2.1.8) precursor - Atriplex hortensis >gi_510574_emb_CAA49425_ (X69770) betaine-aldehyde dehydrogenase [Atriplex hortensis]
Seq. No.	51099
Seq. ID	txt700737019.h1
Method	BLASTN
NCBI GI	g4191813
BLAST score	257
E value	1.0e-143
Match length	281
% identity	87
NCBI Description	Glycine max mRNA for alpha' subunit of beta-conglycinin, complete cds
Seq. No.	51100
Seq. ID	txt700737034.h1
Method	BLASTN
NCBI GI	g1431744
BLAST score	46
E value	3.0e-17
Match length	74
% identity	92

NCBI Description	Glycine max sucrose binding protein (sbp) mRNA, complete cds

Seq. No.	51101
Seq. ID	txt700737038.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	222
E value	1.0e-122
Match length	278
% identity	95
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	51102
Seq. ID	txt700737081.h1
Method	BLASTX
NCBI GI	g2160692
BLAST score	397
E value	6.0e-39
Match length	93
% identity	73
NCBI Description	(U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	51103
Seq. ID	txt700737102.h1
Method	BLASTN
NCBI GI	g1046277
BLAST score	62
E value	2.0e-26
Match length	78
% identity	95
NCBI Description	Phaseolus vulgaris embryo-specific acidic transcriptional activator PvAlf mRNA, complete cds

Seq. No.	51104
Seq. ID	txt700737131.h1
Method	BLASTN
NCBI GI	g2370311
BLAST score	37
E value	1.0e-11
Match length	97
% identity	85
NCBI Description	Medicago sativa mRNA for DnaJ-like protein

Seq. No.	51105
Seq. ID	txt700737231.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	255
E value	1.0e-141
Match length	255
% identity	86
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No.	51106

Seq. ID	txt700737254.h1
Method	BLASTN
NCBI GI	g169926
BLAST score	220
E value	1.0e-121
Match length	228
% identity	99
NCBI Description	Soybean beta-conglycinin-alpha subunit mRNA, 3' end

Seq. No.	51107
Seq. ID	txt700737412.h1
Method	BLASTN
NCBI GI	g4191813
BLAST score	145
E value	3.0e-76
Match length	153
% identity	99
NCBI Description	Glycine max mRNA for alpha' subunit of beta-conglycinin, complete cds

Seq. No.	51108
Seq. ID	txt700737429.h1
Method	BLASTN
NCBI GI	g18621
BLAST score	47
E value	5.0e-18
Match length	99
% identity	91
NCBI Description	Soybean DNA for glycinin A2B1a subunit

Seq. No.	51109
Seq. ID	txt700737593.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	228
E value	1.0e-125
Match length	236
% identity	99
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	51110
Seq. ID	txt700737605.h1
Method	BLASTN
NCBI GI	g1431744
BLAST score	83
E value	2.0e-39
Match length	111
% identity	94
NCBI Description	Glycine max sucrose binding protein (sbp) mRNA, complete cds

Seq. No.	51111
Seq. ID	txt700737615.h1
Method	BLASTN
NCBI GI	g4191813
BLAST score	100
E value	1.0e-49

Match length	100
% identity	100
NCBI Description	Glycine max mRNA for alpha' subunit of beta-conglycinin, complete cds

Seq. No.	51112
Seq. ID	txt700737622.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	189
E value	1.0e-102
Match length	189
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	51113
Seq. ID	txt700737638.h1
Method	BLASTN
NCBI GI	g18620
BLAST score	197
E value	1.0e-107
Match length	233
% identity	100
NCBI Description	Soybean mRNA fragment for Gy(4) glycinin

Seq. No.	51114
Seq. ID	txt700737677.h1
Method	BLASTN
NCBI GI	g18619
BLAST score	164
E value	1.0e-87
Match length	164
% identity	65
NCBI Description	Soybean mutant Gy(4) glycinin gene (null-allele)

Seq. No.	51115
Seq. ID	uC-gmflminsoy001b06b1
Method	BLASTX
NCBI GI	g2129636
BLAST score	180
E value	7.0e-19
Match length	125
% identity	54
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	51116
Seq. ID	uC-gmflminsoy001e01b1
Method	BLASTX
NCBI GI	g3738297
BLAST score	339
E value	7.0e-32
Match length	100
% identity	26
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	51117

Seq. ID	uC-gmflminsoy001f04b1
Method	BLASTX
NCBI GI	g480618
BLAST score	275
E value	2.0e-24
Match length	68
% identity	78
NCBI Description	ATAF1 protein - Arabidopsis thaliana (fragment) >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No.	51118
Seq. ID	uC-gmflminsoy001f08b1
Method	BLASTX
NCBI GI	g2244847
BLAST score	260
E value	2.0e-22
Match length	80
% identity	64
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	51119
Seq. ID	uC-gmflminsoy001g03b1
Method	BLASTX
NCBI GI	g4559351
BLAST score	151
E value	8.0e-10
Match length	98
% identity	38
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51120
Seq. ID	uC-gmflminsoy001h05b1
Method	BLASTX
NCBI GI	g3461838
BLAST score	316
E value	5.0e-29
Match length	156
% identity	46
NCBI Description	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	51121
Seq. ID	uC-gmflminsoy001h08b1
Method	BLASTX
NCBI GI	g3834310
BLAST score	428
E value	3.0e-42
Match length	86
% identity	98
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No. 51122

Seq. ID	uC-gmflminsoy002a03b1
Method	BLASTN
NCBI GI	g668997
BLAST score	59
E value	1.0e-24
Match length	131
% identity	86
NCBI Description	Medicago sativa polygalacturonase mRNA, complete cds

Seq. No.	51123
Seq. ID	uC-gmflminsoy002b04b1
Method	BLASTN
NCBI GI	g668997
BLAST score	79
E value	2.0e-36
Match length	215
% identity	84
NCBI Description	Medicago sativa polygalacturonase mRNA, complete cds

Seq. No.	51124
Seq. ID	uC-gmflminsoy002b09b1
Method	BLASTX
NCBI GI	g3695023
BLAST score	155
E value	7.0e-11
Match length	62
% identity	45
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	51125
Seq. ID	uC-gmflminsoy002c05b1
Method	BLASTN
NCBI GI	g548320
BLAST score	37
E value	1.0e-11
Match length	41
% identity	98
NCBI Description	Glycine max dihydrodipicolinate synthase (dapA) mRNA, complete cds

Seq. No.	51126
Seq. ID	uC-gmflminsoy003a08b1
Method	BLASTX
NCBI GI	g4558550
BLAST score	522
E value	3.0e-53
Match length	165
% identity	61
NCBI Description	(AC007138) putative protein transport factor [Arabidopsis thaliana]

Seq. No.	51127
Seq. ID	uC-gmflminsoy003c08b1
Method	BLASTX
NCBI GI	g3776559
BLAST score	650
E value	4.0e-68

Match length	168
% identity	67
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	51128
Seq. ID	uC-gmflminsoy003d02b1
Method	BLASTX
NCBI GI	g2465923
BLAST score	253
E value	1.0e-21
Match length	109
% identity	45
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	51129
Seq. ID	uC-gmflminsoy003d05b1
Method	BLASTN
NCBI GI	g4389416
BLAST score	189
E value	1.0e-102
Match length	261
% identity	93
NCBI Description	Glycine max nitrate reductase (nr2) gene, partial cds

Seq. No.	51130
Seq. ID	uC-gmflminsoy003f11b1
Method	BLASTX
NCBI GI	g4006855
BLAST score	614
E value	6.0e-64
Match length	166
% identity	69
NCBI Description	(Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No.	51131
Seq. ID	uC-gmflminsoy003g04b1
Method	BLASTX
NCBI GI	g3641252
BLAST score	593
E value	2.0e-61
Match length	129
% identity	82
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	51132
Seq. ID	uC-gmflminsoy003g07b1
Method	BLASTX
NCBI GI	g2462838
BLAST score	379
E value	2.0e-36
Match length	143

% identity	57
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	51133
Seq. ID	uC-gmflminsoy005b06b1
Method	BLASTX
NCBI GI	g4467130
BLAST score	252
E value	2.0e-31
Match length	128
% identity	60
NCBI Description	(AL035538) glycosyltransferase like protein [Arabidopsis thaliana]

Seq. No.	51134
Seq. ID	uC-gmflminsoy005g07b1
Method	BLASTX
NCBI GI	g4467111
BLAST score	407
E value	6.0e-40
Match length	109
% identity	69
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	51135
Seq. ID	uC-gmflminsoy007d01b1
Method	BLASTX
NCBI GI	g2497742
BLAST score	167
E value	1.0e-11
Match length	52
% identity	52
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi_995907 (U15153) nonspecific lipid transfer protein precursor [Gossypium hirsutum]

Seq. No.	51136
Seq. ID	uC-gmflminsoy007d11b1
Method	BLASTX
NCBI GI	g3805854
BLAST score	434
E value	6.0e-43
Match length	127
% identity	64
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	51137
Seq. ID	uC-gmflminsoy007e01b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	339
E value	7.0e-32
Match length	112
% identity	54
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	51138

Seq. ID	uC-gmflminsoy008a01b1
Method	BLASTX
NCBI GI	g3297823
BLAST score	263
E value	7.0e-23
Match length	120
% identity	47
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	51139
Seq. ID	uC-gmflminsoy008a12b1
Method	BLASTX
NCBI GI	g3193296
BLAST score	224
E value	2.0e-18
Match length	133
% identity	44
NCBI Description	(AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No.	51140
Seq. ID	uC-gmflminsoy008d01b1
Method	BLASTX
NCBI GI	g3024871
BLAST score	396
E value	2.0e-38
Match length	127
% identity	57
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	51141
Seq. ID	uC-gmflminsoy008e05b1
Method	BLASTN
NCBI GI	g1946337
BLAST score	194
E value	1.0e-105
Match length	239
% identity	98
NCBI Description	Glycine max alternative oxidase (Aox3) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	51142
Seq. ID	uC-gmflminsoy008g10b1
Method	BLASTX
NCBI GI	g4559388
BLAST score	241
E value	2.0e-20
Match length	136
% identity	35
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51143
Seq. ID	uC-gmflminsoy010a03b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37

E value	2.0e-11
Match length	53
% identity	52
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51144
Seq. ID	uC-gmflminsoy010a09b1
Method	BLASTX
NCBI GI	g2088651
BLAST score	192
E value	1.0e-14
Match length	110
% identity	43
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	51145
Seq. ID	uC-gmflminsoy010b02b1
Method	BLASTX
NCBI GI	g4335717
BLAST score	145
E value	5.0e-09
Match length	115
% identity	33
NCBI Description	(AC006248) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	51146
Seq. ID	uC-gmflminsoy010d02b1
Method	BLASTX
NCBI GI	g462187
BLAST score	404
E value	1.0e-39
Match length	102
% identity	79
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_282928_pir__A42906 serine hydroxymethyltransferase - garden pea >gi_169158 (M87649) serine hydroxymethyltransferase [Pisum sativum]

Seq. No.	51147
Seq. ID	uC-gmflminsoy010e10b1
Method	BLASTX
NCBI GI	g1628482
BLAST score	147
E value	3.0e-09
Match length	74
% identity	8
NCBI Description	(X97570) embryogenesis transmembrane protein [Zea mays]

Seq. No.	51148
Seq. ID	uC-gmflminsoy010e11b1
Method	BLASTX
NCBI GI	g861155
BLAST score	596
E value	6.0e-62

Match length	130
% identity	85
NCBI Description	(Z35162) beta-fructofuranosidase; cell wall invertase I; fructosidase [Vicia faba]

Seq. No.	51149
Seq. ID	uC-gmflminsoy010f08b1
Method	BLASTX
NCBI GI	g3063455
BLAST score	373
E value	7.0e-36
Match length	103
% identity	67
NCBI Description	(AC003981) F22O13.17 [Arabidopsis thaliana]

Seq. No.	51150
Seq. ID	uC-gmflminsoy010g07b1
Method	BLASTX
NCBI GI	g2665637
BLAST score	377
E value	3.0e-36
Match length	124
% identity	57
NCBI Description	(AF031087) mismatch repair protein MSH6 [Mus musculus]

Seq. No.	51151
Seq. ID	uC-gmflminsoy010g08b1
Method	BLASTX
NCBI GI	g4388726
BLAST score	251
E value	4.0e-22
Match length	77
% identity	75
NCBI Description	(AC006413) putative 12-oxophytodienoate-10,11-reductase [Arabidopsis thaliana]

Seq. No.	51152
Seq. ID	uC-gmflminsoy010g11b1
Method	BLASTX
NCBI GI	g4335751
BLAST score	430
E value	2.0e-42
Match length	130
% identity	33
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	51153
Seq. ID	uC-gmflminsoy011b02b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	338
E value	1.0e-31
Match length	110
% identity	65
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	51154
Seq. ID	uC-gmflminsoy011d11b1
Method	BLASTX
NCBI GI	g2827546
BLAST score	210
E value	3.0e-17
Match length	74
% identity	50
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	51155
Seq. ID	uC-gmflminsoy011g02b1
Method	BLASTN
NCBI GI	g3337347
BLAST score	35
E value	3.0e-10
Match length	79
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	51156
Seq. ID	uC-gmflminsoy011g08b1
Method	BLASTX
NCBI GI	g4314359
BLAST score	180
E value	3.0e-13
Match length	74
% identity	50
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51157
Seq. ID	uC-gmflminsoy011g12b1
Method	BLASTX
NCBI GI	g4567214
BLAST score	397
E value	8.0e-39
Match length	110
% identity	36
NCBI Description	(AC007113) putative actin-binding protein villin 1 [Arabidopsis thaliana]

Seq. No.	51158
Seq. ID	uC-gmflminsoy012b12b1
Method	BLASTX
NCBI GI	g4539460
BLAST score	140
E value	8.0e-09
Match length	81
% identity	36
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	51159
Seq. ID	uC-gmflminsoy012f01b1
Method	BLASTN
NCBI GI	g515691

BLAST score	260
E value	1.0e-144
Match length	268
% identity	99
NCBI Description	Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds

Seq. No.	51160
Seq. ID	uC-gmflminsoy012f07b1
Method	BLASTX
NCBI GI	g2829923
BLAST score	248
E value	3.0e-21
Match length	77
% identity	37
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	51161
Seq. ID	uC-gmflminsoy012h12b1
Method	BLASTN
NCBI GI	g1304226
BLAST score	104
E value	2.0e-51
Match length	279
% identity	90
NCBI Description	Soybean mRNA for epoxide hydrolase, complete cds

Seq. No.	51162
Seq. ID	uC-gmflminsoy014d08b1
Method	BLASTX
NCBI GI	g4490702
BLAST score	362
E value	1.0e-34
Match length	102
% identity	70
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51163
Seq. ID	uC-gmflminsoy014d11b1
Method	BLASTX
NCBI GI	g2244971
BLAST score	161
E value	6.0e-11
Match length	38
% identity	84
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51164
Seq. ID	uC-gmflminsoy017a12b1
Method	BLASTX
NCBI GI	g3859570
BLAST score	172
E value	2.0e-12
Match length	45
% identity	64
NCBI Description	(AF098753) unknown [Oryza sativa]

Seq. No.	51165
Seq. ID	uC-gmflminsoy017b12b1
Method	BLASTX
NCBI GI	g4115913
BLAST score	417
E value	5.0e-41
Match length	132
% identity	58
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_ (AL049524) putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	51166
Seq. ID	uC-gmflminsoy018c08b1
Method	BLASTX
NCBI GI	g4467125
BLAST score	229
E value	5.0e-19
Match length	102
% identity	44
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	51167
Seq. ID	uC-gmflminsoy018d08b1
Method	BLASTX
NCBI GI	g4263790
BLAST score	667
E value	3.0e-70
Match length	149
% identity	89
NCBI Description	(AC006068) putative ch-TOG protein [Arabidopsis thaliana]

Seq. No.	51168
Seq. ID	uC-gmflminsoy018f07b1
Method	BLASTX
NCBI GI	g3721856
BLAST score	157
E value	2.0e-10
Match length	52
% identity	54
NCBI Description	(AB014057) beta-Amyrin Synthase [Panax ginseng]

Seq. No.	51169
Seq. ID	uC-gmflminsoy018h09b1
Method	BLASTX
NCBI GI	g3758833
BLAST score	441
E value	3.0e-47
Match length	139
% identity	66
NCBI Description	(Y18225) MtN6 [Medicago truncatula]

Seq. No.	51170
Seq. ID	uC-gmflminsoy019a12b1
Method	BLASTX

NCBI GI	g1352075
BLAST score	246
E value	2.0e-21
Match length	63
% identity	65
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_1076460_pir__S52393 beta-galactosidase (EC 3.2.1.23) - wild cabbage >gi_669059_emb_CAA59162_ (X84684) beta-galactosidase [Brassica oleracea]

Seq. No.	51171
Seq. ID	uC-gmflminsoy019e02b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	4.0e-09
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51172
Seq. ID	uC-gmflminsoy019e06b1
Method	BLASTX
NCBI GI	g4220485
BLAST score	339
E value	4.0e-32
Match length	91
% identity	69
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	51173
Seq. ID	uC-gmflminsoy019f04b1
Method	BLASTX
NCBI GI	g4539330
BLAST score	294
E value	9.0e-27
Match length	103
% identity	57
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	51174
Seq. ID	uC-gmflminsoy020a10b1
Method	BLASTX
NCBI GI	g3367534
BLAST score	516
E value	1.0e-52
Match length	115
% identity	82
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	51175
Seq. ID	uC-gmflminsoy020b05b1
Method	BLASTX

NCBI GI g4335731
BLAST score 142
E value 8.0e-09
Match length 56
% identity 41
NCBI Description (AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No. 51176
Seq. ID uC-gmflminsoy020c11b1
Method BLASTN
NCBI GI g2213533
BLAST score 39
E value 8.0e-13
Match length 79
% identity 87
NCBI Description P.sativum mRNA encoding DNA-binding PD1-like protein

Seq. No. 51177
Seq. ID uC-gmflminsoy020e12b1
Method BLASTX
NCBI GI g2443878
BLAST score 147
E value 2.0e-09
Match length 74
% identity 54
NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 51178
Seq. ID uC-gmflminsoy020f01b1
Method BLASTX
NCBI GI g563247
BLAST score 375
E value 2.0e-36
Match length 79
% identity 92
NCBI Description (U16279) acetolactate synthase precursor [Xanthium sp.]

Seq. No. 51179
Seq. ID uC-gmflminsoy020f05b1
Method BLASTX
NCBI GI g3004564
BLAST score 175
E value 1.0e-12
Match length 44
% identity 66
NCBI Description (AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 51180
Seq. ID uC-gmflminsoy021a03b1
Method BLASTN
NCBI GI g1438880
BLAST score 263
E value 1.0e-146
Match length 379
% identity 92
NCBI Description Glycine max choline kinase GmCK2p mRNA, complete cds

Seq. No.	51181
Seq. ID	uC-gmflminsoy021a07b1
Method	BLASTX
NCBI GI	g399227
BLAST score	327
E value	2.0e-30
Match length	140
% identity	49
NCBI Description	CENTROMERIC PROTEIN E (CENP-E PROTEIN) >gi_284038_pir__S28261 centromere protein E - human >gi_29865_emb_CAA78727_ (Z15005) CENP-E [Homo sapiens] >gi_4502781_ref_NP_001804.1_pCENPE_ centromere protein E (312kD)

Seq. No.	51182
Seq. ID	uC-gmflminsoy021c08b1
Method	BLASTX
NCBI GI	g3212879
BLAST score	249
E value	3.0e-21
Match length	120
% identity	44
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	51183
Seq. ID	uC-gmflminsoy021d08b1
Method	BLASTX
NCBI GI	g4335857
BLAST score	278
E value	8.0e-25
Match length	93
% identity	58
NCBI Description	(AF049347) berberine bridge enzyme [Berberis stolonifera]

Seq. No.	51184
Seq. ID	uC-gmflminsoy021g09b1
Method	BLASTX
NCBI GI	g2388586
BLAST score	366
E value	3.0e-35
Match length	90
% identity	74
NCBI Description	(AC000098) Similar to Saccharomyces RAD16 (gb_X78993). [Arabidopsis thaliana]

Seq. No.	51185
Seq. ID	uC-gmflminsoy021g12b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	39
% identity	62
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51186
Seq. ID	uC-gmflminsoy022b07b1
Method	BLASTX
NCBI GI	g4455329
BLAST score	506
E value	2.0e-51
Match length	107
% identity	90
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	51187
Seq. ID	uC-gmflminsoy022c02b1
Method	BLASTX
NCBI GI	g4102600
BLAST score	409
E value	4.0e-40
Match length	87
% identity	86
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	51188
Seq. ID	uC-gmflminsoy022c12b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	45
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51189
Seq. ID	uC-gmflminsoy022d07b1
Method	BLASTX
NCBI GI	g2245028
BLAST score	231
E value	5.0e-19
Match length	135
% identity	33
NCBI Description	(Z97341) limonene cyclase [Arabidopsis thaliana]

Seq. No.	51190
Seq. ID	uC-gmflminsoy022e10b1
Method	BLASTN
NCBI GI	g2264319
BLAST score	36
E value	1.0e-10
Match length	64
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	51191
Seq. ID	uC-gmflminsoy022e11b1
Method	BLASTX
NCBI GI	g2739168
BLAST score	302

E value	2.0e-27
Match length	107
% identity	55
NCBI Description	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]

Seq. No.	51192
Seq. ID	uC-gmflminsoy022g01b1
Method	BLASTX
NCBI GI	g3882211
BLAST score	193
E value	9.0e-15
Match length	102
% identity	43
NCBI Description	(AB018288) KIAA0745 protein [Homo sapiens]

Seq. No.	51193
Seq. ID	uC-gmflminsoy022h04b1
Method	BLASTX
NCBI GI	g3367578
BLAST score	548
E value	3.0e-56
Match length	154
% identity	68
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	51194
Seq. ID	uC-gmflminsoy022h08b1
Method	BLASTX
NCBI GI	g3080375
BLAST score	279
E value	7.0e-25
Match length	127
% identity	48
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]

Seq. No.	51195
Seq. ID	uC-gmflminsoy022h10b1
Method	BLASTN
NCBI GI	g166739
BLAST score	125
E value	8.0e-64
Match length	305
% identity	85
NCBI Description	A.thaliana histone H4 gene, complete cds

Seq. No.	51196
Seq. ID	uC-gmflminsoy023b06b1
Method	BLASTX
NCBI GI	g4151321
BLAST score	429
E value	2.0e-42
Match length	113
% identity	82
NCBI Description	(AF089085) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]

Seq. No.	51197
Seq. ID	uC-gmflminsoy023e06b1
Method	BLASTX
NCBI GI	g3047082
BLAST score	412
E value	2.0e-40
Match length	94
% identity	74
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	51198
Seq. ID	uC-gmflminsoy023e12b1
Method	BLASTX
NCBI GI	g2842424
BLAST score	310
E value	2.0e-28
Match length	140
% identity	44
NCBI Description	(AJ223948) RNA helicase [Homo sapiens]

Seq. No.	51199
Seq. ID	uC-gmflminsoy023g06b1
Method	BLASTX
NCBI GI	g3776567
BLAST score	301
E value	1.0e-27
Match length	98
% identity	62
NCBI Description	(AC005388) Strong similarity to F21B7.33 gi_2809264 from A. thaliana BAC gb_AC002560. EST gb_N65119 comes from this gene. [Arabidopsis thaliana]

Seq. No.	51200
Seq. ID	uC-gmflminsoy024c01b1
Method	BLASTX
NCBI GI	g4580395
BLAST score	301
E value	2.0e-27
Match length	131
% identity	50
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	51201
Seq. ID	uC-gmflminsoy024f09b1
Method	BLASTX
NCBI GI	g3157927
BLAST score	307
E value	4.0e-28
Match length	116
% identity	56
NCBI Description	(AC002131) Contains similarity to GDP-dissociation inhibitor gb_L07918 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	51202
Seq. ID	uC-gmflminsoy024g10b1
Method	BLASTX
NCBI GI	g4204288
BLAST score	211
E value	2.0e-21
Match length	79
% identity	60
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	51203
Seq. ID	uC-gmflminsoy025e05b1
Method	BLASTX
NCBI GI	g1346771
BLAST score	426
E value	6.0e-42
Match length	151
% identity	47
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase (PCK1) - Urochloa panicoides >gi_607752 (U09241) phosphoenolpyruvate carboxykinase [Urochloa panicoides]

Seq. No.	51204
Seq. ID	uC-gmflminsoy025f03b1
Method	BLASTN
NCBI GI	g4249393
BLAST score	43
E value	5.0e-15
Match length	51
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	51205
Seq. ID	uC-gmflminsoy025f12b1
Method	BLASTX
NCBI GI	g461812
BLAST score	187
E value	4.0e-14
Match length	78
% identity	46
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	51206
Seq. ID	uC-gmflminsoy025h02b1
Method	BLASTX
NCBI GI	g3980412
BLAST score	379
E value	1.0e-36
Match length	120
% identity	64

NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.	51207
Seq. ID	uC-gmflminsoy026c03b1
Method	BLASTX
NCBI GI	g2384671
BLAST score	413
E value	1.0e-40
Match length	126
% identity	58
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]
Seq. No.	51208
Seq. ID	uC-gmflminsoy027b07b1
Method	BLASTN
NCBI GI	g3329367
BLAST score	39
E value	1.0e-12
Match length	115
% identity	84
NCBI Description	Arabidopsis thaliana nodulin-like protein mRNA, partial cds
Seq. No.	51209
Seq. ID	uC-gmflminsoy027b11b1
Method	BLASTX
NCBI GI	g1708191
BLAST score	438
E value	1.0e-43
Match length	112
% identity	78
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]
Seq. No.	51210
Seq. ID	uC-gmflminsoy027c02b1
Method	BLASTX
NCBI GI	g4580469
BLAST score	255
E value	3.0e-22
Match length	82
% identity	59
NCBI Description	(AC006081) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	51211
Seq. ID	uC-gmflminsoy027c07b1
Method	BLASTX
NCBI GI	g2642158
BLAST score	150
E value	6.0e-10
Match length	55
% identity	51
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.	51212
Seq. ID	uC-gmflminsoy027f06b1

Method	BLASTX
NCBI GI	g3142290
BLAST score	293
E value	2.0e-26
Match length	141
% identity	52
NCBI Description	(AC002411) Contains similarity to gb_Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	51213
Seq. ID	uC-gmflminsoy027g03b1
Method	BLASTX
NCBI GI	g3953462
BLAST score	148
E value	2.0e-09
Match length	97
% identity	29
NCBI Description	(AC002328) F20N2.7 [Arabidopsis thaliana]

Seq. No.	51214
Seq. ID	uC-gmflminsoy028b01b1
Method	BLASTX
NCBI GI	g21693
BLAST score	300
E value	3.0e-27
Match length	69
% identity	74
NCBI Description	(X66012) cathepsin B [Triticum aestivum]

Seq. No.	51215
Seq. ID	uC-gmflminsoy028h12b1
Method	BLASTX
NCBI GI	g4100433
BLAST score	277
E value	2.0e-24
Match length	97
% identity	61
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	51216
Seq. ID	uC-gmflminsoy029a10b1
Method	BLASTX
NCBI GI	g1488043
BLAST score	368
E value	3.0e-35
Match length	110
% identity	68
NCBI Description	(U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No.	51217
Seq. ID	uC-gmflminsoy029a11b1
Method	BLASTX
NCBI GI	g4469009
BLAST score	280
E value	2.0e-25
Match length	68
% identity	82

NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]
Seq. No.	51218
Seq. ID	uC-gmflminsoy029c08b1
Method	BLASTX
NCBI GI	g2501296
BLAST score	251
E value	2.0e-21
Match length	127
% identity	39
NCBI Description	DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]
Seq. No.	51219
Seq. ID	uC-gmflminsoy029d06b1
Method	BLASTX
NCBI GI	g3212863
BLAST score	546
E value	5.0e-56
Match length	159
% identity	68
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]
Seq. No.	51220
Seq. ID	uC-gmflminsoy029e07b1
Method	BLASTX
NCBI GI	g4263509
BLAST score	263
E value	4.0e-23
Match length	75
% identity	63
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.	51221
Seq. ID	uC-gmflminsoy029h08b1
Method	BLASTX
NCBI GI	g3386617
BLAST score	224
E value	1.0e-18
Match length	61
% identity	79
NCBI Description	(AC004665) putative cell division protein (ftsY) [Arabidopsis thaliana]
Seq. No.	51222
Seq. ID	uC-gmflminsoy030b04b1
Method	BLASTX
NCBI GI	g4580460
BLAST score	585
E value	1.0e-60
Match length	122
% identity	95
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]
Seq. No.	51223

Seq. ID	uC-gmflminsoy030c04b1
Method	BLASTX
NCBI GI	g2982942
BLAST score	209
E value	6.0e-17
Match length	82
% identity	54
NCBI Description	(AE000679) GMP synthase [Aquifex aeolicus]

Seq. No.	51224
Seq. ID	uC-gmflminsoy030d02b1
Method	BLASTX
NCBI GI	g4512698
BLAST score	468
E value	6.0e-47
Match length	109
% identity	77
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51225
Seq. ID	uC-gmflminsoy030d03b1
Method	BLASTX
NCBI GI	g2465923
BLAST score	461
E value	4.0e-46
Match length	110
% identity	78
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	51226
Seq. ID	uC-gmflminsoy030f06b1
Method	BLASTX
NCBI GI	g1707020
BLAST score	209
E value	1.0e-16
Match length	110
% identity	20
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51227
Seq. ID	uC-gmflminsoy030g10b1
Method	BLASTX
NCBI GI	g3747111
BLAST score	151
E value	8.0e-10
Match length	40
% identity	62
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	51228
Seq. ID	uC-gmflminsoy030g11b1
Method	BLASTX
NCBI GI	g4006827
BLAST score	412
E value	2.0e-40
Match length	139

% identity	58
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	51229
Seq. ID	uC-gmflminsoy031a11b1
Method	BLASTX
NCBI GI	g2651300
BLAST score	519
E value	5.0e-53
Match length	127
% identity	76
NCBI Description	(AC002336) putative initiator tRNA phosphoribosyl-transferase [Arabidopsis thaliana]

Seq. No.	51230
Seq. ID	uC-gmflminsoy031d07b1
Method	BLASTX
NCBI GI	g4185136
BLAST score	439
E value	1.0e-43
Match length	113
% identity	75
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	51231
Seq. ID	uC-gmflminsoy031e10b1
Method	BLASTX
NCBI GI	g4335729
BLAST score	218
E value	1.0e-17
Match length	139
% identity	5
NCBI Description	(AC006248) putative salt-inducible protein [Arabidopsis thaliana]

Seq. No.	51232
Seq. ID	uC-gmflminsoy032b06b1
Method	BLASTX
NCBI GI	g2864618
BLAST score	244
E value	8.0e-21
Match length	85
% identity	55
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	51233
Seq. ID	uC-gmflminsoy032b12b1
Method	BLASTX
NCBI GI	g2979554
BLAST score	231
E value	2.0e-19
Match length	93
% identity	56
NCBI Description	(AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No.	51234

Seq. ID	uC-gmflminsoy032f12b1
Method	BLASTX
NCBI GI	g1055161
BLAST score	177
E value	3.0e-13
Match length	86
% identity	22
NCBI Description	(U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans]

Seq. No.	51235
Seq. ID	uC-gmflminsoy032h10b1
Method	BLASTX
NCBI GI	g3063455
BLAST score	301
E value	2.0e-27
Match length	70
% identity	76
NCBI Description	(AC003981) F22O13.17 [Arabidopsis thaliana]

Seq. No.	51236
Seq. ID	uC-gmflminsoy034b02b1
Method	BLASTX
NCBI GI	g3881976
BLAST score	413
E value	2.0e-40
Match length	121
% identity	62
NCBI Description	(AJ012409) hypothetical protein [Homo sapiens]

Seq. No.	51237
Seq. ID	uC-gmflminsoy034d04b1
Method	BLASTX
NCBI GI	g2654868
BLAST score	241
E value	1.0e-20
Match length	105
% identity	56
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	51238
Seq. ID	uC-gmflminsoy034g02b1
Method	BLASTX
NCBI GI	g585973
BLAST score	111
E value	1.0e-11
Match length	56
% identity	73
NCBI Description	FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A fructokinase [Solanum tuberosum]

Seq. No.	51239
Seq. ID	uC-gmflminsoy034g10b1
Method	BLASTX
NCBI GI	g1778378

BLAST score	412
E value	2.0e-40
Match length	99
% identity	82
NCBI Description	(U81289) NAP1Ps [Pisum sativum]

Seq. No.	51240
Seq. ID	uC-gmflminsoy034h07b1
Method	BLASTN
NCBI GI	g1773329
BLAST score	55
E value	2.0e-22
Match length	119
% identity	87
NCBI Description	Mesembryanthemum crystallinum glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	51241
Seq. ID	uC-gmflminsoy035c02b1
Method	BLASTN
NCBI GI	g20995
BLAST score	279
E value	1.0e-155
Match length	359
% identity	94
NCBI Description	Phaseolus vulgaris mRNA for endopeptidase (EP-C1)

Seq. No.	51242
Seq. ID	uC-gmflminsoy035c08b1
Method	BLASTN
NCBI GI	g3309242
BLAST score	108
E value	1.0e-53
Match length	280
% identity	85
NCBI Description	Citrus limon aconitase-iron regulated protein 1 (IRP1) mRNA, complete cds

Seq. No.	51243
Seq. ID	uC-gmflminsoy035d01b1
Method	BLASTN
NCBI GI	g857394
BLAST score	252
E value	1.0e-139
Match length	370
% identity	94
NCBI Description	Glycine max mRNA for mitotic cyclin a2-type, complete cds

Seq. No.	51244
Seq. ID	uC-gmflminsoy035e08b1
Method	BLASTX
NCBI GI	g4234953
BLAST score	218
E value	4.0e-18
Match length	82
% identity	61
NCBI Description	(AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]

Seq. No.	51245
Seq. ID	uC-gmflminsoy036a04b1
Method	BLASTX
NCBI GI	g1076529
BLAST score	483
E value	1.0e-48
Match length	115
% identity	77
NCBI Description	heat shock protein HSP71.2 - garden pea >gi_562006 (U08848) PsHSP71.2 [Pisum sativum] >gi_1771479_emb_CAA67867_ (X99515) heat shock protein hsp70 [Pisum sativum]

Seq. No.	51246
Seq. ID	uC-gmflminsoy036e11b1
Method	BLASTX
NCBI GI	g3702368
BLAST score	189
E value	3.0e-14
Match length	49
% identity	69
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No.	51247
Seq. ID	uC-gmflminsoy036f12b1
Method	BLASTX
NCBI GI	g3201627
BLAST score	474
E value	1.0e-47
Match length	123
% identity	74
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	51248
Seq. ID	uC-gmflminsoy036h04b1
Method	BLASTX
NCBI GI	g4455338
BLAST score	222
E value	3.0e-18
Match length	110
% identity	47
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	51249
Seq. ID	uC-gmflminsoy036h07b1
Method	BLASTN
NCBI GI	g609224
BLAST score	173
E value	2.0e-92
Match length	305
% identity	89
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	51250

Seq. ID	uC-gmflminsoy037d05b1
Method	BLASTX
NCBI GI	g2213598
BLAST score	253
E value	9.0e-22
Match length	131
% identity	24
NCBI Description	(AC000348) T7N9.18 [Arabidopsis thaliana]

Seq. No.	51251
Seq. ID	uC-gmflminsoy040c09b1
Method	BLASTN
NCBI GI	g4101472
BLAST score	83
E value	8.0e-39
Match length	323
% identity	81
NCBI Description	Arabidopsis thaliana K efflux antiporter KEA1 mRNA, complete cds

Seq. No.	51252
Seq. ID	uC-gmflminsoy040e01b1
Method	BLASTX
NCBI GI	g544018
BLAST score	322
E value	6.0e-30
Match length	116
% identity	63
NCBI Description	NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772 nitrate-inducible nitrate transporter - Arabidopsis thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb_L10357 from A. thaliana. ESTs gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688, gb_R29817, gb_R29862, gb_Z34634 and gb_Z34258 come from this gene. [Arabidopsis thaliana]

Seq. No.	51253
Seq. ID	uC-gmflminsoy040f02b1
Method	BLASTX
NCBI GI	g2911040
BLAST score	336
E value	1.0e-31
Match length	90
% identity	69
NCBI Description	(AL021961) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	51254
Seq. ID	uC-gmflminsoy040f07b1
Method	BLASTX
NCBI GI	g3688173
BLAST score	160
E value	4.0e-11
Match length	43
% identity	74
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	51255
Seq. ID	uC-gmflminsoy040h04b1
Method	BLASTX
NCBI GI	g4371285
BLAST score	223
E value	2.0e-18
Match length	75
% identity	59
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51256
Seq. ID	uC-gmflminsoy040h08b1
Method	BLASTX
NCBI GI	g1657855
BLAST score	143
E value	2.0e-09
Match length	67
% identity	48
NCBI Description	(U73216) cold acclimation protein WCOR413 [Triticum aestivum]

Seq. No.	51257
Seq. ID	uC-gmflminsoy041a01b1
Method	BLASTX
NCBI GI	g1352075
BLAST score	171
E value	4.0e-12
Match length	111
% identity	44
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_1076460_pir__S52393 beta-galactosidase (EC 3.2.1.23) - wild cabbage >gi_669059_emb_CAA59162_ (X84684) beta-galactosidase [Brassica oleracea]

Seq. No.	51258
Seq. ID	uC-gmflminsoy041c06b1
Method	BLASTN
NCBI GI	g12147
BLAST score	221
E value	1.0e-121
Match length	365
% identity	92
NCBI Description	Pea chloroplast genes for ATP synthetase subunits beta and epsilon (atpB and atpE)

Seq. No.	51259
Seq. ID	uC-gmflminsoy041c07b1
Method	BLASTN
NCBI GI	g3549651
BLAST score	71
E value	1.0e-31
Match length	127
% identity	89
NCBI Description	Arabidopsis thaliana MAP3K epsilon gene

Seq. No. 51260

Seq. ID	uC-gmflminsoy041g12b1
Method	BLASTX
NCBI GI	g3063708
BLAST score	377
E value	3.0e-36
Match length	129
% identity	52
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	51261
Seq. ID	uC-gmflminsoy042a11b1
Method	BLASTN
NCBI GI	g669002
BLAST score	356
E value	0.0e+00
Match length	360
% identity	100
NCBI Description	Glycine max calnexin mRNA, complete cds

Seq. No.	51262
Seq. ID	uC-gmflminsoy042d07b1
Method	BLASTX
NCBI GI	g2062167
BLAST score	434
E value	6.0e-43
Match length	98
% identity	82
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	51263
Seq. ID	uC-gmflminsoy043a08b1
Method	BLASTX
NCBI GI	g1171161
BLAST score	161
E value	1.0e-11
Match length	46
% identity	65
NCBI Description	(U41472) pectate lyase homolog [Medicago sativa]

Seq. No.	51264
Seq. ID	uC-gmflminsoy043b06b1
Method	BLASTX
NCBI GI	g3142300
BLAST score	175
E value	8.0e-13
Match length	73
% identity	51
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	51265
Seq. ID	uC-gmflminsoy043b10b1
Method	BLASTX
NCBI GI	g3142290

BLAST score	598
E value	4.0e-62
Match length	152
% identity	82
NCBI Description	(AC002411) Contains similarity to gb_Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	51266
Seq. ID	uC-gmflminsoy043e01b1
Method	BLASTX
NCBI GI	g2980770
BLAST score	288
E value	5.0e-26
Match length	83
% identity	70
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	51267
Seq. ID	uC-gmflminsoy043g02b1
Method	BLASTX
NCBI GI	g2244971
BLAST score	488
E value	2.0e-49
Match length	109
% identity	84
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51268
Seq. ID	uC-gmflminsoy044a10b1
Method	BLASTX
NCBI GI	g2062176
BLAST score	306
E value	6.0e-28
Match length	66
% identity	86
NCBI Description	(AC001645) Myb-related transcription activator (MybSt1) isolog [Arabidopsis thaliana]

Seq. No.	51269
Seq. ID	uC-gmflminsoy044b02b1
Method	BLASTX
NCBI GI	g2642448
BLAST score	183
E value	2.0e-13
Match length	153
% identity	13
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51270
Seq. ID	uC-gmflminsoy044b12b1
Method	BLASTX
NCBI GI	g3947735
BLAST score	310
E value	1.0e-28
Match length	109

% identity	57
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	51271
Seq. ID	uC-gmflminsoy044g01b1
Method	BLASTX
NCBI GI	g4138131
BLAST score	340
E value	3.0e-32
Match length	98
% identity	69
NCBI Description	(AJ011828) NDX1 homeobox protein [Lotus japonicus]

Seq. No.	51272
Seq. ID	uC-gmflminsoy044g07b1
Method	BLASTN
NCBI GI	g303900
BLAST score	254
E value	1.0e-141
Match length	327
% identity	28
NCBI Description	Soybean gene for ubiquitin, complete cds

Seq. No.	51273
Seq. ID	uC-gmflminsoy045a12b1
Method	BLASTX
NCBI GI	g3367537
BLAST score	142
E value	4.0e-09
Match length	35
% identity	80
NCBI Description	(AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375. [Arabid

Seq. No.	51274
Seq. ID	uC-gmflminsoy045b03b1
Method	BLASTX
NCBI GI	g2738750
BLAST score	484
E value	8.0e-49
Match length	101
% identity	90
NCBI Description	(AF016305) ATP sulfurylase [Zea mays]

Seq. No.	51275
Seq. ID	uC-gmflminsoy045d11b1
Method	BLASTN
NCBI GI	g2351073
BLAST score	39
E value	2.0e-12
Match length	59
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	51276
Seq. ID	uC-gmflminsoy045e10b1
Method	BLASTX
NCBI GI	g2341032
BLAST score	357
E value	7.0e-34
Match length	127
% identity	61
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	51277
Seq. ID	uC-gmflminsoy045g07b1
Method	BLASTX
NCBI GI	g4263779
BLAST score	178
E value	3.0e-13
Match length	70
% identity	50
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51278
Seq. ID	uC-gmflminsoy046a07b1
Method	BLASTX
NCBI GI	g4567286
BLAST score	327
E value	1.0e-30
Match length	83
% identity	73
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	51279
Seq. ID	uC-gmflminsoy046a09b1
Method	BLASTN
NCBI GI	g256142
BLAST score	283
E value	1.0e-158
Match length	339
% identity	98
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	51280
Seq. ID	uC-gmflminsoy046b02b1
Method	BLASTX
NCBI GI	g2088668
BLAST score	301
E value	3.0e-27
Match length	125
% identity	46
NCBI Description	(AF003130) similar to Achlya ambisexualis antheridiol steroid receptor (NID:g166306) [Caenorhabditis elegans]

Seq. No.	51281
Seq. ID	uC-gmflminsoy046c08b1

Method	BLASTX
NCBI GI	g2245077
BLAST score	260
E value	1.0e-22
Match length	68
% identity	72
NCBI Description	(Z97343) glucanase homolog [Arabidopsis thaliana]

Seq. No.	51282
Seq. ID	uC-gmflminsoy046h12b1
Method	BLASTX
NCBI GI	g3337361
BLAST score	367
E value	2.0e-35
Match length	95
% identity	71
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	51283
Seq. ID	uC-gmflminsoy047a08b1
Method	BLASTX
NCBI GI	g4558659
BLAST score	226
E value	5.0e-19
Match length	68
% identity	63
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.	51284
Seq. ID	uC-gmflminsoy047c02b1
Method	BLASTX
NCBI GI	g4539397
BLAST score	229
E value	2.0e-19
Match length	56
% identity	77
NCBI Description	(AL035526) cellulose synthase-like protein [Arabidopsis thaliana]

Seq. No.	51285
Seq. ID	uC-gmflminsoy047c11b1
Method	BLASTX
NCBI GI	g2244971
BLAST score	176
E value	1.0e-12
Match length	45
% identity	73
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51286
Seq. ID	uC-gmflminsoy047g10b1
Method	BLASTN
NCBI GI	g1695243
BLAST score	36
E value	1.0e-10
Match length	48
% identity	94

NCBI Description	Arabidopsis thaliana homeodomain protein (GLABRA2) gene, complete cds

Seq. No.	51287
Seq. ID	uC-gmflminsoy049c10b1
Method	BLASTX
NCBI GI	g4115917
BLAST score	264
E value	6.0e-23
Match length	61
% identity	70
NCBI Description	(AF118222) contains similarity to PHD-fingers (Pfam:PF00628, score=10.9, E=0.059, N=1) [Arabidopsis thaliana]

Seq. No.	51288
Seq. ID	uC-gmflminsoy049e06b1
Method	BLASTX
NCBI GI	g3395430
BLAST score	145
E value	5.0e-09
Match length	86
% identity	22
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51289
Seq. ID	uC-gmflminsoy049g07b1
Method	BLASTX
NCBI GI	g4263787
BLAST score	183
E value	2.0e-13
Match length	49
% identity	63
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	51290
Seq. ID	uC-gmflminsoy049g11b1
Method	BLASTX
NCBI GI	g2245012
BLAST score	435
E value	5.0e-43
Match length	129
% identity	68
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51291
Seq. ID	uC-gmflminsoy049h06b1
Method	BLASTX
NCBI GI	g3288823
BLAST score	368
E value	2.0e-35
Match length	106
% identity	72
NCBI Description	(AF063852) FUS5 [Arabidopsis thaliana]

Seq. No.	51292
Seq. ID	uC-gmflminsoy052a04b1

Method	BLASTN
NCBI GI	g2760169
BLAST score	37
E value	8.0e-12
Match length	41
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	51293
Seq. ID	uC-gmflminsoy053a06b1
Method	BLASTX
NCBI GI	g2829911
BLAST score	144
E value	4.0e-09
Match length	34
% identity	74
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	51294
Seq. ID	uC-gmflminsoy053b12b1
Method	BLASTX
NCBI GI	g4558673
BLAST score	209
E value	1.0e-16
Match length	122
% identity	35
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51295
Seq. ID	uC-gmflminsoy053c02b1
Method	BLASTX
NCBI GI	g3335060
BLAST score	280
E value	8.0e-25
Match length	152
% identity	38
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	51296
Seq. ID	uC-gmflminsoy053f06b1
Method	BLASTX
NCBI GI	g3643610
BLAST score	146
E value	4.0e-09
Match length	33
% identity	82
NCBI Description	(AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	51297
Seq. ID	uC-gmflminsoy054b03b1
Method	BLASTX
NCBI GI	g1184075
BLAST score	270

E value	1.0e-23
Match length	161
% identity	3
NCBI Description	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No.	51298
Seq. ID	uC-gmflminsoy054b04b1
Method	BLASTX
NCBI GI	g2935342
BLAST score	497
E value	2.0e-50
Match length	112
% identity	88
NCBI Description	(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]

Seq. No.	51299
Seq. ID	uC-gmflminsoy054c05b1
Method	BLASTX
NCBI GI	g2959781
BLAST score	190
E value	2.0e-14
Match length	57
% identity	61
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	51300
Seq. ID	uC-gmflminsoy054d04b1
Method	BLASTX
NCBI GI	g4262174
BLAST score	506
E value	2.0e-51
Match length	121
% identity	75
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	51301
Seq. ID	uC-gmflminsoy054d11b1
Method	BLASTX
NCBI GI	g3894170
BLAST score	264
E value	1.0e-25
Match length	89
% identity	70
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	51302
Seq. ID	uC-gmflminsoy054e06b1
Method	BLASTX
NCBI GI	g3695019
BLAST score	279
E value	7.0e-25
Match length	119
% identity	45

NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 51303
Seq. ID uC-gmflminsoy054g08b1
Method BLASTX
NCBI GI g2347199
BLAST score 345
E value 1.0e-32
Match length 107
% identity 61
NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 51304
Seq. ID uC-gmflminsoy054h05b1
Method BLASTX
NCBI GI g1806142
BLAST score 693
E value 3.0e-73
Match length 147
% identity 88
NCBI Description (X97315) cdc2MsD [Medicago sativa]

Seq. No. 51305
Seq. ID uC-gmflminsoy054h09b1
Method BLASTX
NCBI GI g1055161
BLAST score 157
E value 2.0e-10
Match length 104
% identity 42
NCBI Description (U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans]

Seq. No. 51306
Seq. ID uC-gmflminsoy054h10b1
Method BLASTX
NCBI GI g4371293
BLAST score 257
E value 3.0e-22
Match length 130
% identity 46
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51307
Seq. ID uC-gmflminsoy055a06b1
Method BLASTX
NCBI GI g3426037
BLAST score 479
E value 2.0e-48
Match length 106
% identity 49
NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No. 51308
Seq. ID uC-gmflminsoy055a09b1
Method BLASTX

NCBI GI g2462828
BLAST score 388
E value 1.0e-37
Match length 144
% identity 6
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51309
Seq. ID uC-gmflminsoy055b11b1
Method BLASTX
NCBI GI g2262101
BLAST score 329
E value 1.0e-30
Match length 108
% identity 62
NCBI Description (AC002343) kinesin heavy chain isolog [Arabidopsis thaliana]

Seq. No. 51310
Seq. ID uC-gmflminsoy055b12b1
Method BLASTX
NCBI GI g4049344
BLAST score 305
E value 7.0e-28
Match length 94
% identity 66
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 51311
Seq. ID uC-gmflminsoy055e01b1
Method BLASTX
NCBI GI g4220514
BLAST score 460
E value 5.0e-46
Match length 104
% identity 81
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 51312
Seq. ID uC-gmflminsoy055g07b1
Method BLASTX
NCBI GI g4559351
BLAST score 183
E value 1.0e-13
Match length 131
% identity 38
NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51313
Seq. ID uC-gmflminsoy056a05b1
Method BLASTX
NCBI GI g2459428
BLAST score 171
E value 5.0e-12
Match length 50
% identity 72
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	51314
Seq. ID	uC-gmflminsoy056b11b1
Method	BLASTX
NCBI GI	g1743354
BLAST score	136
E value	3.0e-14
Match length	57
% identity	71
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	51315
Seq. ID	uC-gmflminsoy056c03b1
Method	BLASTX
NCBI GI	g2558654
BLAST score	433
E value	5.0e-43
Match length	106
% identity	76
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	51316
Seq. ID	uC-gmflminsoy056g04b1
Method	BLASTN
NCBI GI	g1438880
BLAST score	174
E value	4.0e-93
Match length	373
% identity	92
NCBI Description	Glycine max choline kinase GmCK2p mRNA, complete cds

Seq. No.	51317
Seq. ID	uC-gmflminsoy057a11b1
Method	BLASTX
NCBI GI	g4559368
BLAST score	396
E value	2.0e-38
Match length	144
% identity	58
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51318
Seq. ID	uC-gmflminsoy057d11b1
Method	BLASTX
NCBI GI	g4567265
BLAST score	316
E value	2.0e-31
Match length	97
% identity	67
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	51319
Seq. ID	uC-gmflminsoy058c04b1
Method	BLASTN
NCBI GI	g3641864
BLAST score	46
E value	7.0e-17

Match length 114
% identity 85
NCBI Description Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-4

Seq. No. 51320
Seq. ID uC-gmflminsoy058e10b1
Method BLASTX
NCBI GI g4115371
BLAST score 239
E value 5.0e-20
Match length 125
% identity 48
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 51321
Seq. ID uC-gmflminsoy058g01b1
Method BLASTX
NCBI GI g3004565
BLAST score 243
E value 1.0e-20
Match length 76
% identity 70
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 51322
Seq. ID uC-gmflminsoy058g06b1
Method BLASTX
NCBI GI g3600054
BLAST score 184
E value 1.0e-13
Match length 62
% identity 48
NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]

Seq. No. 51323
Seq. ID uC-gmflminsoy059a10b1
Method BLASTN
NCBI GI g2062705
BLAST score 37
E value 3.0e-11
Match length 75
% identity 50
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 51324
Seq. ID uC-gmflminsoy059b05b1
Method BLASTX
NCBI GI g4454039
BLAST score 282
E value 1.0e-25
Match length 85
% identity 66
NCBI Description (AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No. 51325

Seq. ID	uC-gmflminsoy059b07b1
Method	BLASTX
NCBI GI	g136057
BLAST score	384
E value	4.0e-37
Match length	106
% identity	69
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	51326
Seq. ID	uC-gmflminsoy059c02b1
Method	BLASTX
NCBI GI	g2827709
BLAST score	199
E value	9.0e-16
Match length	50
% identity	70
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	51327
Seq. ID	uC-gmflminsoy059f08b1
Method	BLASTN
NCBI GI	g170025
BLAST score	105
E value	5.0e-52
Match length	233
% identity	86
NCBI Description	Soybean malate synthase (MS) mRNA, 3' end

Seq. No.	51328
Seq. ID	uC-gmflminsoy059f10b1
Method	BLASTX
NCBI GI	g3334409
BLAST score	182
E value	2.0e-13
Match length	43
% identity	86
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2129765_pir__S71261 V-type proton-ATPase - Arabidopsis thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type proton-ATPase [Arabidopsis thaliana]

Seq. No.	51329
Seq. ID	uC-gmflminsoy061b04b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	36
E value	8.0e-11
Match length	41
% identity	40
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	51330
Seq. ID	uC-gmflminsoy061d12b1

Method	BLASTN
NCBI GI	g1139584
BLAST score	106
E value	2.0e-52
Match length	230
% identity	87
NCBI Description	Lupinus albus tRNA nucleotidyltransferase (CCA1) mRNA, complete cds

Seq. No.	51331
Seq. ID	uC-gmflminsoy061e04b1
Method	BLASTN
NCBI GI	g4103476
BLAST score	32
E value	1.0e-08
Match length	32
% identity	100
NCBI Description	Glycine tomentella small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, pa

Seq. No.	51332
Seq. ID	uC-gmflminsoy061h07b1
Method	BLASTN
NCBI GI	g2317899
BLAST score	292
E value	1.0e-163
Match length	304
% identity	99
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	51333
Seq. ID	uC-gmflminsoy062b01b1
Method	BLASTX
NCBI GI	g3236261
BLAST score	545
E value	4.0e-56
Match length	119
% identity	81
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	51334
Seq. ID	uC-gmflminsoy062d11b1
Method	BLASTX
NCBI GI	g2623299
BLAST score	264
E value	4.0e-23
Match length	96
% identity	58
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51335
Seq. ID	uC-gmflminsoy062g11b1
Method	BLASTX
NCBI GI	g294845

BLAST score	216
E value	1.0e-20
Match length	101
% identity	48
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]

Seq. No.	51336
Seq. ID	uC-gmflminsoy063b06b1
Method	BLASTX
NCBI GI	g1679803
BLAST score	276
E value	2.0e-24
Match length	108
% identity	54
NCBI Description	(D87545) histidine kinase homolog [Arabidopsis thaliana] >gi_2529684 (AC002535) histidine kinase homolog [Arabidopsis thaliana]

Seq. No.	51337
Seq. ID	uC-gmflminsoy063b09b1
Method	BLASTN
NCBI GI	g18644
BLAST score	105
E value	4.0e-52
Match length	149
% identity	93
NCBI Description	Soybean mRNA for HMG-1 like protein

Seq. No.	51338
Seq. ID	uC-gmflminsoy063d09b1
Method	BLASTX
NCBI GI	g4490706
BLAST score	174
E value	1.0e-12
Match length	42
% identity	71
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	51339
Seq. ID	uC-gmflminsoy063f09b1
Method	BLASTX
NCBI GI	g2384669
BLAST score	349
E value	2.0e-33
Match length	89
% identity	75
NCBI Description	(AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]

Seq. No.	51340
Seq. ID	uC-gmflminsoy063g05b1
Method	BLASTN
NCBI GI	g2598656
BLAST score	178
E value	1.0e-95
Match length	286

% identity	91
NCBI Description	Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.	51341
Seq. ID	uC-gmflminsoy063g11b1
Method	BLASTX
NCBI GI	g2914693
BLAST score	307
E value	3.0e-28
Match length	110
% identity	30
NCBI Description	(AC003974) putative protein kinase [Arabidopsis thaliana]

Seq. No.	51342
Seq. ID	uC-gmflminsoy063h08b1
Method	BLASTX
NCBI GI	g1351945
BLAST score	284
E value	5.0e-26
Match length	60
% identity	57
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA2 >gi_533709 (U12546) APETALA2 protein [Arabidopsis thaliana] >gi_2464888_emb_CAB16765_ (Z99707) APETALA2 protein [Arabidopsis thaliana]

Seq. No.	51343
Seq. ID	uC-gmflminsoy063h10b1
Method	BLASTX
NCBI GI	g2497541
BLAST score	184
E value	3.0e-14
Match length	56
% identity	66
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_482936_emb_CAA82222_ (Z28373) pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	51344
Seq. ID	uC-gmflminsoy064a08b1
Method	BLASTX
NCBI GI	g3540281
BLAST score	195
E value	3.0e-15
Match length	83
% identity	22
NCBI Description	(AF056116) All-1 related protein [Fugu rubripes]

Seq. No.	51345
Seq. ID	uC-gmflminsoy064b09b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	32
E value	1.0e-08
Match length	47
% identity	48
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51346
Seq. ID	uC-gmflminsoy064d01b1
Method	BLASTN
NCBI GI	g16508
BLAST score	71
E value	9.0e-32
Match length	171
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	51347
Seq. ID	uC-gmflminsoy064e07b1
Method	BLASTX
NCBI GI	g3176676
BLAST score	147
E value	2.0e-09
Match length	72
% identity	46
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	51348
Seq. ID	uC-gmflminsoy064h10b1
Method	BLASTX
NCBI GI	g4335735
BLAST score	146
E value	3.0e-09
Match length	49
% identity	59
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51349
Seq. ID	uC-gmflminsoy065c01b1
Method	BLASTX
NCBI GI	g4185599
BLAST score	209
E value	6.0e-17
Match length	76
% identity	49
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	51350
Seq. ID	uC-gmflminsoy065d06b1
Method	BLASTX
NCBI GI	g2654868
BLAST score	230
E value	5.0e-19
Match length	107
% identity	45
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	51351

Seq. ID	uC-gmflminsoy065e04b1
Method	BLASTX
NCBI GI	g2105430
BLAST score	328
E value	1.0e-30
Match length	114
% identity	54
NCBI Description	(U97079) U5-116kD [Mus musculus]

Seq. No.	51352
Seq. ID	uC-gmflminsoy065f03b1
Method	BLASTX
NCBI GI	g2244847
BLAST score	176
E value	4.0e-13
Match length	53
% identity	62
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	51353
Seq. ID	uC-gmflminsoy065g06b1
Method	BLASTX
NCBI GI	g3924611
BLAST score	188
E value	3.0e-14
Match length	109
% identity	34
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51354
Seq. ID	uC-gmflminsoy066e05b1
Method	BLASTX
NCBI GI	g3925363
BLAST score	278
E value	6.0e-25
Match length	95
% identity	56
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	51355
Seq. ID	uC-gmflminsoy066f02b1
Method	BLASTX
NCBI GI	g3738334
BLAST score	209
E value	4.0e-17
Match length	81
% identity	60
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	51356
Seq. ID	uC-gmflminsoy066f03b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	159
E value	3.0e-11
Match length	48

% identity	31
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	51357
Seq. ID	uC-gmflminsoy066f09b1
Method	BLASTX
NCBI GI	g3914472
BLAST score	325
E value	3.0e-30
Match length	88
% identity	75
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	51358
Seq. ID	uC-gmflminsoy067a08b1
Method	BLASTX
NCBI GI	g3335350
BLAST score	231
E value	1.0e-19
Match length	74
% identity	61
NCBI Description	(AC004512) Similar to gb_Z84386 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus. [Arabidopsis thaliana]

Seq. No.	51359
Seq. ID	uC-gmflminsoy067e02b1
Method	BLASTN
NCBI GI	g349158
BLAST score	192
E value	1.0e-104
Match length	332
% identity	90
NCBI Description	Vigna aconitifolia AIR carboxylase (purE) mRNA, partial cds

Seq. No.	51360
Seq. ID	uC-gmflminsoy067f04b1
Method	BLASTX
NCBI GI	g4262186
BLAST score	440
E value	9.0e-44
Match length	125
% identity	69
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	51361
Seq. ID	uC-gmflminsoy067g12b1
Method	BLASTN
NCBI GI	g2213424
BLAST score	100
E value	5.0e-49
Match length	244

% identity	86
NCBI Description	Citrus paradisi mRNA for hypothetical protein

Seq. No.	51362
Seq. ID	uC-gmflminsoy067h06b1
Method	BLASTX
NCBI GI	g4455202
BLAST score	240
E value	2.0e-20
Match length	90
% identity	50
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No.	51363
Seq. ID	uC-gmflminsoy068b01b1
Method	BLASTX
NCBI GI	g4097547
BLAST score	238
E value	4.0e-20
Match length	70
% identity	34
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	51364
Seq. ID	uC-gmflminsoy068c01b1
Method	BLASTX
NCBI GI	g3643603
BLAST score	464
E value	1.0e-46
Match length	132
% identity	73
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	51365
Seq. ID	uC-gmflminsoy068h03b1
Method	BLASTX
NCBI GI	g4206196
BLAST score	170
E value	2.0e-12
Match length	53
% identity	62
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51366
Seq. ID	uC-gmflminsoy069a07b1
Method	BLASTX
NCBI GI	g710626
BLAST score	217
E value	1.0e-17
Match length	76
% identity	55
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	51367

Seq. ID	uC-gmflminsoy069e06b1
Method	BLASTN
NCBI GI	g4164158
BLAST score	98
E value	8.0e-48
Match length	246
% identity	85
NCBI Description	Passiflora edulis mRNA for ethylene receptor, complete cds

Seq. No.	51368
Seq. ID	uC-gmflminsoy069g11b1
Method	BLASTX
NCBI GI	g3152595
BLAST score	611
E value	9.0e-64
Match length	137
% identity	83
NCBI Description	(AC002986) Similar to D. melanogaster sno gene gb_U95760. EST gb_N97148 and gb_Z26221 come from this gene. [Arabidopsis thaliana]

Seq. No.	51369
Seq. ID	uC-gmflminsoy069h02b1
Method	BLASTX
NCBI GI	g2852449
BLAST score	358
E value	3.0e-34
Match length	89
% identity	81
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No.	51370
Seq. ID	uC-gmflminsoy069h09b1
Method	BLASTN
NCBI GI	g3985958
BLAST score	39
E value	2.0e-12
Match length	151
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	51371
Seq. ID	uC-gmflminsoy070d04b1
Method	BLASTX
NCBI GI	g3287696
BLAST score	345
E value	4.0e-33
Match length	74
% identity	88
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	51372

Seq. ID	uC-gmflminsoy070e07b1
Method	BLASTN
NCBI GI	g456713
BLAST score	179
E value	4.0e-96
Match length	339
% identity	28
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	51373
Seq. ID	uC-gmflminsoy070e11b1
Method	BLASTX
NCBI GI	g4406775
BLAST score	214
E value	3.0e-17
Match length	83
% identity	48
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	51374
Seq. ID	uC-gmflminsoy070h01b1
Method	BLASTX
NCBI GI	g4432859
BLAST score	184
E value	4.0e-14
Match length	65
% identity	57
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	51375
Seq. ID	uC-gmflminsoy071d01b2
Method	BLASTX
NCBI GI	g3360289
BLAST score	334
E value	3.0e-31
Match length	122
% identity	31
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	51376
Seq. ID	uC-gmflminsoy071d06b2
Method	BLASTX
NCBI GI	g404690
BLAST score	315
E value	3.0e-29
Match length	112
% identity	56
NCBI Description	(L19075) cytochrome P450 [Catharanthus roseus]

Seq. No.	51377
Seq. ID	uC-gmflminsoy071e01b2
Method	BLASTX
NCBI GI	g2499570
BLAST score	248
E value	4.0e-21
Match length	68

% identity	69
NCBI Description	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) >gi_414332 (L07941) L-isoaspartyl methyltransferase [Triticum aestivum]

Seq. No.	51378
Seq. ID	uC-gmflminsoy071e02b2
Method	BLASTX
NCBI GI	g4263695
BLAST score	355
E value	1.0e-33
Match length	144
% identity	28
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No.	51379
Seq. ID	uC-gmflminsoy071h07b2
Method	BLASTX
NCBI GI	g3193293
BLAST score	161
E value	4.0e-11
Match length	113
% identity	37
NCBI Description	(AF069298) contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375) [Arabidopsis thaliana]

Seq. No.	51380
Seq. ID	uC-gmflminsoy072a03b1
Method	BLASTX
NCBI GI	g3540206
BLAST score	189
E value	3.0e-14
Match length	125
% identity	35
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	51381
Seq. ID	uC-gmflminsoy072d09b1
Method	BLASTX
NCBI GI	g2791896
BLAST score	173
E value	1.0e-12
Match length	83
% identity	45
NCBI Description	(Y08997) 146kDa nuclear protein [Xenopus laevis]

Seq. No.	51382
Seq. ID	uC-gmflminsoy072e08b1
Method	BLASTX
NCBI GI	g2494165
BLAST score	192
E value	1.0e-14
Match length	54

% identity	65
NCBI Description	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No.	51383
Seq. ID	uC-gmflminsoy074h02b1
Method	BLASTX
NCBI GI	g731675
BLAST score	330
E value	8.0e-31
Match length	118
% identity	55
NCBI Description	HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION >gi_626631_pir__S46811 hypothetical protein YHR074w - yeast (Saccharomyces cerevisiae) >gi_500832 (U10556) Yhr074wp [Saccharomyces cerevisiae]

Seq. No.	51384
Seq. ID	uC-gmflminsoy075e11b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	2.0e-09
Match length	34
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51385
Seq. ID	uC-gmflminsoy075g04b1
Method	BLASTN
NCBI GI	g4098318
BLAST score	254
E value	1.0e-141
Match length	474
% identity	88
NCBI Description	Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds

Seq. No.	51386
Seq. ID	uC-gmflminsoy076c12b1
Method	BLASTX
NCBI GI	g1345132
BLAST score	199
E value	2.0e-15
Match length	141
% identity	3
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	51387
Seq. ID	uC-gmflminsoy076e12b1
Method	BLASTX
NCBI GI	g3063713
BLAST score	149

E value	2.0e-09
Match length	68
% identity	50
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	51388
Seq. ID	uC-gmflminsoy076h12b1
Method	BLASTX
NCBI GI	g2760839
BLAST score	383
E value	4.0e-37
Match length	118
% identity	66
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	51389
Seq. ID	uC-gmflminsoy077b05b1
Method	BLASTX
NCBI GI	g3402711
BLAST score	233
E value	1.0e-19
Match length	80
% identity	35
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	51390
Seq. ID	uC-gmflminsoy077b07b1
Method	BLASTX
NCBI GI	g2262101
BLAST score	525
E value	1.0e-53
Match length	133
% identity	79
NCBI Description	(AC002343) kinesin heavy chain isolog [Arabidopsis thaliana]

Seq. No.	51391
Seq. ID	uC-gmflminsoy077c06b1
Method	BLASTX
NCBI GI	g2146727
BLAST score	247
E value	2.0e-21
Match length	90
% identity	49
NCBI Description	cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 - Arabidopsis thaliana (fragment) >gi_598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	51392
Seq. ID	uC-gmflminsoy077c12b1
Method	BLASTX
NCBI GI	g3786324
BLAST score	180
E value	3.0e-13
Match length	87
% identity	44

NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]

Seq. No.	51393
Seq. ID	uC-gmflminsoy077f02b1
Method	BLASTX
NCBI GI	g3850588
BLAST score	469
E value	4.0e-47
Match length	138
% identity	71
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No.	51394
Seq. ID	uC-gmflminsoy077g02b1
Method	BLASTX
NCBI GI	g2244934
BLAST score	314
E value	5.0e-29
Match length	64
% identity	92
NCBI Description	(Z97339) similarity to SYNAPTOBREVIN-RELATED PROTEIN [Arabidopsis thaliana]

Seq. No.	51395
Seq. ID	uC-gmflminsoy078a05b1
Method	BLASTX
NCBI GI	g1363984
BLAST score	262
E value	5.0e-23
Match length	83
% identity	60
NCBI Description	V(D)J recombinational signal sequence-dependent DNA joining protein 2 - mouse >gi_1066815 (M88489) nonamer binding protein [Mus musculus]

Seq. No.	51396
Seq. ID	uC-gmflminsoy078a09b1
Method	BLASTX
NCBI GI	g3559816
BLAST score	633
E value	2.0e-66
Match length	132
% identity	94
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	51397
Seq. ID	uC-gmflminsoy078d12b1
Method	BLASTX
NCBI GI	g4262222
BLAST score	343
E value	2.0e-32
Match length	118
% identity	62

NCBI Description	(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]

Seq. No.	51398
Seq. ID	uC-gmflminsoy078g10b1
Method	BLASTX
NCBI GI	g3033380
BLAST score	362
E value	1.0e-34
Match length	105
% identity	68
NCBI Description	(AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No.	51399
Seq. ID	uC-gmflminsoy079b05b1
Method	BLASTX
NCBI GI	g4049353
BLAST score	369
E value	2.0e-35
Match length	123
% identity	55
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	51400
Seq. ID	uC-gmflminsoy079d04b1
Method	BLASTN
NCBI GI	g18775
BLAST score	110
E value	5.0e-55
Match length	202
% identity	93
NCBI Description	G.max tufA gene for chloroplast translation elongation factor EF-Tu

Seq. No.	51401
Seq. ID	uC-gmflminsoy079e07b1
Method	BLASTX
NCBI GI	g3096949
BLAST score	202
E value	6.0e-16
Match length	84
% identity	55
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	51402
Seq. ID	uC-gmflminsoy079f07b1
Method	BLASTX
NCBI GI	g2129772
BLAST score	344
E value	1.0e-32
Match length	97
% identity	63
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	51403
Seq. ID	uC-gmflminsoy079f11b1
Method	BLASTX
NCBI GI	g4432841
BLAST score	517
E value	1.0e-52
Match length	148
% identity	66
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51404
Seq. ID	uC-gmflminsoy080e10b1
Method	BLASTN
NCBI GI	g402635
BLAST score	114
E value	2.0e-57
Match length	214
% identity	88
NCBI Description	L.albus gene for beta-tubulin

Seq. No.	51405
Seq. ID	uC-gmflminsoy080g01b1
Method	BLASTX
NCBI GI	g3236240
BLAST score	594
E value	1.0e-61
Match length	127
% identity	87
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	51406
Seq. ID	uC-gmflminsoy081b03b1
Method	BLASTX
NCBI GI	g2275202
BLAST score	326
E value	2.0e-30
Match length	92
% identity	65
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	51407
Seq. ID	uC-gmflminsoy081b05b1
Method	BLASTX
NCBI GI	g3023522
BLAST score	404
E value	2.0e-39
Match length	109
% identity	68
NCBI Description	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_2454309 (AF002705) beta prime COP [Rattus norvegicus]

Seq. No.	51408
Seq. ID	uC-gmflminsoy081b08b1

Method	BLASTX
NCBI GI	g1809257
BLAST score	223
E value	1.0e-24
Match length	117
% identity	50
NCBI Description	(U59316) serine/threonine protein kinase Pto [Lycopersicon esculentum]

Seq. No.	51409
Seq. ID	uC-gmflminsoy081d02b1
Method	BLASTX
NCBI GI	g4455240
BLAST score	269
E value	1.0e-23
Match length	131
% identity	49
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	51410
Seq. ID	uC-gmflminsoy081f03b1
Method	BLASTX
NCBI GI	g1938569
BLAST score	252
E value	9.0e-22
Match length	113
% identity	47
NCBI Description	(U97189) strong similarity to thw P13/P14 family of kinases [Caenorhabditis elegans]

Seq. No.	51411
Seq. ID	uC-gmflminsoy082e01b1
Method	BLASTX
NCBI GI	g4006868
BLAST score	187
E value	3.0e-14
Match length	63
% identity	60
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	51412
Seq. ID	uC-gmflminsoy083b06b1
Method	BLASTX
NCBI GI	g3426048
BLAST score	377
E value	2.0e-36
Match length	126
% identity	56
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	51413
Seq. ID	uC-gmflminsoy083g02b1
Method	BLASTX
NCBI GI	g3892054
BLAST score	261
E value	4.0e-23

Match length 82
% identity 59
NCBI Description (AC002330) putative glycosyltransferase [Arabidopsis thaliana]

Seq. No. 51414
Seq. ID uC-gmflminsoy084e05b1
Method BLASTX
NCBI GI g3643608
BLAST score 149
E value 1.0e-09
Match length 123
% identity 31
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51415
Seq. ID uC-gmflminsoy084f11b1
Method BLASTX
NCBI GI g2832658
BLAST score 160
E value 4.0e-11
Match length 39
% identity 79
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 51416
Seq. ID uC-gmflminsoy084g12b1
Method BLASTX
NCBI GI g4490721
BLAST score 207
E value 1.0e-20
Match length 65
% identity 78
NCBI Description (AL035709) squalene epoxidase-like protein [Arabidopsis thaliana]

Seq. No. 51417
Seq. ID uC-gmflminsoy089d06b1
Method BLASTX
NCBI GI g1397319
BLAST score 147
E value 3.0e-09
Match length 71
% identity 41
NCBI Description (U61953) No definition line found [Caenorhabditis elegans]

Seq. No. 51418
Seq. ID uC-gmflminsoy089f02b1
Method BLASTX
NCBI GI g2244876
BLAST score 270
E value 2.0e-30
Match length 107
% identity 63
NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51419

Seq. ID	uC-gmflminsoy089g02b1
Method	BLASTX
NCBI GI	g4314358
BLAST score	434
E value	3.0e-43
Match length	106
% identity	77
NCBI Description	(AC006340) putative kinesin heavy chain protein [Arabidopsis thaliana]

Seq. No.	51420
Seq. ID	uC-gmflminsoy089g05b1
Method	BLASTX
NCBI GI	g3335366
BLAST score	417
E value	4.0e-41
Match length	104
% identity	74
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	51421
Seq. ID	uC-gmflminsoy091e03b1
Method	BLASTX
NCBI GI	g3688600
BLAST score	191
E value	8.0e-18
Match length	64
% identity	73
NCBI Description	(AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq. No.	51422
Seq. ID	uC-gmflminsoy091f08b1
Method	BLASTX
NCBI GI	g2618687
BLAST score	274
E value	3.0e-24
Match length	100
% identity	58
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51423
Seq. ID	uC-gmflminsoy091g03b1
Method	BLASTX
NCBI GI	g2772934
BLAST score	274
E value	2.0e-24
Match length	94
% identity	57
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	51424
Seq. ID	uC-gmflminsoy093d10b1
Method	BLASTX
NCBI GI	g3402711
BLAST score	254
E value	3.0e-22

Match length 68
% identity 37
NCBI Description (AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No. 51425
Seq. ID uC-gmflminsoy097c03b1
Method BLASTX
NCBI GI g549059
BLAST score 158
E value 9.0e-11
Match length 49
% identity 63
NCBI Description T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA) (CCT-GAMMA) (MATRICIN) >gi_631654_pir__S43062 CCT (chaperonin containing TCP-1) gamma chain - mouse >gi_468552_emb_CAA83431_ (Z31556) CCT (chaperonin containing TCP-1) gamma subunit [Mus musculus]

Seq. No. 51426
Seq. ID uC-gmflminsoy097d01b1
Method BLASTN
NCBI GI g18764
BLAST score 328
E value 0.0e+00
Match length 344
% identity 99
NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 51427
Seq. ID uC-gmflminsoy097e02b1
Method BLASTN
NCBI GI g1335861
BLAST score 84
E value 7.0e-40
Match length 152
% identity 91
NCBI Description Glycine max clathrin heavy chain mRNA, complete cds

Seq. No. 51428
Seq. ID uC-gmflminsoy097f05b1
Method BLASTX
NCBI GI g2651295
BLAST score 199
E value 8.0e-16
Match length 75
% identity 56
NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51429
Seq. ID uC-gmflminsoy098d05b1
Method BLASTX
NCBI GI g3560166
BLAST score 236
E value 8.0e-20
Match length 125
% identity 43

NCBI Description	(AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]

Seq. No.	51430
Seq. ID	uC-gmflminsoy098g12b1
Method	BLASTN
NCBI GI	g2654107
BLAST score	210
E value	1.0e-114
Match length	402
% identity	88
NCBI Description	Pisum sativum cytosine-5 DNA methyltransferase mRNA, complete cds

Seq. No.	51431
Seq. ID	uC-gmflminsoy099a02b1
Method	BLASTX
NCBI GI	g4559342
BLAST score	262
E value	2.0e-23
Match length	56
% identity	84
NCBI Description	(AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No.	51432
Seq. ID	uC-gmflminsoy099a08b1
Method	BLASTN
NCBI GI	g2832639
BLAST score	62
E value	2.0e-26
Match length	122
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	51433
Seq. ID	uC-gmflminsoy099b01b1
Method	BLASTX
NCBI GI	g1363492
BLAST score	195
E value	4.0e-15
Match length	54
% identity	65
NCBI Description	outer envelope membrane protein OEP75 precursor - garden pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No.	51434
Seq. ID	uC-gmflminsoy099c06b1
Method	BLASTN
NCBI GI	g4558461
BLAST score	87
E value	1.0e-41
Match length	123
% identity	93

NCBI Description	Medicago sativa subsp. X varia cell cycle switch protein (ccs52) mRNA, complete cds
Seq. No.	51435
Seq. ID	uC-gmflminsoy099e02b1
Method	BLASTX
NCBI GI	g3158476
BLAST score	409
E value	2.0e-40
Match length	91
% identity	86
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]
Seq. No.	51436
Seq. ID	uC-gmflminsoy099e11b1
Method	BLASTX
NCBI GI	g4455367
BLAST score	407
E value	4.0e-40
Match length	87
% identity	63
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]
Seq. No.	51437
Seq. ID	uC-gmflminsoy099f01b1
Method	BLASTN
NCBI GI	g4324966
BLAST score	250
E value	1.0e-138
Match length	258
% identity	99
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds
Seq. No.	51438
Seq. ID	uC-gmflminsoy099g07b1
Method	BLASTX
NCBI GI	g1362152
BLAST score	388
E value	7.0e-38
Match length	90
% identity	79
NCBI Description	ribosomal protein S6 kinase homolog (clone Aspk11) - oat >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal protein S6 kinase [Avena sativa]
Seq. No.	51439
Seq. ID	uC-gmflminsoy099h08b1
Method	BLASTX
NCBI GI	g4314363
BLAST score	177
E value	6.0e-13
Match length	99
% identity	19
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.	51440
Seq. ID	uC-gmflminsoy100a11b1

Method	BLASTN
NCBI GI	g2921511
BLAST score	64
E value	1.0e-27
Match length	68
% identity	99
NCBI Description	Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds

Seq. No.	51441
Seq. ID	uC-gmflminsoy100c09b1
Method	BLASTX
NCBI GI	g3540180
BLAST score	393
E value	3.0e-38
Match length	116
% identity	76
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	51442
Seq. ID	uC-gmflminsoy100e03b1
Method	BLASTX
NCBI GI	g3341692
BLAST score	184
E value	5.0e-14
Match length	81
% identity	52
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	51443
Seq. ID	uC-gmflminsoy100h07b1
Method	BLASTX
NCBI GI	g4544438
BLAST score	145
E value	2.0e-09
Match length	78
% identity	40
NCBI Description	(AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51444
Seq. ID	uC-gmflminsoy108c09b1
Method	BLASTX
NCBI GI	g1402912
BLAST score	278
E value	4.0e-25
Match length	85
% identity	60
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	51445
Seq. ID	uC-gmflminsoy108d03b1
Method	BLASTX
NCBI GI	g1272349
BLAST score	166
E value	4.0e-12
Match length	50
% identity	60
NCBI Description	(U51740) secreted glycoprotein 3 [Ipomoea trifida]

Seq. No.	51446
Seq. ID	uC-gmflminsoy108d08b1
Method	BLASTX
NCBI GI	g4056568
BLAST score	182
E value	1.0e-13
Match length	76
% identity	15
NCBI Description	(U90944) PDI-like protein [Zea mays]

Seq. No.	51447
Seq. ID	uC-gmflminsoy108e06b1
Method	BLASTX
NCBI GI	g3169174
BLAST score	250
E value	2.0e-21
Match length	91
% identity	57
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	51448
Seq. ID	uC-gmflminsoy109a01b1
Method	BLASTX
NCBI GI	g4263510
BLAST score	198
E value	1.0e-15
Match length	93
% identity	43
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51449
Seq. ID	uC-gmflminsoy109a08b1
Method	BLASTX
NCBI GI	g2618698
BLAST score	212
E value	1.0e-17
Match length	79
% identity	62
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	51450
Seq. ID	uC-gmflminsoy109c11b1
Method	BLASTN
NCBI GI	g4521152
BLAST score	81
E value	9.0e-38
Match length	211
% identity	87
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	51451
Seq. ID	uC-gmflminsoy109d02b1
Method	BLASTX
NCBI GI	g2558664

BLAST score	212
E value	1.0e-17
Match length	69
% identity	54
NCBI Description	(AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51452
Seq. ID	uC-gmflminsoy109e03b1
Method	BLASTX
NCBI GI	g3947735
BLAST score	164
E value	1.0e-11
Match length	57
% identity	54
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	51453
Seq. ID	uC-gmflminsoy109e09b1
Method	BLASTX
NCBI GI	g4432839
BLAST score	261
E value	3.0e-23
Match length	72
% identity	44
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	51454
Seq. ID	uC-gmflminsoy109g09b1
Method	BLASTX
NCBI GI	g1935019
BLAST score	404
E value	8.0e-40
Match length	91
% identity	86
NCBI Description	(Z93774) sucrose transport protein [Vicia faba]

Seq. No.	51455
Seq. ID	uC-gmflminsoy115d11b1
Method	BLASTX
NCBI GI	g3915737
BLAST score	211
E value	2.0e-17
Match length	56
% identity	75
NCBI Description	IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon esculentum]

Seq. No.	51456
Seq. ID	uC-gmflminsoy115g10b1
Method	BLASTX
NCBI GI	g4240120
BLAST score	197
E value	2.0e-15
Match length	46
% identity	72
NCBI Description	(AB007801) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	51457
Seq. ID	uC-gmflminsoy117c04b1
Method	BLASTX
NCBI GI	g2961346
BLAST score	397
E value	1.0e-38
Match length	118
% identity	67
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	51458
Seq. ID	uC-gmflminsoy117e11b1
Method	BLASTN
NCBI GI	g170042
BLAST score	135
E value	5.0e-70
Match length	221
% identity	93
NCBI Description	Glycine max cv Prize protein kinase mRNA

Seq. No.	51459
Seq. ID	uC-gmflminsoy117g04b1
Method	BLASTX
NCBI GI	g629670
BLAST score	173
E value	2.0e-12
Match length	75
% identity	51
NCBI Description	hypothetical protein - tomato

Seq. No.	51460
Seq. ID	uC-gmflminsoy117h06b1
Method	BLASTX
NCBI GI	g82307
BLAST score	469
E value	4.0e-47
Match length	99
% identity	86
NCBI Description	myb protein 306 - garden snapdragon >gi_256828_bbs_115017 Myb oncoprotein homolog {clone 306} [Antirrhinum majus=snapdragons, J1:522, flowers, Peptide, 316 aa]

Seq. No.	51461
Seq. ID	uC-gmflminsoy118b05b1
Method	BLASTX
NCBI GI	g1707007
BLAST score	216
E value	2.0e-17
Match length	121
% identity	9
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51462
Seq. ID	uC-gmflminsoy118b06b1
Method	BLASTX

NCBI GI	g2894599
BLAST score	282
E value	3.0e-25
Match length	62
% identity	85
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	51463
Seq. ID	uC-gmflminsoy118c02b1
Method	BLASTN
NCBI GI	g169958
BLAST score	115
E value	7.0e-58
Match length	226
% identity	91
NCBI Description	Glycine max G-box binding factor (GBF2A) mRNA, 3' end

Seq. No.	51464
Seq. ID	uC-gmflminsoy118e01b1
Method	BLASTX
NCBI GI	g4539363
BLAST score	197
E value	2.0e-15
Match length	72
% identity	51
NCBI Description	(AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	51465
Seq. ID	uC-gmflminsoy119g12b1
Method	BLASTN
NCBI GI	g456713
BLAST score	235
E value	1.0e-129
Match length	283
% identity	28
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	51466
Seq. ID	uC-gmflminsoy119h04b1
Method	BLASTX
NCBI GI	g2827658
BLAST score	412
E value	2.0e-40
Match length	142
% identity	55
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	51467
Seq. ID	uC-gmflminsoy120b10b1
Method	BLASTX
NCBI GI	g4006858
BLAST score	166
E value	4.0e-12
Match length	60
% identity	58
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	51468
Seq. ID	uC-gmflminsoy120d03b1
Method	BLASTX
NCBI GI	g3548803
BLAST score	152
E value	5.0e-23
Match length	76
% identity	76
NCBI Description	(AC005313) putative DNA-binding protein [Arabidopsis thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No.	51469
Seq. ID	uC-gmflminsoy120d10b1
Method	BLASTN
NCBI GI	g3184053
BLAST score	40
E value	2.0e-13
Match length	64
% identity	91
NCBI Description	Pisum sativum mRNA for MADS-box transcription factor

Seq. No.	51470
Seq. ID	uC-gmflminsoy120e10b1
Method	BLASTN
NCBI GI	g166411
BLAST score	141
E value	1.0e-73
Match length	277
% identity	88
NCBI Description	Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No.	51471
Seq. ID	uC-gmflminsoy120f07b1
Method	BLASTX
NCBI GI	g1402879
BLAST score	259
E value	9.0e-23
Match length	90
% identity	58
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495247_emb_CAA66220_ (X97616) orf 05 [Arabidopsis thaliana]

Seq. No.	51472
Seq. ID	uC-gmrominsoy0001a02b1
Method	BLASTX
NCBI GI	g3688209
BLAST score	181
E value	2.0e-13
Match length	120
% identity	49
NCBI Description	(AJ010093) MAP3K beta 1 protein kinase [Brassica napus]

Seq. No.	51473
Seq. ID	uC-gmrominsoy0001f09a1

Method	BLASTX
NCBI GI	g4097880
BLAST score	202
E value	3.0e-16
Match length	64
% identity	66
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	51474
Seq. ID	uC-gmrominsoy0001f12b1
Method	BLASTX
NCBI GI	g3549667
BLAST score	176
E value	5.0e-13
Match length	58
% identity	60
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	51475
Seq. ID	uC-gmrominsoy026b03b1
Method	BLASTN
NCBI GI	g1667372
BLAST score	163
E value	1.0e-86
Match length	327
% identity	83
NCBI Description	M.sativa MMK4 mRNA for protein kinase

Seq. No.	51476
Seq. ID	uC-gmrominsoy026f12b1
Method	BLASTX
NCBI GI	g4567235
BLAST score	338
E value	1.0e-31
Match length	122
% identity	55
NCBI Description	(AC007119) putative phosphatidylinositol/phophatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No.	51477
Seq. ID	uC-gmrominsoy027a07b1
Method	BLASTX
NCBI GI	g3122625
BLAST score	291
E value	1.0e-26
Match length	81
% identity	70
NCBI Description	PROBABLE 26S PROTEASE REGULATORY SUBUNIT S10B >gi_2394434 (AF024493) strong similarity to the AAA family of ATPases [Caenorhabditis elegans]

Seq. No.	51478
Seq. ID	uC-gmrominsoy027f01b1
Method	BLASTN
NCBI GI	g18588
BLAST score	233

E value	1.0e-128
Match length	435
% identity	100
NCBI Description	Soybean gene 3 for chalcone synthetase protein

Seq. No.	51479
Seq. ID	uC-gmrominsoy028b05b1
Method	BLASTN
NCBI GI	g849135
BLAST score	103
E value	1.0e-50
Match length	115
% identity	97
NCBI Description	Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete cds

Seq. No.	51480
Seq. ID	uC-gmrominsoy028c01b1
Method	BLASTX
NCBI GI	g2606077
BLAST score	362
E value	2.0e-34
Match length	137
% identity	53
NCBI Description	(AF030301) auxin-induced protein [Helianthus annuus]

Seq. No.	51481
Seq. ID	uC-gmrominsoy028h07b1
Method	BLASTX
NCBI GI	g1084404
BLAST score	156
E value	2.0e-10
Match length	64
% identity	47
NCBI Description	hypothetical protein - tomato >gi_667069 (L22186) ORF [Lycopersicon esculentum]

Seq. No.	51482
Seq. ID	uC-gmrominsoy029f11b1
Method	BLASTX
NCBI GI	g1084393
BLAST score	217
E value	2.0e-17
Match length	61
% identity	64
NCBI Description	peroxidase (EC 1.11.1.7) precursor - parsley >gi_559235 (L36981) anionic peroxidase [Petroselinum crispum]

Seq. No.	51483
Seq. ID	uC-gmrominsoy030b07b1
Method	BLASTX
NCBI GI	g1109873
BLAST score	285
E value	1.0e-25
Match length	65
% identity	41
NCBI Description	(U41542) Similar to protein disulfide isomerase; coded for

by C. elegans cDNA CEESB65F; coded for by C. elegans cDNA CEESH23FB; coded for by C. elegans cDNA CEESH23FC; coded for by C. elegans cDNA CEESN70F; coded for by C. elegans cDNA CEESO

Seq. No.	51484
Seq. ID	uC-gmrominsoy030e11b1
Method	BLASTX
NCBI GI	g3377820
BLAST score	190
E value	2.0e-14
Match length	52
% identity	69
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	51485
Seq. ID	uC-gmrominsoy030f12b1
Method	BLASTX
NCBI GI	g4490702
BLAST score	273
E value	4.0e-24
Match length	85
% identity	64
NCBI Description	(AL035680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51486
Seq. ID	uC-gmrominsoy031a03b1
Method	BLASTX
NCBI GI	g1663545
BLAST score	252
E value	1.0e-21
Match length	89
% identity	57
NCBI Description	(U55807) disease resistance protein homolog [Glycine max]

Seq. No.	51487
Seq. ID	uC-gmrominsoy032c02b1
Method	BLASTN
NCBI GI	g1808591
BLAST score	61
E value	5.0e-26
Match length	157
% identity	85
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	51488
Seq. ID	uC-gmrominsoy032c08b1
Method	BLASTN
NCBI GI	g4389416
BLAST score	433
E value	0.0e+00
Match length	497
% identity	97
NCBI Description	Glycine max nitrate reductase (nr2) gene, partial cds

Seq. No. 51489

Seq. ID	uC-gmrominsoy032c09b1
Method	BLASTN
NCBI GI	g169980
BLAST score	112
E value	4.0e-56
Match length	211
% identity	89
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	51490
Seq. ID	uC-gmrominsoy032d03b1
Method	BLASTX
NCBI GI	g1778378
BLAST score	386
E value	3.0e-37
Match length	144
% identity	60
NCBI Description	(U81289) NAP1Ps [Pisum sativum]

Seq. No.	51491
Seq. ID	uC-gmrominsoy033g02b1
Method	BLASTX
NCBI GI	g1465818
BLAST score	197
E value	4.0e-15
Match length	63
% identity	54
NCBI Description	(U64855) coded for by C. elegans cDNA CEESS16F; coded for by C. elegans cDNA yk76b10.3; coded for by C. elegans cDNA yk14d4.3; coded for by C. elegans cDNA CEESS16F; coded for by C. elegans cDNA yk49a11.5; coded for by C. elegans cDNA yk48c6

Seq. No.	51492
Seq. ID	uC-gmrominsoy033h02b1
Method	BLASTX
NCBI GI	g1825661
BLAST score	239
E value	4.0e-20
Match length	74
% identity	58
NCBI Description	(U88175) similar to protein-S isoprenylsysteine O-methyltransferase; coded for by C. elegans cDNA yk119c9.5; coded for by C. elegans cDN [Caenorhabditis elegans]

Seq. No.	51493
Seq. ID	uC-gmrominsoy034e05b1
Method	BLASTX
NCBI GI	g3152594
BLAST score	429
E value	2.0e-42
Match length	137
% identity	8
NCBI Description	(AC002986) Contains repeats similar to RECA protein gb_L26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]

Seq. No.	51494
Seq. ID	uC-gmrominsoy034e12b1
Method	BLASTX
NCBI GI	g4097880
BLAST score	249
E value	7.0e-22
Match length	69
% identity	74
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	51495
Seq. ID	uC-gmrominsoy034f02b1
Method	BLASTX
NCBI GI	g2499127
BLAST score	164
E value	2.0e-11
Match length	117
% identity	34
NCBI Description	VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) >gi_1362584_pir__A57245 VAMP-binding protein VAP-33 - California sea hare >gi_1000369 (U36779) vesicle-associated membrane protein/synaptobrevin binding protein [Aplysia californica]

Seq. No.	51496
Seq. ID	uC-gmrominsoy034f03b1
Method	BLASTX
NCBI GI	g2160189
BLAST score	218
E value	8.0e-18
Match length	108
% identity	43
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	51497
Seq. ID	uC-gmrominsoy034f06b1
Method	BLASTX
NCBI GI	g422811
BLAST score	207
E value	2.0e-16
Match length	114
% identity	39
NCBI Description	dnaJ protein homolog - human

Seq. No.	51498
Seq. ID	uC-gmrominsoy034g03b1
Method	BLASTX
NCBI GI	g3355308
BLAST score	203
E value	7.0e-16
Match length	137
% identity	33
NCBI Description	(AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

Seq. No.	51499
Seq. ID	uC-gmrominsoy035a09b1
Method	BLASTN
NCBI GI	g20680
BLAST score	55
E value	1.0e-22
Match length	103
% identity	88
NCBI Description	P.sativum mRNA of cDNA clone 26g

Seq. No.	51500
Seq. ID	uC-gmrominsoy035a10b1
Method	BLASTX
NCBI GI	g2462837
BLAST score	497
E value	2.0e-50
Match length	112
% identity	84
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51501
Seq. ID	uC-gmrominsoy035b11b1
Method	BLASTX
NCBI GI	g3402684
BLAST score	470
E value	3.0e-47
Match length	129
% identity	72
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51502
Seq. ID	uC-gmrominsoy039b12b1
Method	BLASTX
NCBI GI	g393707
BLAST score	293
E value	2.0e-28
Match length	101
% identity	72
NCBI Description	(X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No.	51503
Seq. ID	uC-gmrominsoy039d01b1
Method	BLASTX
NCBI GI	g4406775
BLAST score	140
E value	1.0e-17
Match length	93
% identity	52
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	51504
Seq. ID	uC-gmrominsoy039d12b1
Method	BLASTX
NCBI GI	g2244876
BLAST score	491
E value	1.0e-49
Match length	127

% identity	84
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51505
Seq. ID	uC-gmrominsoy040a08b1
Method	BLASTX
NCBI GI	g2501484
BLAST score	153
E value	5.0e-10
Match length	121
% identity	33
NCBI Description	PUTATIVE UDP-GLUCURONOSYLTRANSFERASE UGT5 PRECURSOR (UDPGT) >gi_3876754_emb_CAA85328_ (Z36752) similar to UDP-glucuronosyltransferase; cDNA EST EMBL:D27910 comes from this gene; cDNA EST EMBL:D27909 comes from this gene [Caenorhabditis elegans]

Seq. No.	51506
Seq. ID	uC-gmrominsoy040b06b1
Method	BLASTX
NCBI GI	g3894387
BLAST score	160
E value	8.0e-11
Match length	120
% identity	6
NCBI Description	(AF053995) Hcr2-0B [Lycopersicon esculentum]

Seq. No.	51507
Seq. ID	uC-gmrominsoy040d07b1
Method	BLASTX
NCBI GI	g2809481
BLAST score	265
E value	3.0e-23
Match length	101
% identity	57
NCBI Description	(AF042839) calmodulin [Oryza sativa]

Seq. No.	51508
Seq. ID	uC-gmrominsoy040f06b1
Method	BLASTX
NCBI GI	g710626
BLAST score	306
E value	7.0e-28
Match length	86
% identity	69
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	51509
Seq. ID	uC-gmrominsoy040g02b1
Method	BLASTN
NCBI GI	g1667372
BLAST score	244
E value	1.0e-135
Match length	391

% identity	91
NCBI Description	M.sativa MMK4 mRNA for protein kinase

Seq. No.	51510
Seq. ID	uC-gmrominsoy040g12b1
Method	BLASTX
NCBI GI	g3668077
BLAST score	172
E value	3.0e-12
Match length	79
% identity	48
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51511
Seq. ID	uC-gmrominsoy040h01b1
Method	BLASTX
NCBI GI	g2160185
BLAST score	513
E value	3.0e-52
Match length	121
% identity	73
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	51512
Seq. ID	uC-gmrominsoy041a02b1
Method	BLASTX
NCBI GI	g4454039
BLAST score	390
E value	7.0e-38
Match length	113
% identity	65
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	51513
Seq. ID	uC-gmrominsoy041b09b1
Method	BLASTX
NCBI GI	g3255965
BLAST score	461
E value	3.0e-46
Match length	118
% identity	36
NCBI Description	(Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]

Seq. No.	51514
Seq. ID	uC-gmrominsoy042g08b1
Method	BLASTX
NCBI GI	g2148043
BLAST score	291
E value	3.0e-26
Match length	114
% identity	43
NCBI Description	S-receptor kinase A14 precursor - Brassica napus >gi_392557 (U00443) S-receptor kinase [Brassica napus]

Seq. No.	51515

Seq. ID	uC-gmrominsoy042h06b1
Method	BLASTX
NCBI GI	g3875291
BLAST score	178
E value	1.0e-13
Match length	62
% identity	17
NCBI Description	(Z81489) Similarity to Human host cell factor C1 (SW:P51610); cDNA EST yk205a3.5 comes from this gene; cDNA EST yk216b10.5 comes from this gene; cDNA EST yk277h9.3 comes from this gene; cDNA EST yk277h9.5 comes from this gene; ... >gi_3877454_emb_CAB03122_ (Z81087) Similarity to Human host cell factor C1 (SW:P51610); cDNA EST yk205a3.5 comes from this gene; cDNA EST yk216b10.5 comes from this gene; cDNA EST yk277h9.3 comes from this gene; cDNA EST yk277h9.5 comes from this gene;

Seq. No.	51516
Seq. ID	uC-gmrominsoy043a11b1
Method	BLASTX
NCBI GI	g1079063
BLAST score	150
E value	1.0e-09
Match length	135
% identity	37
NCBI Description	deep orange protein - fruit fly (Drosophila melanogaster) >gi_798832_emb_CAA60382_ (X86683) deep orange (dor) [Drosophila melanogaster]

Seq. No.	51517
Seq. ID	uC-gmrominsoy043b10b1
Method	BLASTX
NCBI GI	g1345132
BLAST score	158
E value	1.0e-10
Match length	121
% identity	7
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	51518
Seq. ID	uC-gmrominsoy043c10b1
Method	BLASTX
NCBI GI	g4567279
BLAST score	205
E value	4.0e-16
Match length	113
% identity	41
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	51519
Seq. ID	uC-gmrominsoy043d02b1
Method	BLASTX
NCBI GI	g2495184

BLAST score 351
E value 2.0e-59
Match length 130
% identity 92
NCBI Description PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO) >gi_1877018_dbj_BAA11820_ (D83139) protoporphyrinogen oxidase [Arabidopsis thaliana]

Seq. No. 51520
Seq. ID uC-gmrominsoy043g08b1
Method BLASTX
NCBI GI g1078946
BLAST score 358
E value 4.0e-34
Match length 121
% identity 32
NCBI Description gelsolin - American lobster >gi_452313_emb_CAA82650_ (Z29534) gelsolin [Homarus americanus] >gi_453697_dbj_BAA05629_ (D26582) lobster cytoplasmic gelsolin [Homarus americanus]

Seq. No. 51521
Seq. ID uC-gmrominsoy043h02b1
Method BLASTX
NCBI GI g2982452
BLAST score 361
E value 1.0e-34
Match length 105
% identity 65
NCBI Description (AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No. 51522
Seq. ID uC-gmrominsoy044a04b1
Method BLASTX
NCBI GI g2959767
BLAST score 448
E value 1.0e-44
Match length 128
% identity 62
NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No. 51523
Seq. ID uC-gmrominsoy044c04b1
Method BLASTX
NCBI GI g132944
BLAST score 149
E value 2.0e-09
Match length 28
% identity 96
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi_806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 51524

Seq. ID	uC-gmrominsoy044d05b1
Method	BLASTX
NCBI GI	g2981475
BLAST score	433
E value	6.0e-43
Match length	110
% identity	72
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	51525
Seq. ID	uC-gmrominsoy044f12b1
Method	BLASTX
NCBI GI	g4454051
BLAST score	573
E value	3.0e-59
Match length	157
% identity	65
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	51526
Seq. ID	uC-gmrominsoy044g12b1
Method	BLASTX
NCBI GI	g4007734
BLAST score	205
E value	4.0e-16
Match length	125
% identity	38
NCBI Description	(AL034447) putative transmembrane protein [Streptomyces coelicolor]

Seq. No.	51527
Seq. ID	uC-gmrominsoy045d03b1
Method	BLASTN
NCBI GI	g2293133
BLAST score	190
E value	1.0e-102
Match length	346
% identity	89
NCBI Description	Globodera rostochiensis glyceraldehyde-3-phosphate-dehydrogenase (gpd-1) mRNA, partial cds

Seq. No.	51528
Seq. ID	uC-gmrominsoy045f01b1
Method	BLASTX
NCBI GI	g2854182
BLAST score	458
E value	7.0e-46
Match length	94
% identity	94
NCBI Description	(AF045644) similar to the ARF family of ATP-binding proteins [Caenorhabditis elegans]

Seq. No.	51529
Seq. ID	uC-gmrominsoy045h05b1

Method	BLASTN
NCBI GI	g886099
BLAST score	276
E value	1.0e-154
Match length	363
% identity	96
NCBI Description	Glycine max putative water channel protein (Pip1) mRNA, complete cds

Seq. No.	51530
Seq. ID	uC-gmrominsoy046a09b1
Method	BLASTX
NCBI GI	g3461820
BLAST score	183
E value	1.0e-13
Match length	55
% identity	55
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	51531
Seq. ID	uC-gmrominsoy046d07b1
Method	BLASTX
NCBI GI	g3779024
BLAST score	146
E value	2.0e-09
Match length	70
% identity	47
NCBI Description	(AC005171) unknown protein [Arabidopsis thaliana]

Seq. No.	51532
Seq. ID	uC-gmrominsoy046g12b1
Method	BLASTN
NCBI GI	g255407
BLAST score	87
E value	8.0e-42
Match length	111
% identity	95
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	51533
Seq. ID	uC-gmrominsoy047b05b1
Method	BLASTX
NCBI GI	g4102600
BLAST score	696
E value	1.0e-73
Match length	145
% identity	88
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	51534
Seq. ID	uC-gmrominsoy047b09b1
Method	BLASTX
NCBI GI	g1184075
BLAST score	346
E value	1.0e-32

Match length	144
% identity	2
NCBI Description	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No.	51535
Seq. ID	uC-gmrominsoy047c02b1
Method	BLASTX
NCBI GI	g3249105
BLAST score	172
E value	7.0e-13
Match length	59
% identity	56
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	51536
Seq. ID	uC-gmrominsoy047e12b1
Method	BLASTX
NCBI GI	g2736514
BLAST score	465
E value	1.0e-46
Match length	142
% identity	58
NCBI Description	(AF039052) similar to ribophorin I [Caenorhabditis elegans]

Seq. No.	51537
Seq. ID	uC-gmrominsoy047h06b1
Method	BLASTN
NCBI GI	g1938226
BLAST score	52
E value	3.0e-20
Match length	199
% identity	82
NCBI Description	M.sativa mRNA for carbonic anhydrase

Seq. No.	51538
Seq. ID	uC-gmrominsoy048b03b1
Method	BLASTX
NCBI GI	g124727
BLAST score	151
E value	8.0e-10
Match length	92
% identity	3
NCBI Description	INVOLUCRIN >gi_2144795_pir__I36911 involucrin L - douroucouli >gi_176558 (M25313) involucrin (large allele) [Aotus trivirgatus]

Seq. No.	51539
Seq. ID	uC-gmrominsoy048c11b1
Method	BLASTX
NCBI GI	g2499223
BLAST score	315
E value	5.0e-29
Match length	122
% identity	56

NCBI Description	HYPOTHETICAL 63.1 KD PROTEIN R07E4.4 IN CHROMOSOME X >gi_1049394 (U39652) similar to guanosine-diphosphatase from S. cerevisiae, (PIR:P32621) [Caenorhabditis elegans]

Seq. No.	51540
Seq. ID	uC-gmrominsoy048e08b1
Method	BLASTX
NCBI GI	g4558671
BLAST score	352
E value	3.0e-33
Match length	133
% identity	55
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51541
Seq. ID	uC-gmrominsoy048f06b1
Method	BLASTX
NCBI GI	g465981
BLAST score	358
E value	4.0e-34
Match length	117
% identity	68
NCBI Description	HYPOTHETICAL 95.6 KD PROTEIN ZC21.2 IN CHROMOSOME III >gi_630741_pir__S44873 ZC21.2 protein - Caenorhabditis elegans >gi_289732 (L16685) homology with transient receptor potential protein; putative [Caenorhabditis elegans]

Seq. No.	51542
Seq. ID	uC-gmrominsoy049a01b1
Method	BLASTX
NCBI GI	g4567311
BLAST score	279
E value	7.0e-25
Match length	81
% identity	64
NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No.	51543
Seq. ID	uC-gmrominsoy049b03b1
Method	BLASTX
NCBI GI	g3169065
BLAST score	215
E value	2.0e-17
Match length	111
% identity	42
NCBI Description	(AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe]

Seq. No.	51544
Seq. ID	uC-gmrominsoy049b06b1
Method	BLASTX
NCBI GI	g3878427
BLAST score	333
E value	4.0e-31
Match length	129
% identity	51

NCBI Description	(Z81099) predicted using Genefinder; Similarity to Slime mould WD40 repeat protein (SW:P54686); cDNA EST EMBL:M89013 comes from this gene; cDNA EST EMBL:M89299 comes from this gene; cDNA EST EMBL:D70935 comes from this gene; cD
Seq. No.	51545
Seq. ID	uC-gmrominsoy049d08b1
Method	BLASTX
NCBI GI	g2894607
BLAST score	271
E value	9.0e-24
Match length	121
% identity	47
NCBI Description	(AL021889) NAM (no apical meristem) - like protein [Arabidopsis thaliana]
Seq. No.	51546
Seq. ID	uC-gmrominsoy050b03b1
Method	BLASTX
NCBI GI	g135422
BLAST score	703
E value	2.0e-74
Match length	154
% identity	86
NCBI Description	TUBULIN ALPHA-4 CHAIN >gi_88945_pir__A25873 tubulin alpha chain (version 2) - human >gi_2119265_pir__I77427 alpha-tubulin isotype M-alpha-6 - mouse >gi_202215 (M13444) alpha-tubulin isotype M-alpha-6 [Mus musculus]
Seq. No.	51547
Seq. ID	uC-gmrominsoy050c03b1
Method	BLASTX
NCBI GI	g4204304
BLAST score	175
E value	6.0e-13
Match length	34
% identity	88
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	51548
Seq. ID	uC-gmrominsoy050h02b1
Method	BLASTX
NCBI GI	g4206640
BLAST score	256
E value	5.0e-22
Match length	161
% identity	42
NCBI Description	(AF072858) zinc transporter ZAT [Arabidopsis thaliana]
Seq. No.	51549
Seq. ID	uC-gmrominsoy053d10b1
Method	BLASTX
NCBI GI	g3334144
BLAST score	145
E value	4.0e-09
Match length	30

% identity	87
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	51550
Seq. ID	uC-gmrominsoy053e09b1
Method	BLASTN
NCBI GI	g3128135
BLAST score	41
E value	8.0e-14
Match length	73
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	51551
Seq. ID	uC-gmrominsoy053f02b1
Method	BLASTX
NCBI GI	g3875268
BLAST score	433
E value	8.0e-43
Match length	116
% identity	69
NCBI Description	(Z77655) similar to Transthyretin-like family [Caenorhabditis elegans]

Seq. No.	51552
Seq. ID	uC-gmrominsoy055f01b1
Method	BLASTX
NCBI GI	g3122254
BLAST score	111
E value	3.0e-11
Match length	58
% identity	69
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) >gi_2642164 (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51553
Seq. ID	uC-gmrominsoy055g05b1
Method	BLASTN
NCBI GI	g1208536
BLAST score	359
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Glycine max guanine nucleotide regulatory protein (rab2) mRNA, complete cds

Seq. No.	51554
Seq. ID	uC-gmrominsoy055h03b1
Method	BLASTN
NCBI GI	g156758
BLAST score	184
E value	5.0e-99
Match length	392
% identity	87

NCBI Description	D.melanogaster actin gene, complete cds, locus 5C
Seq. No.	51555
Seq. ID	uC-gmrominsoy057a08b1
Method	BLASTX
NCBI GI	g4249388
BLAST score	373
E value	8.0e-36
Match length	95
% identity	74
NCBI Description	(AC005966) Similar to gb_AF025438 Opa-interacting protein (OIP2) from Homo sapiens. [Arabidopsis thaliana]
Seq. No.	51556
Seq. ID	uC-gmrominsoy058e01b1
Method	BLASTX
NCBI GI	g1173209
BLAST score	304
E value	6.0e-28
Match length	67
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal protein S16 protein - upland cotton >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
Seq. No.	51557
Seq. ID	uC-gmrominsoy058e11b1
Method	BLASTN
NCBI GI	g16508
BLAST score	84
E value	1.0e-39
Match length	148
% identity	89
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds
Seq. No.	51558
Seq. ID	uC-gmrominsoy059e03b1
Method	BLASTX
NCBI GI	g1172636
BLAST score	443
E value	4.0e-44
Match length	105
% identity	82
NCBI Description	PROBABLE 26S PROTEASE REGULATORY SUBUNIT 6B >gi_529215 (U12965) similar to CDC48/PAS1/SEC18 family; highest similarity to 26S protease subunit 4, member of eukaryotic ATPase family [Caenorhabditis elegans]
Seq. No.	51559
Seq. ID	uC-gmrominsoy060b09b1
Method	BLASTX
NCBI GI	g3024444
BLAST score	200
E value	1.0e-15

Match length	50
% identity	70
NCBI Description	SERINE/THREONINE-PROTEIN KINASE PRP4 HOMOLOG >gi_1399462 (U48736) serine/threonine-protein kinase PRP4h [Homo sapiens] >gi_4506125_ref_NP_003904.1_pPRP4_ UNKNOWN

Seq. No.	51560
Seq. ID	uC-gmrominsoy060b11b1
Method	BLASTX
NCBI GI	g4105633
BLAST score	152
E value	2.0e-18
Match length	98
% identity	54
NCBI Description	(AF048982) putative ethylene receptor [Arabidopsis thaliana]

Seq. No.	51561
Seq. ID	uC-gmrominsoy061b02b1
Method	BLASTX
NCBI GI	g1169228
BLAST score	201
E value	1.0e-15
Match length	46
% identity	74
NCBI Description	RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639 helicase-like protein - Wood tobacco >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris]

Seq. No.	51562
Seq. ID	uC-gmrominsoy062b11b1
Method	BLASTX
NCBI GI	g2213586
BLAST score	231
E value	3.0e-19
Match length	112
% identity	66
NCBI Description	(AC000348) T7N9.6 [Arabidopsis thaliana]

Seq. No.	51563
Seq. ID	uC-gmrominsoy062g02b1
Method	BLASTX
NCBI GI	g4101591
BLAST score	311
E value	1.0e-28
Match length	125
% identity	50
NCBI Description	(AF005051) aspartyl aminopeptidase [Mus musculus]

Seq. No.	51564
Seq. ID	uC-gmrominsoy065e09b1
Method	BLASTX
NCBI GI	g2914706
BLAST score	277
E value	2.0e-24
Match length	65

% identity	77
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	51565
Seq. ID	uC-gmrominsoy067a01b1
Method	BLASTX
NCBI GI	g1495804
BLAST score	222
E value	1.0e-18
Match length	63
% identity	68
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	51566
Seq. ID	uC-gmrominsoy067f05b1
Method	BLASTX
NCBI GI	g2586082
BLAST score	305
E value	5.0e-28
Match length	110
% identity	55
NCBI Description	(U72725) retrofit [Oryza longistaminata]

Seq. No.	51567
Seq. ID	uC-gmrominsoy069e02b1
Method	BLASTX
NCBI GI	g2624328
BLAST score	230
E value	5.0e-19
Match length	89
% identity	49
NCBI Description	(AJ002894) OsGRP2 [Oryza sativa]

Seq. No.	51568
Seq. ID	uC-gmrominsoy069g08b1
Method	BLASTX
NCBI GI	g3947735
BLAST score	227
E value	1.0e-18
Match length	144
% identity	36
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	51569
Seq. ID	uC-gmrominsoy072h11b1
Method	BLASTX
NCBI GI	g416758
BLAST score	216
E value	9.0e-18
Match length	84
% identity	76
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	51570

Seq. ID	uC-gmrominsoy073c12b1
Method	BLASTX
NCBI GI	g3450842
BLAST score	191
E value	2.0e-14
Match length	56
% identity	71
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	51571
Seq. ID	uC-gmrominsoy073d10b1
Method	BLASTX
NCBI GI	g2191171
BLAST score	267
E value	2.0e-23
Match length	70
% identity	61
NCBI Description	(AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) [Arabidopsis thaliana]

Seq. No.	51572
Seq. ID	uC-gmrominsoy073e04b1
Method	BLASTX
NCBI GI	g3005931
BLAST score	189
E value	3.0e-14
Match length	126
% identity	39
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]

Seq. No.	51573
Seq. ID	uC-gmrominsoy073f11b1
Method	BLASTX
NCBI GI	g1230630
BLAST score	186
E value	7.0e-14
Match length	68
% identity	49
NCBI Description	(U50310) weak similarity to human synapsin Ib (PIR:B35363) [Caenorhabditis elegans]

Seq. No.	51574
Seq. ID	uC-gmrominsoy074c06b1
Method	BLASTX
NCBI GI	g1707139
BLAST score	331
E value	5.0e-31
Match length	94
% identity	69
NCBI Description	(U80836) similar to mitochrondrial 2-oxoglutarate/malate carrier protein [Caenorhabditis elegans]

Seq. No.	51575
Seq. ID	uC-gmrominsoy074f01b1
Method	BLASTX
NCBI GI	g3337361

BLAST score	443
E value	3.0e-44
Match length	98
% identity	85
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	51576
Seq. ID	uC-gmrominsoy074h11b1
Method	BLASTX
NCBI GI	g2911073
BLAST score	243
E value	1.0e-20
Match length	95
% identity	49
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	51577
Seq. ID	uC-gmrominsoy079a01b1
Method	BLASTX
NCBI GI	g4455231
BLAST score	148
E value	2.0e-09
Match length	74
% identity	59
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	51578
Seq. ID	uC-gmrominsoy079d01b1
Method	BLASTX
NCBI GI	g2244785
BLAST score	504
E value	4.0e-51
Match length	145
% identity	71
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51579
Seq. ID	uC-gmrominsoy080g12b1
Method	BLASTX
NCBI GI	g3805845
BLAST score	318
E value	2.0e-29
Match length	98
% identity	60
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	51580
Seq. ID	uC-gmrominsoy081a01b1
Method	BLASTX
NCBI GI	g1063400
BLAST score	256
E value	5.0e-22
Match length	55
% identity	89
NCBI Description	(X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No.	51581

Seq. ID	uC-gmrominsoy081d01b1
Method	BLASTX
NCBI GI	g2245030
BLAST score	141
E value	1.0e-08
Match length	35
% identity	80
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	51582
Seq. ID	uC-gmrominsoy081g07b1
Method	BLASTX
NCBI GI	g2213600
BLAST score	316
E value	4.0e-29
Match length	127
% identity	48
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	51583
Seq. ID	uC-gmrominsoy085c11b1
Method	BLASTX
NCBI GI	g2920587
BLAST score	144
E value	3.0e-09
Match length	55
% identity	44
NCBI Description	(AF038362) TBP-associated factor 172 [Homo sapiens] >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo sapiens]

Seq. No.	51584
Seq. ID	uC-gmrominsoy086a07b1
Method	BLASTX
NCBI GI	g1076389
BLAST score	367
E value	3.0e-35
Match length	77
% identity	51
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	51585
Seq. ID	uC-gmrominsoy086a11b1
Method	BLASTX
NCBI GI	g3746069
BLAST score	156
E value	2.0e-10
Match length	128
% identity	33
NCBI Description	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	51586
Seq. ID	uC-gmrominsoy086g10b1

Method	BLASTX
NCBI GI	g3367596
BLAST score	204
E value	1.0e-21
Match length	90
% identity	62
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	51587
Seq. ID	uC-gmrominsoy087a10b1
Method	BLASTX
NCBI GI	g629564
BLAST score	215
E value	3.0e-17
Match length	43
% identity	95
NCBI Description	ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis thaliana

Seq. No.	51588
Seq. ID	uC-gmrominsoy087c04b1
Method	BLASTX
NCBI GI	g138364
BLAST score	252
E value	4.0e-22
Match length	76
% identity	67
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	51589
Seq. ID	uC-gmrominsoy087d05b1
Method	BLASTN
NCBI GI	g166421
BLAST score	174
E value	5.0e-93
Match length	330
% identity	88
NCBI Description	Medicago sativa ubiquitin carrier protein mRNA, complete cds

Seq. No.	51590
Seq. ID	uC-gmrominsoy087g12b1
Method	BLASTX
NCBI GI	g4580717
BLAST score	273
E value	2.0e-37
Match length	91
% identity	87
NCBI Description	(AF136161) phosphoenolpyruvate carboxykinase 2 [Urochloa panicoides]

Seq. No.	51591
Seq. ID	uC-gmrominsoy088e04b1
Method	BLASTX

NCBI GI	g2281115
BLAST score	187
E value	2.0e-14
Match length	46
% identity	78
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	51592
Seq. ID	uC-gmrominsoy088g09b1
Method	BLASTN
NCBI GI	g166411
BLAST score	167
E value	5.0e-89
Match length	315
% identity	88
NCBI Description	Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No.	51593
Seq. ID	uC-gmrominsoy089d12b1
Method	BLASTX
NCBI GI	g2494321
BLAST score	407
E value	7.0e-40
Match length	93
% identity	80
NCBI Description	PROBABLE INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi_3877497_emb_CAA90247_ (Z49967) similar to initiation factor 5A; cDNA EST EMBL:D75952 comes from this gene; cDNA EST EMBL:D74070 comes from this gene; cDNA EST EMBL:D74623 comes from this gene; cDNA EST EMBL:D74571 comes from this gene; cDNA EST EMBL

Seq. No.	51594
Seq. ID	uC-gmrominsoy089g10b1
Method	BLASTX
NCBI GI	g1123105
BLAST score	146
E value	3.0e-09
Match length	111
% identity	28
NCBI Description	(U42438) similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans]

Seq. No.	51595
Seq. ID	uC-gmrominsoy089h07b1
Method	BLASTX
NCBI GI	g4454467
BLAST score	140
E value	1.0e-08
Match length	46
% identity	59
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	51596
Seq. ID	uC-gmrominsoy090e08b1
Method	BLASTN

NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 41
% identity 63
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 51597
Seq. ID uC-gmrominsoy090f11b1
Method BLASTX
NCBI GI g4006915
BLAST score 302
E value 2.0e-27
Match length 136
% identity 51
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51598
Seq. ID uC-gmrominsoy091e05b1
Method BLASTX
NCBI GI g4263704
BLAST score 268
E value 1.0e-23
Match length 117
% identity 51
NCBI Description (AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No. 51599
Seq. ID uC-gmrominsoy091f12b1
Method BLASTX
NCBI GI g2979543
BLAST score 289
E value 2.0e-26
Match length 67
% identity 90
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51600
Seq. ID uC-gmrominsoy091g04b1
Method BLASTX
NCBI GI g1848214
BLAST score 238
E value 2.0e-33
Match length 96
% identity 74
NCBI Description (Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]

Seq. No. 51601
Seq. ID uC-gmrominsoy092a09b1
Method BLASTX
NCBI GI g2062175
BLAST score 233
E value 3.0e-27
Match length 110
% identity 63

NCBI Description	(AC001645) hypothetical protein [Arabidopsis thaliana]
Seq. No.	51602
Seq. ID	uC-gmrominsoy092a10b1
Method	BLASTN
NCBI GI	g170065
BLAST score	265
E value	1.0e-147
Match length	309
% identity	12
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds
Seq. No.	51603
Seq. ID	uC-gmrominsoy092g02b1
Method	BLASTX
NCBI GI	g1001311
BLAST score	301
E value	1.0e-27
Match length	100
% identity	56
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]
Seq. No.	51604
Seq. ID	uC-gmrominsoy092h04b1
Method	BLASTX
NCBI GI	g4103324
BLAST score	241
E value	1.0e-20
Match length	56
% identity	88
NCBI Description	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]
Seq. No.	51605
Seq. ID	uC-gmrominsoy093e05b1
Method	BLASTN
NCBI GI	g166411
BLAST score	188
E value	1.0e-101
Match length	376
% identity	88
NCBI Description	Medicago sativa NADH-glutamate synthase mRNA, comlete cds
Seq. No.	51606
Seq. ID	uC-gmrominsoy093f06b1
Method	BLASTX
NCBI GI	g1931645
BLAST score	201
E value	1.0e-15
Match length	78
% identity	53
NCBI Description	(U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
Seq. No.	51607
Seq. ID	uC-gmrominsoy094f04b1
Method	BLASTN

NCBI GI	g2104678
BLAST score	63
E value	3.0e-27
Match length	163
% identity	85
NCBI Description	V.faba mRNA for transcription factor containing HMG-box

Seq. No.	51608
Seq. ID	uC-gmrominsoy094g03b1
Method	BLASTX
NCBI GI	g1617274
BLAST score	205
E value	2.0e-16
Match length	61
% identity	64
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	51609
Seq. ID	uC-gmrominsoy095e09b1
Method	BLASTX
NCBI GI	g961442
BLAST score	251
E value	1.0e-21
Match length	93
% identity	28
NCBI Description	(D63875) KIAA0155 gene product is related to C.elegans B0464.2 protein. [Homo sapiens]

Seq. No.	51610
Seq. ID	uC-gmrominsoy098d02b1
Method	BLASTX
NCBI GI	g1002796
BLAST score	355
E value	1.0e-33
Match length	99
% identity	66
NCBI Description	(U33915) Cpm10 [Craterostigma plantagineum]

Seq. No.	51611
Seq. ID	uC-gmrominsoy098e09b1
Method	BLASTX
NCBI GI	g2443881
BLAST score	229
E value	5.0e-19
Match length	51
% identity	82
NCBI Description	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]

Seq. No.	51612
Seq. ID	uC-gmrominsoy098h10b1
Method	BLASTN
NCBI GI	g463251
BLAST score	131
E value	2.0e-67
Match length	303
% identity	86

NCBI Description	M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5
Seq. No.	51613
Seq. ID	uC-gmrominsoy100e04b1
Method	BLASTX
NCBI GI	g1931642
BLAST score	375
E value	4.0e-36
Match length	134
% identity	49
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
Seq. No.	51614
Seq. ID	uC-gmrominsoy100f03b1
Method	BLASTX
NCBI GI	g4454043
BLAST score	300
E value	3.0e-27
Match length	115
% identity	38
NCBI Description	(AL035394) putative receptor kinase [Arabidopsis thaliana]
Seq. No.	51615
Seq. ID	uC-gmrominsoy100f08b1
Method	BLASTX
NCBI GI	g2119045
BLAST score	404
E value	2.0e-39
Match length	125
% identity	67
NCBI Description	small nuclear ribonucleoprotein U1A - potato >gi_1050840_emb_CAA90282_ (Z49990) U1snRNP-specific protein, U1A [Solanum tuberosum]
Seq. No.	51616
Seq. ID	uC-gmrominsoy101f03b1
Method	BLASTN
NCBI GI	g170019
BLAST score	69
E value	6.0e-31
Match length	129
% identity	88
NCBI Description	Soybean maturation protein (MAT1) gene, complete cds
Seq. No.	51617
Seq. ID	uC-gmrominsoy102a08b1
Method	BLASTN
NCBI GI	g2055227
BLAST score	46
E value	1.0e-16
Match length	177
% identity	91
NCBI Description	Glycine max mRNA for SRC1, complete cds
Seq. No.	51618
Seq. ID	uC-gmrominsoy102f03b1

Method	BLASTX
NCBI GI	g3879851
BLAST score	350
E value	4.0e-33
Match length	123
% identity	56
NCBI Description	(Z81592) predicted using Genefinder; cDNA EST yk400g3.3 comes from this gene; cDNA EST EMBL:C08162 comes from this gene; cDNA EST EMBL:C09805 comes from this gene; cDNA EST yk400g3.5 comes from this gene; cDNA EST yk336d10.3 co

Seq. No.	51619
Seq. ID	uC-gmrominsoy102g05b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	6.0e-09
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51620
Seq. ID	uC-gmrominsoy103d10b1
Method	BLASTX
NCBI GI	g3935147
BLAST score	509
E value	1.0e-51
Match length	148
% identity	68
NCBI Description	(AC005106) T25N20.11 [Arabidopsis thaliana]

Seq. No.	51621
Seq. ID	uC-gmrominsoy103e12b1
Method	BLASTX
NCBI GI	g417696
BLAST score	262
E value	8.0e-23
Match length	65
% identity	66
NCBI Description	DNA-DIRECTED RNA POLYMERASES I, II, AND III 8.3 KD POLYPEPTIDE (ABC10-BETA) (ABC8) >gi_1362277_pir__S48885 DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB10 - yeast (Saccharomyces cerevisiae) >gi_295635 (L11274) subunit ABC10beta shared by DNA dependant RNA polymerases I, II, and III [Saccharomyces cerevisiae] >gi_385569_bbs_133380 (S62098) RNA polymerase II subunit RPB10 [yeast, Peptide, 70 aa] [Saccharomyces cerevisiae] >gi_1420491_emb_CAA99425_ (Z75118) ORF YOR210w [Saccharomyces cerevisiae]

Seq. No.	51622
Seq. ID	uC-gmrominsoy103f07b1
Method	BLASTX
NCBI GI	g1947015
BLAST score	188
E value	3.0e-14
Match length	105

% identity	33
NCBI Description	(AF000263) Similar to phenylalanyl-tRNA synthetase; coded for by C. elegans cDNA yk174a7.3; coded for by C. elegans cDNA yk174a7.5; coded for by C. elegans cDNA CEESP75F; coded for by C. elegans cDNA CEESV94F; coded for by C. elegans cDNA CE

Seq. No.	51623
Seq. ID	uC-gmrominsoy103h03b1
Method	BLASTX
NCBI GI	g2633727
BLAST score	270
E value	1.0e-23
Match length	116
% identity	49
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	51624
Seq. ID	uC-gmrominsoy103h12b1
Method	BLASTX
NCBI GI	g1871199
BLAST score	193
E value	6.0e-15
Match length	85
% identity	45
NCBI Description	(U91318) pM5 (3' partial) [Homo sapiens]

Seq. No.	51625
Seq. ID	uC-gmrominsoy104a04b1
Method	BLASTX
NCBI GI	g4008402
BLAST score	224
E value	2.0e-18
Match length	82
% identity	49
NCBI Description	(Z82286) predicted using Genefinder; similar to Fatty acid desaturase; cDNA EST EMBL:M89244 comes from this gene; cDNA EST EMBL:D32410 comes from this gene; cDNA EST EMBL:D34903 comes from this gene; cDNA EST yk437d4.3 comes fr

Seq. No.	51626
Seq. ID	uC-gmrominsoy104e04b1
Method	BLASTX
NCBI GI	g4455259
BLAST score	159
E value	9.0e-11
Match length	103
% identity	40
NCBI Description	(AL035523) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	51627
Seq. ID	uC-gmrominsoy104f05b1
Method	BLASTX
NCBI GI	g4522008
BLAST score	379
E value	1.0e-36

Match length	100
% identity	70
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51628
Seq. ID	uC-gmrominsoy104g05b1
Method	BLASTX
NCBI GI	g3785973
BLAST score	172
E value	2.0e-12
Match length	60
% identity	65
NCBI Description	(AC005560) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	51629
Seq. ID	uC-gmrominsoy104h03b1
Method	BLASTN
NCBI GI	g2924733
BLAST score	34
E value	1.0e-09
Match length	70
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	51630
Seq. ID	uC-gmrominsoy105g05b1
Method	BLASTX
NCBI GI	g3785989
BLAST score	425
E value	7.0e-42
Match length	158
% identity	53
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	51631
Seq. ID	uC-gmrominsoy105h11b1
Method	BLASTX
NCBI GI	g1888357
BLAST score	233
E value	5.0e-20
Match length	74
% identity	64
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	51632
Seq. ID	uC-gmrominsoy106b07b1
Method	BLASTN
NCBI GI	g161676
BLAST score	56
E value	1.0e-22
Match length	279
% identity	81
NCBI Description	Nematode muscle tropomyosin mRNA, complete cds

Seq. No.	51633
Seq. ID	uC-gmrominsoy106c11b1
Method	BLASTX
NCBI GI	g2829870
BLAST score	186
E value	6.0e-14
Match length	132
% identity	34
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	51634
Seq. ID	uC-gmrominsoy106d03b1
Method	BLASTX
NCBI GI	g3608155
BLAST score	288
E value	1.0e-25
Match length	100
% identity	66
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	51635
Seq. ID	uC-gmrominsoy107a12b1
Method	BLASTX
NCBI GI	g3549671
BLAST score	257
E value	3.0e-22
Match length	84
% identity	61
NCBI Description	(AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51636
Seq. ID	uC-gmrominsoy107f04b1
Method	BLASTX
NCBI GI	g3935157
BLAST score	388
E value	1.0e-37
Match length	130
% identity	63
NCBI Description	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No.	51637
Seq. ID	uC-gmrominsoy108c12b1
Method	BLASTX
NCBI GI	g2244915
BLAST score	221
E value	6.0e-18
Match length	115
% identity	36
NCBI Description	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq. No.	51638
Seq. ID	uC-gmrominsoy108f10b1
Method	BLASTX
NCBI GI	g416650
BLAST score	293
E value	2.0e-26

Match length	134
% identity	45
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN PGNT35/PCNT111) >gi_100304_pir__S16268 auxin-induced protein (clone pGNT35) - common tobacco >gi_19797_emb_CAA39706_ (X56265) auxin-induced protein [Nicotiana tabacum] >gi_19801_emb_CAA39710_ (X56269) auxin-induced protein [Nicotiana tabacum]

Seq. No.	51639
Seq. ID	uC-gmrominsoy109d01b1
Method	BLASTX
NCBI GI	g1352190
BLAST score	197
E value	1.0e-15
Match length	72
% identity	56
NCBI Description	CROSS-PATHWAY CONTROL PROTEIN 1 >gi_168793 (J03262) cross-pathway control protein 1 [Neurospora crassa]

Seq. No.	51640
Seq. ID	uC-gmrominsoy109e03b1
Method	BLASTX
NCBI GI	g416873
BLAST score	189
E value	3.0e-14
Match length	105
% identity	48
NCBI Description	3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH) >gi_111295_pir__A32867 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) precursor - rat (fragment) >gi_556389 (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus norvegicus]

Seq. No.	51641
Seq. ID	uC-gmrominsoy111a03b1
Method	BLASTX
NCBI GI	g3413712
BLAST score	614
E value	4.0e-64
Match length	121
% identity	85
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51642
Seq. ID	uC-gmrominsoy111d10b1
Method	BLASTX
NCBI GI	g3218521
BLAST score	267
E value	1.0e-33
Match length	119
% identity	60
NCBI Description	(AL023874) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=73.05; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P78381; 2-match_description=UDP-GALACTOSE TRANSLOCATOR (UDP-

Seq. No.	51643
Seq. ID	uC-gmrominsoy111g09b1
Method	BLASTX
NCBI GI	g2982431
BLAST score	408
E value	8.0e-40
Match length	161
% identity	3
NCBI Description	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]

Seq. No.	51644
Seq. ID	uC-gmrominsoy111h04b1
Method	BLASTX
NCBI GI	g1903019
BLAST score	253
E value	1.0e-21
Match length	88
% identity	59
NCBI Description	(Y10580) polycomb group [Arabidopsis thaliana]

Seq. No.	51645
Seq. ID	uC-gmrominsoy112a08b1
Method	BLASTX
NCBI GI	g4325354
BLAST score	141
E value	1.0e-08
Match length	70
% identity	44
NCBI Description	(AF128395) contains similarity to retrovirus-related polyproteins and to CCHC zinc finger protein (Pfam: PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]

Seq. No.	51646
Seq. ID	uC-gmrominsoy112c05b1
Method	BLASTN
NCBI GI	g2547219
BLAST score	61
E value	6.0e-26
Match length	172
% identity	88
NCBI Description	Meloidogyne arenaria

Seq. No.	51647
Seq. ID	uC-gmrominsoy112g04b1
Method	BLASTN
NCBI GI	g3869071
BLAST score	33
E value	4.0e-09
Match length	83
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	51648
Seq. ID	uC-gmrominsoy112h04b1

Method	BLASTX
NCBI GI	g2258469
BLAST score	191
E value	1.0e-14
Match length	88
% identity	51
NCBI Description	(AF009179) replication protein A1 [Oryza sativa]

Seq. No.	51649
Seq. ID	uC-gmrominsoy113a07b1
Method	BLASTN
NCBI GI	g1707369
BLAST score	42
E value	2.0e-14
Match length	122
% identity	84
NCBI Description	A.thaliana mRNA for arginine/serine-rich splicing factor, RSp41

Seq. No.	51650
Seq. ID	uC-gmrominsoy113f07b1
Method	BLASTX
NCBI GI	g2258317
BLAST score	192
E value	1.0e-14
Match length	103
% identity	42
NCBI Description	(AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]

Seq. No.	51651
Seq. ID	uC-gmrominsoy114b10b1
Method	BLASTX
NCBI GI	g2244900
BLAST score	200
E value	2.0e-15
Match length	69
% identity	55
NCBI Description	(Z97338) similarity to hypothetical protein HYP1 - Arabidopsis [Arabidopsis thaliana]

Seq. No.	51652
Seq. ID	uC-gmrominsoy115c07b1
Method	BLASTX
NCBI GI	g1945494
BLAST score	520
E value	5.0e-53
Match length	145
% identity	68
NCBI Description	(U56965) C. elegans heat shock 70 kd protein C precursor, HSP-3 or HSP70C [Caenorhabditis elegans]

Seq. No.	51653
Seq. ID	uC-gmrominsoy115d06b1
Method	BLASTX
NCBI GI	g4415918
BLAST score	143

E value	9.0e-09
Match length	124
% identity	15
NCBI Description	(AC006282) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51654
Seq. ID	uC-gmrominsoy115e02b1
Method	BLASTX
NCBI GI	g3875410
BLAST score	342
E value	3.0e-32
Match length	127
% identity	55
NCBI Description	(Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	51655
Seq. ID	uC-gmrominsoy115e11b1
Method	BLASTX
NCBI GI	g3941448
BLAST score	469
E value	4.0e-47
Match length	93
% identity	89
NCBI Description	(AF062878) putative transcription factor [Arabidopsis thaliana]

Seq. No.	51656
Seq. ID	uC-gmrominsoy115f02b1
Method	BLASTX
NCBI GI	g1173066
BLAST score	496
E value	3.0e-50
Match length	134
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L8 >gi_293233 (M99055) ribosomal protein L8 [Aedes albopictus]

Seq. No.	51657
Seq. ID	uC-gmrominsoy116b07b1
Method	BLASTX
NCBI GI	g2290528
BLAST score	472
E value	1.0e-47
Match length	93
% identity	94
NCBI Description	(U94746) ATAN11 [Arabidopsis thaliana]

Seq. No.	51658
Seq. ID	uC-gmrominsoy116d10b1
Method	BLASTN
NCBI GI	g2656025
BLAST score	33
E value	6.0e-09
Match length	89
% identity	84

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7
Seq. No.	51659
Seq. ID	uC-gmrominsoy116e08b1
Method	BLASTX
NCBI GI	g1169228
BLAST score	199
E value	2.0e-15
Match length	51
% identity	67
NCBI Description	RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639 helicase-like protein - Wood tobacco >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris]
Seq. No.	51660
Seq. ID	uC-gmrominsoy117d10b1
Method	BLASTX
NCBI GI	g3880548
BLAST score	167
E value	6.0e-12
Match length	69
% identity	42
NCBI Description	(Z82073) similar to Fatty acid desaturase; cDNA EST yk412h2.3 comes from this gene; cDNA EST yk412h2.5 comes from this gene; cDNA EST EMBL:C12226 comes from this gene [Caenorhabditis elegans]
Seq. No.	51661
Seq. ID	uC-gmrominsoy119a11b1
Method	BLASTX
NCBI GI	g3881459
BLAST score	261
E value	3.0e-23
Match length	66
% identity	68
NCBI Description	(Z68753) predicted using Genefinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this gene
Seq. No.	51662
Seq. ID	uC-gmrominsoy119d03b1
Method	BLASTX
NCBI GI	g3406737
BLAST score	167
E value	3.0e-12
Match length	41
% identity	83
NCBI Description	(AF080546) S-adenosyl-L-homocysteine hydrolase [Anopheles gambiae]
Seq. No.	51663
Seq. ID	uC-gmrominsoy120a11b1
Method	BLASTX

NCBI GI	g4455261
BLAST score	302
E value	1.0e-27
Match length	68
% identity	78
NCBI Description	(AL035353) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	51664
Seq. ID	uC-gmrominsoy120c04b1
Method	BLASTX
NCBI GI	g2668492
BLAST score	259
E value	2.0e-22
Match length	123
% identity	42
NCBI Description	(D89981) metal-transporting P-type ATPase [Arabidopsis thaliana]

Seq. No.	51665
Seq. ID	uC-gmrominsoy121a12b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	33
E value	6.0e-09
Match length	37
% identity	59
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	51666
Seq. ID	uC-gmrominsoy121b01b1
Method	BLASTN
NCBI GI	g1395190
BLAST score	38
E value	2.0e-12
Match length	86
% identity	86
NCBI Description	Spinacia oleracea L. mRNA for 26S proteasome ATPase subunit, complete cds

Seq. No.	51667
Seq. ID	uC-gmrominsoy121c10b1
Method	BLASTX
NCBI GI	g3892059
BLAST score	176
E value	1.0e-12
Match length	109
% identity	35
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	51668
Seq. ID	uC-gmrominsoy121f11b1
Method	BLASTX
NCBI GI	g3757522
BLAST score	145
E value	1.0e-09

Match length	32
% identity	84
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	51669
Seq. ID	uC-gmrominsoy122d07b1
Method	BLASTX
NCBI GI	g4467148
BLAST score	400
E value	5.0e-39
Match length	143
% identity	62
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	51670
Seq. ID	uC-gmrominsoy122e04b1
Method	BLASTX
NCBI GI	g3874297
BLAST score	177
E value	7.0e-13
Match length	89
% identity	36
NCBI Description	(Z37139) predicted using Genefinder; cDNA EST yk307h3.3 comes from this gene; cDNA EST yk307h3.5 comes from this gene [Caenorhabditis elegans] >gi_3876661_emb_CAA84320_ (Z34799) predicted using Genefinder; cDNA EST yk307h3.3 comes from this gene; cDNA EST yk307h3.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	51671
Seq. ID	uC-gmrominsoy123d03b1
Method	BLASTX
NCBI GI	g3875406
BLAST score	383
E value	4.0e-37
Match length	111
% identity	64
NCBI Description	(Z81052) predicted using Genefinder; Similarity to Human pyruvate carboxylase (TR:G458236); cDNA EST EMBL:Z14488 comes from this gene; cDNA EST EMBL:Z14499 comes from this gene; cDNA EST EMBL:D27998 comes from this gene; cDNA E

Seq. No.	51672
Seq. ID	uC-gmrominsoy123e07b1
Method	BLASTX
NCBI GI	g283527
BLAST score	249
E value	2.0e-21
Match length	77
% identity	61
NCBI Description	acetyl-CoA acetyltransferase homolog - Caenorhabditis elegans >gi_156194 (M77697) acetyl-CoA acetyltransferase [Caenorhabditis elegans]

Seq. No.	51673
Seq. ID	uC-gmrominsoy123f01b1
Method	BLASTX

NCBI GI	g3881291
BLAST score	315
E value	3.0e-29
Match length	93
% identity	69
NCBI Description	(AL032659) predicted using Genefinder; cDNA EST EMBL:Z14528 comes from this gene [Caenorhabditis elegans]

Seq. No.	51674
Seq. ID	uC-gmrominsoy123f10b1
Method	BLASTN
NCBI GI	g2293111
BLAST score	160
E value	9.0e-85
Match length	284
% identity	89
NCBI Description	V.faba mRNA for potassium channel

Seq. No.	51675
Seq. ID	uC-gmrominsoy124d09b1
Method	BLASTX
NCBI GI	g4455182
BLAST score	139
E value	5.0e-09
Match length	40
% identity	62
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	51676
Seq. ID	uC-gmrominsoy124h06b1
Method	BLASTX
NCBI GI	g1421730
BLAST score	215
E value	2.0e-17
Match length	81
% identity	47
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	51677
Seq. ID	uC-gmrominsoy125c09b1
Method	BLASTN
NCBI GI	g3204107
BLAST score	55
E value	2.0e-22
Match length	162
% identity	88
NCBI Description	Cicer arietinum mRNA for putative cytidine or deoxycytidylate deaminase, partial

Seq. No.	51678
Seq. ID	uC-gmrominsoy125f05b1
Method	BLASTX
NCBI GI	g2252852
BLAST score	618
E value	1.0e-64
Match length	133
% identity	85

NCBI Description	(AF013294) similar to the cation transport ATPases family. [Arabidopsis thaliana] >gi_4185853_emb_CAA10659_ (AJ132387) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	51679
Seq. ID	uC-gmrominsoy126a06b1
Method	BLASTN
NCBI GI	g1498333
BLAST score	43
E value	3.0e-15
Match length	63
% identity	92
NCBI Description	Glycine max actin (Soy57) gene, partial cds

Seq. No.	51680
Seq. ID	uC-gmrominsoy126a08b1
Method	BLASTX
NCBI GI	g4249409
BLAST score	353
E value	2.0e-33
Match length	113
% identity	53
NCBI Description	(AC006072) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	51681
Seq. ID	uC-gmrominsoy126d04b1
Method	BLASTX
NCBI GI	g4008380
BLAST score	475
E value	8.0e-48
Match length	113
% identity	80
NCBI Description	(Z69885) predicted using Genefinder; Similarity to Yeast hypothetical protein L8167.6 (PIR Acc. No. S48557); cDNA EST EMBL:D33042 comes from this gene; cDNA EST EMBL:D35774 comes from this gene; cDNA EST EMBL:D75125 comes from

Seq. No.	51682
Seq. ID	uC-gmrominsoy126e04b1
Method	BLASTX
NCBI GI	g3881181
BLAST score	156
E value	2.0e-10
Match length	61
% identity	44
NCBI Description	(Z99281) cDNA EST yk433f11.3 comes from this gene; cDNA EST yk433f11.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	51683
Seq. ID	uC-gmrominsoy127b03b1
Method	BLASTX
NCBI GI	g1255951
BLAST score	262
E value	2.0e-23
Match length	67
% identity	72

NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	51684
Seq. ID	uC-gmrominsoy127c07b1
Method	BLASTX
NCBI GI	g2832698
BLAST score	207
E value	2.0e-16
Match length	76
% identity	49
NCBI Description	(AL021713) starch synthase-like protein [Arabidopsis thaliana]

Seq. No.	51685
Seq. ID	uC-gmrominsoy127c11b1
Method	BLASTX
NCBI GI	g3282239
BLAST score	213
E value	4.0e-17
Match length	74
% identity	69
NCBI Description	(U88966) rapamycin associated protein FRAP2 [Homo sapiens]

Seq. No.	51686
Seq. ID	uC-gmrominsoy127c12b1
Method	BLASTX
NCBI GI	g4566614
BLAST score	330
E value	1.0e-30
Match length	79
% identity	77
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	51687
Seq. ID	uC-gmrominsoy128e02b1
Method	BLASTX
NCBI GI	g3874213
BLAST score	291
E value	3.0e-26
Match length	127
% identity	48
NCBI Description	(Z83217) Similarity to Drosophila White protein (SW:WHIT_DROME); cDNA EST EMBL:T01609 comes from this gene; cDNA EST EMBL:D67987 comes from this gene; cDNA EST EMBL:D34570 comes from this gene; cDNA EST EMBL:D32839 comes from t

Seq. No.	51688
Seq. ID	uC-gmrominsoy131a03b1
Method	BLASTX
NCBI GI	g3461817
BLAST score	146
E value	1.0e-09
Match length	81
% identity	40
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	51689
Seq. ID	uC-gmrominsoy131b05b1
Method	BLASTX
NCBI GI	g1666096
BLAST score	240
E value	3.0e-20
Match length	116
% identity	43
NCBI Description	(Y09113) dioxygenase [Marah macrocarpus]

Seq. No.	51690
Seq. ID	uC-gmrominsoy135f12b1
Method	BLASTX
NCBI GI	g3860263
BLAST score	195
E value	4.0e-15
Match length	51
% identity	65
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	51691
Seq. ID	uC-gmrominsoy136a10b1
Method	BLASTX
NCBI GI	g2498731
BLAST score	202
E value	7.0e-16
Match length	60
% identity	70
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	51692
Seq. ID	uC-gmrominsoy136e05b1
Method	BLASTN
NCBI GI	g3641869
BLAST score	119
E value	3.0e-60
Match length	279
% identity	86
NCBI Description	Cicer arietinum epicotyl EST, clone Can133

Seq. No.	51693
Seq. ID	uC-gmrominsoy137b09b1
Method	BLASTX
NCBI GI	g1805654
BLAST score	372
E value	8.0e-36
Match length	119
% identity	67
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No. 51694

Seq. ID	uC-gmrominsoy138a09b1
Method	BLASTX
NCBI GI	g1723536
BLAST score	151
E value	2.0e-10
Match length	46
% identity	63
NCBI Description	PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) >gi_1256531_emb_CAA94637_ (Z70691) eukaryotic translation initiation factor 3 beta subunit [Schizosaccharomyces pombe]

Seq. No.	51695
Seq. ID	uC-gmrominsoy138h05b1
Method	BLASTX
NCBI GI	g4454482
BLAST score	393
E value	4.0e-38
Match length	122
% identity	62
NCBI Description	(AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51696
Seq. ID	uC-gmrominsoy138h06b1
Method	BLASTN
NCBI GI	g16508
BLAST score	116
E value	1.0e-58
Match length	164
% identity	93
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	51697
Seq. ID	uC-gmrominsoy139e05b1
Method	BLASTX
NCBI GI	g2244815
BLAST score	208
E value	1.0e-16
Match length	62
% identity	63
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51698
Seq. ID	uC-gmrominsoy140d07b1
Method	BLASTX
NCBI GI	g1652434
BLAST score	265
E value	2.0e-23
Match length	101
% identity	57
NCBI Description	(D90905) N-acetylglutamate kinase [Synechocystis sp.]

Seq. No.	51699
Seq. ID	uC-gmrominsoy141g01b1
Method	BLASTX

NCBI GI	g3212869
BLAST score	550
E value	1.0e-56
Match length	111
% identity	91
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	51700
Seq. ID	uC-gmrominsoy142b02b1
Method	BLASTN
NCBI GI	g4115336
BLAST score	113
E value	9.0e-57
Match length	289
% identity	22
NCBI Description	Pisum sativum (Alaska) ubiquitin (PUB3) gene, complete cds

Seq. No.	51701
Seq. ID	uC-gmrominsoy145c09b1
Method	BLASTX
NCBI GI	g1362578
BLAST score	186
E value	3.0e-14
Match length	55
% identity	54
NCBI Description	thin filament-associated protein UNC-87, short form - Caenorhabditis elegans >gi_498328 (U04711) uses first of two potential start sites [Caenorhabditis elegans] >gi_498331 (U04712) uses the first of two potential start codons; second of two alternatively spliced products [Caenorhabditis elegans]

Seq. No.	51702
Seq. ID	uC-gmrominsoy153a02b1
Method	BLASTX
NCBI GI	g3122853
BLAST score	213
E value	4.0e-17
Match length	133
% identity	27
NCBI Description	WD-REPEAT PROTEIN SAZD >gi_1082863_pir__A49367 transducin homolog sazD - human >gi_414536 (U02609) transducin-like protein [Homo sapiens]

Seq. No.	51703
Seq. ID	uC-gmrominsoy153c07b1
Method	BLASTX
NCBI GI	g2995321
BLAST score	377
E value	2.0e-36
Match length	129
% identity	57
NCBI Description	(Z68759) amino acid carrier [Ricinus communis]

Seq. No.	51704
Seq. ID	uC-gmrominsoy153g06b1
Method	BLASTN

NCBI GI g218261
BLAST score 82
E value 2.0e-38
Match length 186
% identity 86
NCBI Description Soybean mRNA for early nodulin

Seq. No. 51705
Seq. ID uC-gmrominsoy153g07b1
Method BLASTX
NCBI GI g3881877
BLAST score 507
E value 1.0e-51
Match length 122
% identity 69
NCBI Description (Z95123) predicted using Genefinder; Similarity to Rat acyl-CoA desaturase (SW:ACOD_RAT); cDNA EST yk445a4.5 comes from this gene; cDNA EST yk445a4.3 comes from this gene [Caenorhabditis elegans]

Seq. No. 51706
Seq. ID uC-gmrominsoy154g07b1
Method BLASTN
NCBI GI g167066
BLAST score 82
E value 3.0e-38
Match length 130
% identity 91
NCBI Description Hordeum vulgare L-lactate dehydrogenase mRNA, complete cds

Seq. No. 51707
Seq. ID uC-gmrominsoy154h09b1
Method BLASTX
NCBI GI g2708331
BLAST score 335
E value 2.0e-31
Match length 110
% identity 59
NCBI Description (AF038557) ligand gated channel-like protein [Arabidopsis thaliana]

Seq. No. 51708
Seq. ID uC-gmrominsoy155c07b1
Method BLASTX
NCBI GI g861392
BLAST score 282
E value 3.0e-25
Match length 119
% identity 46
NCBI Description (U29096) coded for by C. elegans cDNA yk44f2.5; similar to P59 protein (HSP binding immunophilin) and to TPR domain [Caenorhabditis elegans] >gi_4104228 (AF034085) UNC-45 [Caenorhabditis elegans]

Seq. No. 51709
Seq. ID uC-gmrominsoy156a02b1
Method BLASTX

NCBI GI	g2443329
BLAST score	352
E value	3.0e-33
Match length	149
% identity	54
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	51710
Seq. ID	uC-gmrominsoy156c05b1
Method	BLASTX
NCBI GI	g3123025
BLAST score	152
E value	6.0e-10
Match length	124
% identity	33
NCBI Description	VITELLOGENIN 6 PRECURSOR >gi_1515337 (U35449) vitellogenin [Oscheius sp. 'CEW1']

Seq. No.	51711
Seq. ID	uC-gmrominsoy156h11b1
Method	BLASTX
NCBI GI	g4512663
BLAST score	182
E value	2.0e-13
Match length	107
% identity	13
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544470_gb_AAD22377.1_AC006580_9 (AC006580) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51712
Seq. ID	uC-gmrominsoy158c10b1
Method	BLASTX
NCBI GI	g3876865
BLAST score	149
E value	2.0e-09
Match length	80
% identity	36
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	51713
Seq. ID	uC-gmrominsoy162e10b1
Method	BLASTX
NCBI GI	g1175759
BLAST score	220
E value	6.0e-18
Match length	92
% identity	43
NCBI Description	PROBABLE ZINC PROTEASE PQQL >gi_1074746_pir__E64171 hypothetical protein HI1368 - Haemophilus influenzae (strain Rd KW20) >gi_1574200 (U32816) zinc protease, putative [Haemophilus influenzae Rd]

Seq. No. 51714

Seq. ID	uC-gmrominsoy162f03b1
Method	BLASTX
NCBI GI	g4559396
BLAST score	198
E value	6.0e-16
Match length	68
% identity	56
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	51715
Seq. ID	uC-gmrominsoy164c02b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	47
% identity	49
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51716
Seq. ID	uC-gmrominsoy164e11b1
Method	BLASTX
NCBI GI	g3386594
BLAST score	250
E value	2.0e-21
Match length	122
% identity	45
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana] >gi_3702344 (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51717
Seq. ID	uC-gmrominsoy164h11b1
Method	BLASTX
NCBI GI	g1708868
BLAST score	382
E value	7.0e-37
Match length	144
% identity	25
NCBI Description	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN PRECURSOR (LRP) >gi_1078879_pir__A47437 LDL-receptor-related protein - Caenorhabditis elegans >gi_156360 (M96150) LDL receptor-related protein [Caenorhabditis elegans] >gi_3876533_emb_CAA98124_ (Z73907) predicted using Genefinder; Identity to C.elegans Low density lipid (LDL) receptor-related protein (TR:G156360); cDNA EST EMBL:D37747 comes from this gene; cDNA EST EMBL:D35129 comes from this gene; cDNA EST EMBL:D3458

Seq. No.	51718
Seq. ID	uC-gmrominsoy165b12b1
Method	BLASTX
NCBI GI	g2960144
BLAST score	265
E value	3.0e-23
Match length	112
% identity	42

NCBI Description	(AL022121) hypothetical protein Rv3720 [Mycobacterium tuberculosis]

Seq. No.	51719
Seq. ID	uC-gmrominsoy165c11b1
Method	BLASTX
NCBI GI	g3875408
BLAST score	236
E value	7.0e-20
Match length	102
% identity	51
NCBI Description	(Z81052) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D70121 comes from this gene; cDNA EST EMBL:D65665 comes from this gene; cDNA EST EMBL:D66139 comes from this gene; cDNA EST EMBL:D66385 comes from this gen

Seq. No.	51720
Seq. ID	uC-gmrominsoy165e10b1
Method	BLASTX
NCBI GI	g3292827
BLAST score	587
E value	6.0e-61
Match length	123
% identity	86
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	51721
Seq. ID	uC-gmrominsoy165f07b1
Method	BLASTX
NCBI GI	g3021280
BLAST score	147
E value	3.0e-09
Match length	102
% identity	33
NCBI Description	(AL022347) serine /threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	51722
Seq. ID	uC-gmrominsoy168b06b1
Method	BLASTX
NCBI GI	g4033577
BLAST score	388
E value	1.0e-37
Match length	115
% identity	68
NCBI Description	(AJ001208) APS reductase [Brassica juncea]

Seq. No.	51723
Seq. ID	uC-gmrominsoy168g02b1
Method	BLASTN
NCBI GI	g1370202
BLAST score	134
E value	3.0e-69
Match length	234
% identity	89
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAN1A

Seq. No.	51724
Seq. ID	uC-gmrominsoy169c06b1
Method	BLASTX
NCBI GI	g1518540
BLAST score	298
E value	4.0e-27
Match length	75
% identity	77
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	51725
Seq. ID	uC-gmrominsoy170c03b1
Method	BLASTX
NCBI GI	g3367521
BLAST score	235
E value	8.0e-20
Match length	77
% identity	60
NCBI Description	(AC004392) Similar to gb_U08285 membrane-associated salt-inducible protein from Nicotiana tabacum. ESTs gb_T44131 and gb_T04378 come from this gene. [Arabidopsis thaliana]

Seq. No.	51726
Seq. ID	uC-gmrominsoy171c02b1
Method	BLASTX
NCBI GI	g2765817
BLAST score	368
E value	3.0e-35
Match length	121
% identity	69
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	51727
Seq. ID	uC-gmrominsoy171c09b1
Method	BLASTX
NCBI GI	g4415933
BLAST score	420
E value	2.0e-41
Match length	117
% identity	67
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]

Seq. No.	51728
Seq. ID	uC-gmrominsoy172a10b1
Method	BLASTX
NCBI GI	g2500392
BLAST score	515
E value	2.0e-52
Match length	115

% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN SA HOMOLOG (RIBOSOME-ASSOCIATED PROTEIN 1) >gi_1039443 (U36470) putative ribosome-associated protein [Neurospora crassa]

Seq. No.	51729
Seq. ID	uC-gmrominsoy172b07b1
Method	BLASTX
NCBI GI	g4539301
BLAST score	404
E value	2.0e-39
Match length	146
% identity	56
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	51730
Seq. ID	uC-gmrominsoy172c06b1
Method	BLASTN
NCBI GI	g169980
BLAST score	359
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	51731
Seq. ID	uC-gmrominsoy172d07b1
Method	BLASTX
NCBI GI	g4093157
BLAST score	264
E value	5.0e-23
Match length	71
% identity	82
NCBI Description	(AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana]

Seq. No.	51732
Seq. ID	uC-gmrominsoy172g02b1
Method	BLASTX
NCBI GI	g107350
BLAST score	185
E value	1.0e-13
Match length	145
% identity	32
NCBI Description	Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5 protein [Homo sapiens]

Seq. No.	51733
Seq. ID	uC-gmrominsoy174a01b1
Method	BLASTN
NCBI GI	g1518539
BLAST score	203
E value	1.0e-110
Match length	235
% identity	97
NCBI Description	Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No.	51734
Seq. ID	uC-gmrominsoy174g05b1
Method	BLASTX
NCBI GI	g2291114
BLAST score	273
E value	4.0e-24
Match length	122
% identity	43
NCBI Description	(AF016413) similar to the NUPC family of transporters [Caenorhabditis elegans]

Seq. No.	51735
Seq. ID	uC-gmrominsoy174h07b1
Method	BLASTX
NCBI GI	g3980417
BLAST score	166
E value	1.0e-11
Match length	88
% identity	40
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	51736
Seq. ID	uC-gmrominsoy175c10b1
Method	BLASTX
NCBI GI	g3335060
BLAST score	207
E value	6.0e-17
Match length	64
% identity	62
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	51737
Seq. ID	uC-gmrominsoy175d01b1
Method	BLASTN
NCBI GI	g18662
BLAST score	113
E value	4.0e-57
Match length	153
% identity	93
NCBI Description	Glycine max hsp 70 gene

Seq. No.	51738
Seq. ID	uC-gmrominsoy175f01b1
Method	BLASTX
NCBI GI	g2213590
BLAST score	314
E value	7.0e-29
Match length	149
% identity	45
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	51739
Seq. ID	uC-gmrominsoy175h07b1
Method	BLASTX

NCBI GI g1800223
BLAST score 165
E value 1.0e-11
Match length 88
% identity 40
NCBI Description (U65018) mannosyltransferase [Dictyostelium discoideum]

Seq. No. 51740
Seq. ID uC-gmrominsoy176f01b1
Method BLASTX
NCBI GI g3549665
BLAST score 338
E value 9.0e-32
Match length 130
% identity 61
NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 51741
Seq. ID uC-gmrominsoy176h07b1
Method BLASTX
NCBI GI g3790587
BLAST score 284
E value 2.0e-25
Match length 74
% identity 73
NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No. 51742
Seq. ID uC-gmrominsoy177h10b1
Method BLASTX
NCBI GI g3461848
BLAST score 241
E value 1.0e-20
Match length 84
% identity 60
NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No. 51743
Seq. ID uC-gmrominsoy178a04b1
Method BLASTX
NCBI GI g1098902
BLAST score 451
E value 4.0e-45
Match length 118
% identity 72
NCBI Description (U34773) DEAD-box protein [Drosophila melanogaster]

Seq. No. 51744
Seq. ID uC-gmrominsoy178a05b1
Method BLASTX
NCBI GI g4176548
BLAST score 583
E value 2.0e-60
Match length 127
% identity 80
NCBI Description (AL035259) putative Ca-calmodulin-dependent

serine-threonine-protein kinase [Schizosaccharomyces pombe]

Seq. No.	51745
Seq. ID	uC-gmrominsoy178e04b1
Method	BLASTX
NCBI GI	g4006829
BLAST score	284
E value	2.0e-25
Match length	74
% identity	78
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	51746
Seq. ID	uC-gmrominsoy178f03b1
Method	BLASTX
NCBI GI	g136107
BLAST score	229
E value	3.0e-25
Match length	107
% identity	56
NCBI Description	TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL AMINOPEPTIDASE) >gi_1082875_pir__S54376 tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880 (M73047) tripeptidyl peptidase II [Homo sapiens] >gi_4507657_ref_NP_003282.1_pTPP2_ tripeptidyl peptidase II

Seq. No.	51747
Seq. ID	uC-gmrominsoy178g10b1
Method	BLASTX
NCBI GI	g2435519
BLAST score	321
E value	9.0e-30
Match length	132
% identity	58
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	51748
Seq. ID	uC-gmrominsoy179a12b1
Method	BLASTX
NCBI GI	g1943843
BLAST score	340
E value	6.0e-32
Match length	125
% identity	51
NCBI Description	(U97407) similar to the tyrosinase family [Caenorhabditis elegans]

Seq. No.	51749
Seq. ID	uC-gmrominsoy179c02b1
Method	BLASTX
NCBI GI	g2062169
BLAST score	315
E value	5.0e-29
Match length	111
% identity	60

NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	51750
Seq. ID	uC-gmrominsoy179d03b1
Method	BLASTX
NCBI GI	g2335108
BLAST score	388
E value	2.0e-37
Match length	99
% identity	78
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	51751
Seq. ID	uC-gmrominsoy179d07b1
Method	BLASTX
NCBI GI	g2315733
BLAST score	201
E value	1.0e-15
Match length	130
% identity	39
NCBI Description	(AF016679) similar to the type-B carboxylesterase/lipase family [Caenorhabditis elegans]

Seq. No.	51752
Seq. ID	uC-gmrominsoy179e09b1
Method	BLASTX
NCBI GI	g4454012
BLAST score	396
E value	2.0e-38
Match length	91
% identity	75
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	51753
Seq. ID	uC-gmrominsoy180a01b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	2.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51754
Seq. ID	uC-gmrominsoy180a11b1
Method	BLASTX
NCBI GI	g2829918
BLAST score	200
E value	2.0e-15
Match length	73
% identity	64
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	51755

Seq. ID uC-gmrominsoy180c06b1
Method BLASTX
NCBI GI g3341679
BLAST score 397
E value 6.0e-39
Match length 97
% identity 79
NCBI Description (AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No. 51756
Seq. ID uC-gmrominsoy180g05b1
Method BLASTX
NCBI GI g3395436
BLAST score 139
E value 1.0e-08
Match length 41
% identity 56
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 51757
Seq. ID uC-gmrominsoy181e07b1
Method BLASTN
NCBI GI g1326160
BLAST score 56
E value 6.0e-23
Match length 117
% identity 94
NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No. 51758
Seq. ID uC-gmrominsoy182c04b1
Method BLASTN
NCBI GI g4097879
BLAST score 67
E value 1.0e-29
Match length 111
% identity 90
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No. 51759
Seq. ID uC-gmrominsoy182c09b1
Method BLASTX
NCBI GI g3183346
BLAST score 174
E value 4.0e-13
Match length 65
% identity 49
NCBI Description HYPOTHETICAL 67.7 KD PROTEIN C23C11.03 IN CHROMOSOME I >gi_2330767_emb_CAB11156_ (Z98559) SPAC23C11.03; len:598aa, similar eg. to YJR002W, YJX2_YEAST, P47083, hypothetical 67.0 kd protein, (593aa), fasta scores, opt:855, E():0, (33.0% identity in 610 aa overlap) [Schizosaccharomyces pombe]

Seq. No. 51760

Seq. ID	uC-gmrominsoy182g05b1
Method	BLASTX
NCBI GI	g1514649
BLAST score	733
E value	5.0e-78
Match length	151
% identity	93
NCBI Description	(X86021) potassium channel [Solanum tuberosum]

Seq. No.	51761
Seq. ID	uC-gmrominsoy183b06b1
Method	BLASTX
NCBI GI	g3096947
BLAST score	203
E value	7.0e-30
Match length	118
% identity	63
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	51762
Seq. ID	uC-gmrominsoy183d01b1
Method	BLASTX
NCBI GI	g1669599
BLAST score	324
E value	5.0e-30
Match length	143
% identity	50
NCBI Description	(D88746) AR791 [Arabidopsis thaliana]

Seq. No.	51763
Seq. ID	uC-gmrominsoy183f08b1
Method	BLASTX
NCBI GI	g542656
BLAST score	422
E value	1.0e-41
Match length	130
% identity	64
NCBI Description	multicatalytic endopeptidase complex (EC 3.4.99.46) chain XC9 (clone 1) - clawed frog

Seq. No.	51764
Seq. ID	uC-gmrominsoy183f10b1
Method	BLASTX
NCBI GI	g4006870
BLAST score	298
E value	5.0e-27
Match length	111
% identity	58
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	51765
Seq. ID	uC-gmrominsoy185f11b1
Method	BLASTX
NCBI GI	g3831469
BLAST score	145
E value	4.0e-09

Match length	44
% identity	64
NCBI Description	(AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51766
Seq. ID	uC-gmrominsoy186e11b1
Method	BLASTN
NCBI GI	g170065
BLAST score	194
E value	1.0e-105
Match length	431
% identity	11
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	51767
Seq. ID	uC-gmrominsoy187a05b1
Method	BLASTX
NCBI GI	g2252849
BLAST score	172
E value	1.0e-12
Match length	90
% identity	39
NCBI Description	(AF013294) contains similarity to gag proteins [Arabidopsis thaliana]

Seq. No.	51768
Seq. ID	uC-gmrominsoy187g11b1
Method	BLASTX
NCBI GI	g3785980
BLAST score	159
E value	5.0e-17
Match length	90
% identity	53
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51769
Seq. ID	uC-gmrominsoy187h05b1
Method	BLASTX
NCBI GI	g629722
BLAST score	530
E value	3.0e-54
Match length	109
% identity	83
NCBI Description	finger protein pcp1 - potato >gi_563623_emb_CAA57772_ (X82328) putative DNA/RNA binding protein [Solanum tuberosum]

Seq. No.	51770
Seq. ID	uC-gmrominsoy188c10b1
Method	BLASTX
NCBI GI	g4314375
BLAST score	153
E value	2.0e-10
Match length	58
% identity	52
NCBI Description	(AC006232) putative RNA-binding glycine rich protein

(RGP-2) [Arabidopsis thaliana]

Seq. No.	51771
Seq. ID	uC-gmrominsoy188g07b1
Method	BLASTX
NCBI GI	g3738325
BLAST score	260
E value	1.0e-22
Match length	62
% identity	85
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No.	51772
Seq. ID	uC-gmrominsoy188g10b1
Method	BLASTX
NCBI GI	g2495724
BLAST score	151
E value	9.0e-10
Match length	60
% identity	45
NCBI Description	HYPOTHETICAL PROTEIN KIAA0249 >gi_1665767_dbj_BAA13380_ (D87436) Similar to Human KIAA0188 protein [Homo sapiens]

Seq. No.	51773
Seq. ID	uC-gmrominsoy189c10b1
Method	BLASTX
NCBI GI	g3128206
BLAST score	369
E value	2.0e-35
Match length	111
% identity	67
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	51774
Seq. ID	uC-gmrominsoy189f01b1
Method	BLASTX
NCBI GI	g2213599
BLAST score	185
E value	6.0e-14
Match length	103
% identity	42
NCBI Description	(AC000348) T7N9.19 [Arabidopsis thaliana]

Seq. No.	51775
Seq. ID	uC-gmrominsoy189g01b1
Method	BLASTX
NCBI GI	g1825764
BLAST score	291
E value	2.0e-26
Match length	87
% identity	61
NCBI Description	(U88314) C46H11.11 gene product [Caenorhabditis elegans]

Seq. No.	51776
Seq. ID	uC-gmrominsoy189g10b1
Method	BLASTX

NCBI GI	g4567301
BLAST score	162
E value	3.0e-11
Match length	79
% identity	46
NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No.	51777
Seq. ID	uC-gmrominsoy192d02b1
Method	BLASTX
NCBI GI	g134892
BLAST score	258
E value	4.0e-38
Match length	132
% identity	64
NCBI Description	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi_88607_pir__A29440 signal recognition particle receptor - human >gi_30866_emb_CAA29608_ (X06272) docking protein [Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal recognition particle receptor ('docking protein')

Seq. No.	51778
Seq. ID	uC-gmrominsoy192h09b1
Method	BLASTX
NCBI GI	g4234953
BLAST score	207
E value	2.0e-16
Match length	131
% identity	24
NCBI Description	(AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]

Seq. No.	51779
Seq. ID	uC-gmrominsoy193h11b1
Method	BLASTX
NCBI GI	g1255951
BLAST score	647
E value	7.0e-68
Match length	154
% identity	79
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	51780
Seq. ID	uC-gmrominsoy194b07b1
Method	BLASTX
NCBI GI	g4539423
BLAST score	289
E value	3.0e-26
Match length	65
% identity	86
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	51781
Seq. ID	uC-gmrominsoy194e12b1
Method	BLASTX
NCBI GI	g2224685

BLAST score	167
E value	1.0e-11
Match length	95
% identity	42
NCBI Description	(AB002370) KIAA0372 [Homo sapiens]

Seq. No.	51782
Seq. ID	uC-gmrominsoy195a05b1
Method	BLASTX
NCBI GI	g3426041
BLAST score	265
E value	3.0e-23
Match length	87
% identity	61
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	51783
Seq. ID	uC-gmrominsoy195h02b1
Method	BLASTX
NCBI GI	g4200165
BLAST score	433
E value	7.0e-43
Match length	121
% identity	74
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	51784
Seq. ID	uC-gmrominsoy197e02b1
Method	BLASTX
NCBI GI	g2253010
BLAST score	349
E value	3.0e-33
Match length	75
% identity	81
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	51785
Seq. ID	uC-gmrominsoy197f12b1
Method	BLASTX
NCBI GI	g2191134
BLAST score	160
E value	5.0e-11
Match length	69
% identity	42
NCBI Description	(AF007269) contains weak similarity to Galectin-3 binding protein [Arabidopsis thaliana]

Seq. No.	51786
Seq. ID	uC-gmrominsoy197h01b1
Method	BLASTX
NCBI GI	g3413886
BLAST score	237
E value	7.0e-20
Match length	145
% identity	39
NCBI Description	(AB007931) KIAA0462 protein [Homo sapiens]

Seq. No.	51787
Seq. ID	uC-gmrominsoy197h07b1
Method	BLASTN
NCBI GI	g1675195
BLAST score	124
E value	2.0e-63
Match length	262
% identity	87
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	51788
Seq. ID	uC-gmrominsoy198e07b1
Method	BLASTX
NCBI GI	g3341679
BLAST score	264
E value	4.0e-23
Match length	121
% identity	45
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	51789
Seq. ID	uC-gmrominsoy198f04b1
Method	BLASTN
NCBI GI	g3193311
BLAST score	57
E value	3.0e-23
Match length	195
% identity	94
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	51790
Seq. ID	uC-gmrominsoy198h04b1
Method	BLASTX
NCBI GI	g1853968
BLAST score	414
E value	1.0e-40
Match length	112
% identity	73
NCBI Description	(D88121) CPRD12 protein [Vigna unguiculata]

Seq. No.	51791
Seq. ID	uC-gmrominsoy199a04b1
Method	BLASTX
NCBI GI	g2655008
BLAST score	241
E value	2.0e-20
Match length	78
% identity	60
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]

Seq. No.	51792
Seq. ID	uC-gmrominsoy199c03b1
Method	BLASTX

NCBI GI	g1330401
BLAST score	241
E value	2.0e-20
Match length	72
% identity	67
NCBI Description	(U58762) T27F7.1 gene product [Caenorhabditis elegans]

Seq. No.	51793
Seq. ID	uC-gmrominsoy199c10b1
Method	BLASTX
NCBI GI	g3193320
BLAST score	184
E value	1.0e-13
Match length	83
% identity	43
NCBI Description	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]

Seq. No.	51794
Seq. ID	uC-gmrominsoy199e11b1
Method	BLASTX
NCBI GI	g3335345
BLAST score	198
E value	3.0e-15
Match length	70
% identity	63
NCBI Description	(AC004512) Contains similarity to ABC transporter gb_1651790 from Synechocystis sp. gb_D90900. [Arabidopsis thaliana]

Seq. No.	51795
Seq. ID	uC-gmrominsoy199f11b1
Method	BLASTX
NCBI GI	g4512670
BLAST score	374
E value	6.0e-36
Match length	128
% identity	50
NCBI Description	(AC006931) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	51796
Seq. ID	uC-gmrominsoy200e01b1
Method	BLASTX
NCBI GI	g609350
BLAST score	167
E value	1.0e-11
Match length	118
% identity	38
NCBI Description	(U15099) methionine synthase [Saccharomyces cerevisiae]

Seq. No.	51797
Seq. ID	uC-gmrominsoy200e03b1
Method	BLASTX
NCBI GI	g3122572
BLAST score	436

E value	1.0e-43
Match length	85
% identity	95
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	51798
Seq. ID	uC-gmrominsoy200e08b1
Method	BLASTX
NCBI GI	g3249076
BLAST score	169
E value	4.0e-12
Match length	67
% identity	57
NCBI Description	(AC004473) Similar to beta glucosidase (bg1A) gb_X94986 from Manihot esculenta. [Arabidopsis thaliana]

Seq. No.	51799
Seq. ID	uC-gmrominsoy201c11b1
Method	BLASTX
NCBI GI	g3738297
BLAST score	260
E value	2.0e-22
Match length	90
% identity	14
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	51800
Seq. ID	uC-gmrominsoy202d02b1
Method	BLASTX
NCBI GI	g1708241
BLAST score	351
E value	3.0e-33
Match length	93
% identity	70
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2131285_pir__S58202 HMGS protein - yeast (Saccharomyces cerevisiae) >gi_927536_emb_CAA90557_ (Z50178) unknown [Saccharomyces cerevisiae] >gi_1304355_emb_CAA65437_ (X96617) 3-hydroxy-3-methylglutaryl coenzyme A synthase [Saccharomyces cerevisiae]

Seq. No.	51801
Seq. ID	uC-gmrominsoy204e11b1
Method	BLASTN
NCBI GI	g2062691
BLAST score	33
E value	7.0e-09
Match length	34
% identity	62
NCBI Description	Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	51802
Seq. ID	uC-gmrominsoy205e03b1
Method	BLASTX
NCBI GI	g2914700
BLAST score	267
E value	1.0e-23
Match length	65
% identity	80
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	51803
Seq. ID	uC-gmrominsoy205g06b1
Method	BLASTX
NCBI GI	g2498629
BLAST score	367
E value	4.0e-35
Match length	134
% identity	13
NCBI Description	TRANSCRIPTIONAL REPRESSOR NF-X1 >gi_2135825_pir__I38869 NFX1 - human >gi_563217 (U15306) NFX1 [Homo sapiens] >gi_4505387_ref_NP_002495.1_pNFX1_ nuclear transcription factor, X-box binding

Seq. No.	51804
Seq. ID	uC-gmrominsoy205g12b1
Method	BLASTX
NCBI GI	g2465925
BLAST score	299
E value	4.0e-27
Match length	81
% identity	69
NCBI Description	(AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	51805
Seq. ID	uC-gmrominsoy206c02b1
Method	BLASTX
NCBI GI	g3874137
BLAST score	541
E value	1.0e-55
Match length	124
% identity	75
NCBI Description	(Z68334) Similarity to Rat chloride channel protein (PIR Acc. No. S47327); cDNA EST yk354e5.3 comes from this gene [Caenorhabditis elegans] >gi_3880174_emb_CAA90949_ (Z54216) Similarity to Rat chloride channel protein (PIR Acc. No. S47327); cDNA EST yk354e5.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	51806
Seq. ID	uC-gmrominsoy206c12b1
Method	BLASTN
NCBI GI	g313143
BLAST score	144
E value	3.0e-75

Match length	233
% identity	93
NCBI Description	A.medicago MSK-1 mRNA for protein kinase

Seq. No.	51807
Seq. ID	uC-gmrominsoy206h10b1
Method	BLASTX
NCBI GI	g1086263
BLAST score	191
E value	1.0e-14
Match length	90
% identity	52
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	51808
Seq. ID	uC-gmrominsoy207f03b1
Method	BLASTX
NCBI GI	g1552379
BLAST score	253
E value	2.0e-22
Match length	60
% identity	80
NCBI Description	(Y08155) pectin methylesterase [Silene latifolia ssp. alba]

Seq. No.	51809
Seq. ID	uC-gmrominsoy207g07b1
Method	BLASTX
NCBI GI	g1076413
BLAST score	263
E value	7.0e-23
Match length	110
% identity	46
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_2146776_pir__S67482 serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_608577 (L34076) serine acetyltransferase [Arabidopsis thaliana] >gi_608677_emb_CAA84371_ (Z34888) serine acetyltransferase [Arabidopsis thaliana] >gi_1093493_prf__2104212A Ser acetyltransferase [Arabidopsis thaliana]

Seq. No.	51810
Seq. ID	uC-gmrominsoy207h03b1
Method	BLASTX
NCBI GI	g3121981
BLAST score	396
E value	1.0e-38
Match length	115
% identity	66
NCBI Description	PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10) >gi_1142710 (U28042) similar to DEAD box RNA helicases [Homo sapiens] >gi_1589113_prf__2210303A RNA helicase [Homo sapiens]

Seq. No.	51811
Seq. ID	uC-gmrominsoy208c10b1
Method	BLASTX

NCBI GI	g345829
BLAST score	477
E value	6.0e-48
Match length	141
% identity	60
NCBI Description	ubiquitin carrier protein E2 - human

Seq. No.	51812
Seq. ID	uC-gmrominsoy208e05b1
Method	BLASTX
NCBI GI	g4006865
BLAST score	191
E value	9.0e-15
Match length	65
% identity	62
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	51813
Seq. ID	uC-gmrominsoy208f10b1
Method	BLASTX
NCBI GI	g2351580
BLAST score	449
E value	7.0e-45
Match length	88
% identity	97
NCBI Description	(U82433) thymidine diphospho-glucose 4-6-dehydratase homolog [Prunus armeniaca]

Seq. No.	51814
Seq. ID	uC-gmrominsoy208h06b1
Method	BLASTX
NCBI GI	g1184072
BLAST score	154
E value	3.0e-10
Match length	106
% identity	36
NCBI Description	(U40766) COL-1 [Meloidogyne incognita]

Seq. No.	51815
Seq. ID	uC-gmrominsoy209a07b1
Method	BLASTX
NCBI GI	g416866
BLAST score	353
E value	1.0e-33
Match length	113
% identity	58
NCBI Description	CYANIDE HYDRATASE (FORMAMIDE HYDROLYASE) >gi_323021_pir__JQ1613 cyanide hydratase (EC 4.2.1.66) - imperfect fungus (Gloeocercospora sorghi) >gi_168197 (M99044) cyanide hydratase [Gloeocercospora sorghi]

Seq. No.	51816
Seq. ID	uC-gmrominsoy210f04b1
Method	BLASTX
NCBI GI	g3695393
BLAST score	178
E value	5.0e-13

Match length	68
% identity	53
NCBI Description	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]

Seq. No.	51817
Seq. ID	uC-gmrominsoy211d09b1
Method	BLASTX
NCBI GI	g2342685
BLAST score	311
E value	1.0e-28
Match length	95
% identity	62
NCBI Description	(AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No.	51818
Seq. ID	uC-gmrominsoy213a12b1
Method	BLASTX
NCBI GI	g4185599
BLAST score	162
E value	3.0e-11
Match length	91
% identity	42
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	51819
Seq. ID	uC-gmrominsoy213c07b1
Method	BLASTN
NCBI GI	g4544381
BLAST score	34
E value	2.0e-09
Match length	140
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	51820
Seq. ID	uC-gmrominsoy213h12b1
Method	BLASTX
NCBI GI	g3236238
BLAST score	404
E value	1.0e-39
Match length	116
% identity	70
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	51821
Seq. ID	uC-gmrominsoy214d03b1
Method	BLASTX
NCBI GI	g3876398
BLAST score	295

E value	6.0e-27
Match length	95
% identity	59
NCBI Description	(Z81068) similar to Pyruvate kinase; cDNA EST yk206a12.5 comes from this gene; cDNA EST yk437b7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	51822
Seq. ID	uC-gmrominsoy214d10b1
Method	BLASTX
NCBI GI	g3249068
BLAST score	271
E value	7.0e-24
Match length	131
% identity	44
NCBI Description	(AC004473) Contains similarity to zinc-binding protein (PWA33) gb_L04190 from Pleurodeles waltlii. [Arabidopsis thaliana]

Seq. No.	51823
Seq. ID	uC-gmrominsoy214f03b1
Method	BLASTX
NCBI GI	g466104
BLAST score	202
E value	9.0e-16
Match length	119
% identity	34
NCBI Description	HYPOTHETICAL 51.6 KD PROTEIN ZK353.8 IN CHROMOSOME III >gi_1078910_pir__S44655 ZK353.8 protein - Caenorhabditis elegans >gi_289758 (L15313) putative [Caenorhabditis elegans]

Seq. No.	51824
Seq. ID	uC-gmrominsoy215c06b1
Method	BLASTX
NCBI GI	g4115359
BLAST score	240
E value	3.0e-20
Match length	129
% identity	5
NCBI Description	(AC005957) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	51825
Seq. ID	uC-gmrominsoy215d02b1
Method	BLASTX
NCBI GI	g4097880
BLAST score	200
E value	5.0e-16
Match length	75
% identity	60
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	51826
Seq. ID	uC-gmrominsoy216c12b1
Method	BLASTX
NCBI GI	g3850588

BLAST score	250
E value	2.0e-21
Match length	106
% identity	52
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No.	51827
Seq. ID	uC-gmrominsoy217a12b1
Method	BLASTN
NCBI GI	g1326160
BLAST score	67
E value	2.0e-29
Match length	173
% identity	95
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	51828
Seq. ID	uC-gmrominsoy217f11b1
Method	BLASTN
NCBI GI	g1370204
BLAST score	53
E value	5.0e-21
Match length	69
% identity	94
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAN1B

Seq. No.	51829
Seq. ID	uC-gmrominsoy217h10b1
Method	BLASTX
NCBI GI	g1903357
BLAST score	477
E value	5.0e-48
Match length	140
% identity	61
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	51830
Seq. ID	uC-gmrominsoy218d04b1
Method	BLASTX
NCBI GI	g2281115
BLAST score	197
E value	3.0e-15
Match length	48
% identity	77
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	51831
Seq. ID	uC-gmrominsoy218e10b1
Method	BLASTX
NCBI GI	g3415117
BLAST score	425
E value	4.0e-42

Match length	97
% identity	30
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	51832
Seq. ID	uC-gmrominsoy219a07b1
Method	BLASTX
NCBI GI	g2738996
BLAST score	270
E value	8.0e-24
Match length	119
% identity	53
NCBI Description	(AF022457) CYP97B2p [Glycine max]

Seq. No.	51833
Seq. ID	uC-gmrominsoy220a02b1
Method	BLASTX
NCBI GI	g100099
BLAST score	182
E value	6.0e-14
Match length	69
% identity	71
NCBI Description	DNA-binding protein VBP1 - fava bean >gi_1372966 (M81827) CREB-like protein [Vicia faba]

Seq. No.	51834
Seq. ID	uC-gmrominsoy220b05b1
Method	BLASTX
NCBI GI	g3540188
BLAST score	425
E value	5.0e-42
Match length	112
% identity	70
NCBI Description	(AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	51835
Seq. ID	uC-gmrominsoy220f03b1
Method	BLASTN
NCBI GI	g1675195
BLAST score	114
E value	2.0e-57
Match length	240
% identity	87
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	51836
Seq. ID	uC-gmrominsoy220h07b1
Method	BLASTX
NCBI GI	g423793
BLAST score	173
E value	3.0e-12
Match length	84
% identity	43
NCBI Description	carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56) >gi_402521_dbj_BAA03399_ (D14529) esterase V [Pseudomonas sp.]

Seq. No.	51837
Seq. ID	uC-gmrominsoy221h11b1
Method	BLASTX
NCBI GI	g4314388
BLAST score	654
E value	1.0e-68
Match length	149
% identity	85
NCBI Description	(AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51838
Seq. ID	uC-gmrominsoy222c06b1
Method	BLASTN
NCBI GI	g1498333
BLAST score	91
E value	7.0e-44
Match length	188
% identity	90
NCBI Description	Glycine max actin (Soy57) gene, partial cds

Seq. No.	51839
Seq. ID	uC-gmrominsoy222d08b1
Method	BLASTN
NCBI GI	g1808591
BLAST score	116
E value	1.0e-58
Match length	176
% identity	91
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	51840
Seq. ID	uC-gmrominsoy222f05b1
Method	BLASTX
NCBI GI	g2335096
BLAST score	222
E value	3.0e-18
Match length	105
% identity	37
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51841
Seq. ID	uC-gmrominsoy222g09b1
Method	BLASTX
NCBI GI	g3608155
BLAST score	465
E value	9.0e-47
Match length	113
% identity	81
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	51842
Seq. ID	uC-gmrominsoy223d02b1
Method	BLASTX
NCBI GI	g282963
BLAST score	232
E value	3.0e-19

Match length	48
% identity	92
NCBI Description	transforming protein (myb) homolog (clone myb.Ph2) - garden petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia x hybrida]

Seq. No.	51843
Seq. ID	uC-gmrominsoy223h06b1
Method	BLASTX
NCBI GI	g3287677
BLAST score	304
E value	1.0e-27
Match length	94
% identity	61
NCBI Description	(AC003979) Contains similarity to transcription factor (TINY) isolog T02O04.22 gb_2062174 from A. thaliana BAC gb_AC001645. [Arabidopsis thaliana]

Seq. No.	51844
Seq. ID	uC-gmrominsoy224c08b1
Method	BLASTX
NCBI GI	g2394274
BLAST score	249
E value	2.0e-29
Match length	128
% identity	61
NCBI Description	(AF017061) vasopressin-activated calcium mobilizing putative receptor protein [Homo sapiens]

Seq. No.	51845
Seq. ID	uC-gmrominsoy225h11b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	2.0e-09
Match length	43
% identity	47
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51846
Seq. ID	uC-gmrominsoy226b09b1
Method	BLASTX
NCBI GI	g2285875
BLAST score	233
E value	2.0e-19
Match length	127
% identity	39
NCBI Description	(D85682) synaptojanin [Bos taurus]

Seq. No.	51847
Seq. ID	uC-gmrominsoy226h11b1
Method	BLASTN
NCBI GI	g459961
BLAST score	179
E value	4.0e-96
Match length	179
% identity	100

NCBI Description	Glycine max proplastid omega-6 desaturase mRNA, complete cds

Seq. No.	51848
Seq. ID	uC-gmrominsoy227b07b1
Method	BLASTN
NCBI GI	g4220641
BLAST score	35
E value	4.0e-10
Match length	55
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	51849
Seq. ID	uC-gmrominsoy227h10b1
Method	BLASTX
NCBI GI	g2252842
BLAST score	149
E value	2.0e-09
Match length	146
% identity	31
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	51850
Seq. ID	uC-gmrominsoy228c10b1
Method	BLASTX
NCBI GI	g1707010
BLAST score	224
E value	2.0e-18
Match length	108
% identity	47
NCBI Description	(U78721) mitochondrial carrier protein isolog [Arabidopsis thaliana]

Seq. No.	51851
Seq. ID	uC-gmrominsoy228f03b1
Method	BLASTX
NCBI GI	g1049340
BLAST score	236
E value	1.0e-19
Match length	82
% identity	54
NCBI Description	(U39644) similar to other C. elegans cuticular collagens [Caenorhabditis elegans]

Seq. No.	51852
Seq. ID	uC-gmrominsoy229c02b1
Method	BLASTX
NCBI GI	g1002800
BLAST score	456
E value	1.0e-45
Match length	95
% identity	86
NCBI Description	(U33917) Cpm7 [Craterostigma plantagineum]

Seq. No.	51853

Seq. ID	uC-gmrominsoy229d04b1
Method	BLASTX
NCBI GI	g2496966
BLAST score	142
E value	1.0e-08
Match length	91
% identity	41
NCBI Description	HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III >gi_726395 (U23172) No definition line found [Caenorhabditis elegans]

Seq. No.	51854
Seq. ID	uC-gmrominsoy229g05b1
Method	BLASTX
NCBI GI	g1109872
BLAST score	342
E value	4.0e-32
Match length	95
% identity	67
NCBI Description	(U41542) weak similarity to yeast hypothetical protein in CDC1 region (SP:YHQ8_YEAST,P38817) [Caenorhabditis elegans]

Seq. No.	51855
Seq. ID	uC-gmrominsoy230a03b1
Method	BLASTX
NCBI GI	g2252828
BLAST score	329
E value	2.0e-37
Match length	114
% identity	75
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	51856
Seq. ID	uC-gmrominsoy230d02b1
Method	BLASTX
NCBI GI	g138364
BLAST score	250
E value	5.0e-22
Match length	71
% identity	68
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	51857
Seq. ID	uC-gmrominsoy230f05b1
Method	BLASTX
NCBI GI	g3929361
BLAST score	258
E value	2.0e-22
Match length	91
% identity	54
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1246816_emb_CAA64794_ (X95547) ferredoxin-like iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]

Seq. No.	51858
Seq. ID	uC-gmrominsoy231b06b1
Method	BLASTX
NCBI GI	g2129575
BLAST score	249
E value	2.0e-21
Match length	52
% identity	87
NCBI Description	DNA repair protein homolog XPBara - Arabidopsis thaliana

Seq. No.	51859
Seq. ID	uC-gmrominsoy231b12b1
Method	BLASTX
NCBI GI	g1707090
BLAST score	317
E value	3.0e-29
Match length	130
% identity	52
NCBI Description	(U80451) coded for by C. elegans cDNA yk106e10.3; coded for by C. elegans cDNA yk106e10.5; coded for by C. elegans cDNA yk51g3.5; coded for by C. elegans cDNA yk67h1.5; coded for by C. elegans cDNA yk113c12.5; belongs to the GST superfamily

Seq. No.	51860
Seq. ID	uC-gmrominsoy231d11b1
Method	BLASTX
NCBI GI	g1943797
BLAST score	220
E value	8.0e-18
Match length	93
% identity	42
NCBI Description	(U97194) Similar to cyclin [Caenorhabditis elegans]

Seq. No.	51861
Seq. ID	uC-gmrominsoy231f05b1
Method	BLASTN
NCBI GI	g4039114
BLAST score	52
E value	3.0e-20
Match length	291
% identity	92
NCBI Description	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds

Seq. No.	51862
Seq. ID	uC-gmrominsoy232c07b1
Method	BLASTN
NCBI GI	g1163180
BLAST score	162
E value	4.0e-86
Match length	277
% identity	90
NCBI Description	Glycine max arginine decarboxylase mRNA, complete cds

Seq. No.	51863
Seq. ID	uC-gmrominsoy233a12b1

Method	BLASTN
NCBI GI	g1006804
BLAST score	53
E value	5.0e-21
Match length	88
% identity	95
NCBI Description	Vigna radiata 1-aminocyclopropane-1-carboxylic acid synthase (VRACS6) mRNA, complete cds

Seq. No.	51864
Seq. ID	uC-gmrominsoy233d02b1
Method	BLASTN
NCBI GI	g4009327
BLAST score	177
E value	6.0e-95
Match length	345
% identity	88
NCBI Description	Plecoglossus altivelis gene for beta-actin, partial cds

Seq. No.	51865
Seq. ID	uC-gmrominsoy233d10b1
Method	BLASTX
NCBI GI	g1353179
BLAST score	268
E value	1.0e-23
Match length	96
% identity	54
NCBI Description	HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV >gi_1086618 (U41011) similar to S. cerevisiae regulatory protein APA1 (PIR:S43122) [Caenorhabditis elegans]

Seq. No.	51866
Seq. ID	uC-gmrominsoy233e03b1
Method	BLASTX
NCBI GI	g3875751
BLAST score	408
E value	5.0e-40
Match length	115
% identity	39
NCBI Description	(Z81499) similar to myosin heavy chain; cDNA EST EMBL:T02297 comes from this gene; cDNA EST EMBL:T00788 comes from this gene; cDNA EST yk202c10.3 comes from this gene; cDNA EST yk202c10.5 comes from this gene; cDNA EST yk205b2.... >gi_3876585_emb_CAB05505_ (Z83107) similar to myosin heavy chain; cDNA EST EMBL:T02297 comes from this gene; cDNA EST EMBL:T00788 comes from this gene; cDNA EST yk202c10.3 comes from this gene; cDNA EST yk202c10.5 comes from this gene; cDNA EST yk205b2

Seq. No.	51867
Seq. ID	uC-gmrominsoy233g05b1
Method	BLASTX
NCBI GI	g1353179
BLAST score	183
E value	9.0e-14
Match length	89
% identity	48

NCBI Description	HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV >gi_1086618 (U41011) similar to S. cerevisiae regulatory protein APA1 (PIR:S43122) [Caenorhabditis elegans]

Seq. No.	51868
Seq. ID	uC-gmrominsoy234c04b1
Method	BLASTX
NCBI GI	g3980413
BLAST score	159
E value	7.0e-11
Match length	76
% identity	46
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	51869
Seq. ID	uC-gmrominsoy234f09b1
Method	BLASTX
NCBI GI	g2062167
BLAST score	274
E value	3.0e-24
Match length	85
% identity	60
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	51870
Seq. ID	uC-gmrominsoy234f11b1
Method	BLASTX
NCBI GI	g2370232
BLAST score	217
E value	1.0e-17
Match length	47
% identity	83
NCBI Description	(AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No.	51871
Seq. ID	uC-gmrominsoy235b10b1
Method	BLASTX
NCBI GI	g2736325
BLAST score	209
E value	1.0e-16
Match length	69
% identity	54
NCBI Description	(AF038615) Similar to farnesyltransferase alpha subunit [Caenorhabditis elegans]

Seq. No.	51872
Seq. ID	uC-gmrominsoy235d05b1
Method	BLASTX
NCBI GI	g3093294
BLAST score	553
E value	6.0e-57
Match length	143
% identity	37
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	51873

Seq. ID uC-gmrominsoy235e03b1
Method BLASTX
NCBI GI g3881379
BLAST score 281
E value 5.0e-25
Match length 105
% identity 38
NCBI Description (Z49131) similar to cystathionine beta-synthase; cDNA EST EMBL:D73726 comes from this gene; cDNA EST EMBL:D71124 comes from this gene; cDNA EST EMBL:D71812 comes from this gene; cDNA EST yk503c8.3 comes from this gene; cDNA EST

Seq. No. 51874
Seq. ID uC-gmrominsoy235h02b1
Method BLASTN
NCBI GI g18590
BLAST score 159
E value 3.0e-84
Match length 310
% identity 86
NCBI Description G.max GH3 gene for auxin-regulated protein

Seq. No. 51875
Seq. ID uC-gmrominsoy235h12b1
Method BLASTN
NCBI GI g4097879
BLAST score 47
E value 3.0e-17
Match length 71
% identity 92
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No. 51876
Seq. ID uC-gmrominsoy236c02b1
Method BLASTX
NCBI GI g4218011
BLAST score 392
E value 5.0e-38
Match length 140
% identity 54
NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana] >gi_4309721_gb_AAD15491_ (AC006439) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 51877
Seq. ID uC-gmrominsoy236f01b1
Method BLASTX
NCBI GI g4107323
BLAST score 649
E value 3.0e-68
Match length 136
% identity 90
NCBI Description (AL035077) 60s ribosomal protein l10 [Schizosaccharomyces pombe]

Seq. No. 51878

Seq. ID	uC-gmrominsoy238c05b1
Method	BLASTX
NCBI GI	g2190419
BLAST score	637
E value	9.0e-67
Match length	129
% identity	89
NCBI Description	(Y13632) dem [Lycopersicon esculentum]

Seq. No.	51879
Seq. ID	uC-gmrominsoy238g11b1
Method	BLASTX
NCBI GI	g4262595
BLAST score	305
E value	5.0e-28
Match length	99
% identity	64
NCBI Description	(AF125955) similar to L-lactate dehydrogenases (Pfam:PF00056, Score=318.1, E=1.1e-91, N=1) [Caenorhabditis elegans]

Seq. No.	51880
Seq. ID	uC-gmrominsoy238g12b1
Method	BLASTX
NCBI GI	g4559333
BLAST score	156
E value	1.0e-10
Match length	109
% identity	32
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	51881
Seq. ID	uC-gmrominsoy240g01b1
Method	BLASTX
NCBI GI	g138364
BLAST score	138
E value	8.0e-09
Match length	43
% identity	65
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	51882
Seq. ID	uC-gmrominsoy241a05b1
Method	BLASTX
NCBI GI	g2492504
BLAST score	471
E value	2.0e-47
Match length	107
% identity	42
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_1669660_emb_CAA70565_ (Y09396) protein of AAA family [Capsicum annuum]

Seq. No.	51883

Seq. ID	uC-gmrominsoy241b04b1
Method	BLASTN
NCBI GI	g169988
BLAST score	338
E value	0.0e+00
Match length	370
% identity	98
NCBI Description	Glycine max NADP-specific isocitrate dehydrogenase (idh1) mRNA, 3' end

Seq. No.	51884
Seq. ID	uC-gmrominsoy241c08b1
Method	BLASTX
NCBI GI	g3193290
BLAST score	354
E value	1.0e-33
Match length	142
% identity	49
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido

Seq. No.	51885
Seq. ID	uC-gmrominsoy241d03b1
Method	BLASTX
NCBI GI	g1495259
BLAST score	312
E value	1.0e-28
Match length	142
% identity	46
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]

Seq. No.	51886
Seq. ID	uC-gmrominsoy241g04b1
Method	BLASTX
NCBI GI	g4572671
BLAST score	249
E value	3.0e-21
Match length	86
% identity	53
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	51887
Seq. ID	uC-gmrominsoy241g05b1
Method	BLASTX
NCBI GI	g3158376
BLAST score	264
E value	5.0e-23
Match length	108
% identity	53
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	51888
Seq. ID	uC-gmrominsoy241g09b1

Method	BLASTX
NCBI GI	g416864
BLAST score	212
E value	5.0e-17
Match length	122
% identity	36
NCBI Description	CYCLOHEXIMIDE RESISTANCE PROTEIN >gi_170849 (M64932) cyclohexamide resistance protein [Candida maltosa]

Seq. No.	51889
Seq. ID	uC-gmrominsoy243a11b1
Method	BLASTX
NCBI GI	g4262236
BLAST score	358
E value	3.0e-34
Match length	98
% identity	74
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	51890
Seq. ID	uC-gmrominsoy243f11b1
Method	BLASTN
NCBI GI	g4103958
BLAST score	59
E value	2.0e-24
Match length	71
% identity	96
NCBI Description	Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele, complete cds

Seq. No.	51891
Seq. ID	uC-gmrominsoy244a10b1
Method	BLASTX
NCBI GI	g2245124
BLAST score	413
E value	2.0e-40
Match length	123
% identity	67
NCBI Description	(Z97343) protein kinase [Arabidopsis thaliana]

Seq. No.	51892
Seq. ID	uC-gmrominsoy244b09b1
Method	BLASTN
NCBI GI	g1107480
BLAST score	144
E value	3.0e-75
Match length	335
% identity	40
NCBI Description	Acanthamoeba polyubiquitin gene

Seq. No.	51893
Seq. ID	uC-gmrominsoy244d02b1
Method	BLASTX
NCBI GI	g2129539
BLAST score	155
E value	3.0e-10

Match length	52
% identity	52
NCBI Description	AtJ1 protein - Arabidopsis thaliana >gi_564030 (U16246) AtJ1 [Arabidopsis thaliana]

Seq. No.	51894
Seq. ID	uC-gmrominsoy244e10b1
Method	BLASTX
NCBI GI	g482227
BLAST score	509
E value	1.0e-51
Match length	161
% identity	32
NCBI Description	hypothetical protein T07C4.9 - Caenorhabditis elegans >gi_3879509_emb_CAA82571_ (Z29443) similar to Annexin; cDNA EST EMBL:C10640 comes from this gene; cDNA EST EMBL:C12433 comes from this gene; cDNA EST yk192f7.5 comes from this gene; cDNA EST yk318c1.5 comes from this gene; cDNA EST yk494a12.3 comes from

Seq. No.	51895
Seq. ID	uC-gmrominsoy244f11b1
Method	BLASTX
NCBI GI	g730526
BLAST score	340
E value	8.0e-32
Match length	103
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	51896
Seq. ID	uC-gmrominsoy244h03b1
Method	BLASTX
NCBI GI	g3236241
BLAST score	146
E value	3.0e-09
Match length	88
% identity	43
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	51897
Seq. ID	uC-gmrominsoy244h05b1
Method	BLASTX
NCBI GI	g1170567
BLAST score	211
E value	2.0e-17
Match length	66
% identity	70
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]

Seq. No.	51898

Seq. ID	uC-gmrominsoy244h08b1
Method	BLASTX
NCBI GI	g2576361
BLAST score	151
E value	8.0e-10
Match length	92
% identity	33
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	51899
Seq. ID	uC-gmrominsoy245a11b1
Method	BLASTX
NCBI GI	g2258317
BLAST score	200
E value	2.0e-15
Match length	128
% identity	38
NCBI Description	(AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]

Seq. No.	51900
Seq. ID	uC-gmrominsoy245b03b1
Method	BLASTX
NCBI GI	g2244866
BLAST score	359
E value	3.0e-34
Match length	132
% identity	50
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51901
Seq. ID	uC-gmrominsoy245b12b1
Method	BLASTX
NCBI GI	g4417271
BLAST score	385
E value	4.0e-37
Match length	81
% identity	85
NCBI Description	(AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	51902
Seq. ID	uC-gmrominsoy245d06b1
Method	BLASTN
NCBI GI	g2656028
BLAST score	53
E value	8.0e-21
Match length	121
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	51903
Seq. ID	uC-gmrominsoy245g09b1
Method	BLASTN
NCBI GI	g3821780

BLAST score 33
E value 7.0e-09
Match length 33
% identity 58
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 51904
Seq. ID uC-gmrominsoy245h06b1
Method BLASTX
NCBI GI g3212861
BLAST score 444
E value 4.0e-44
Match length 92
% identity 88
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 51905
Seq. ID uC-gmrominsoy246c02b1
Method BLASTN
NCBI GI g18766
BLAST score 126
E value 2.0e-64
Match length 421
% identity 83
NCBI Description Soybean Tgm5 transposable element

Seq. No. 51906
Seq. ID uC-gmrominsoy247a07b1
Method BLASTX
NCBI GI g1055107
BLAST score 309
E value 2.0e-28
Match length 113
% identity 49
NCBI Description (U39995) No definition line found [Caenorhabditis elegans]

Seq. No. 51907
Seq. ID uC-gmrominsoy247c08b1
Method BLASTX
NCBI GI g4490335
BLAST score 165
E value 1.0e-11
Match length 113
% identity 35
NCBI Description (AL035656) receptor kinase-like protein [Arabidopsis thaliana]

Seq. No. 51908
Seq. ID uC-gmrominsoy247c11b1
Method BLASTX
NCBI GI g417059
BLAST score 315
E value 4.0e-29
Match length 116
% identity 50
NCBI Description GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) >gi_543538_pir__JN0716 glutamate--ammonia ligase (EC

6.3.1.2) - spiny lobster >gi_160786 (M96798) glutamine synthetase [Panulirus argus]

Seq. No.	51909
Seq. ID	uC-gmrominsoy247d09b1
Method	BLASTX
NCBI GI	g2492633
BLAST score	184
E value	7.0e-26
Match length	91
% identity	68
NCBI Description	PROBABLE GLUTARYL-COA DEHYDROGENASE PRECURSOR (GCD) >gi_3877512_emb_CAA91333_ (Z66513) similar to acyl-CoA dehydrogenase; cDNA EST EMBL:D70283 comes from this gene; cDNA EST EMBL:D66714 comes from this gene; cDNA EST EMBL:D70641 comes from this gene; cDNA EST EMBL:D70573 comes from this gene; cDNA EST EM

Seq. No.	51910
Seq. ID	uC-gmrominsoy248a09b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	3.0e-10
Match length	36
% identity	60
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	51911
Seq. ID	uC-gmrominsoy248g07b1
Method	BLASTX
NCBI GI	g619738
BLAST score	619
E value	1.0e-64
Match length	163
% identity	71
NCBI Description	(U18781) alcohol dehydrogenase [Caenorhabditis elegans]

Seq. No.	51912
Seq. ID	uC-gmrominsoy250g08b1
Method	BLASTN
NCBI GI	g1236948
BLAST score	249
E value	1.0e-138
Match length	305
% identity	96
NCBI Description	Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No.	51913
Seq. ID	uC-gmrominsoy253e06b1
Method	BLASTX
NCBI GI	g2497504
BLAST score	152
E value	7.0e-10
Match length	58
% identity	50
NCBI Description	PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97)

(DISCS, LARGE HOMOLOG 1) >gi_2135397_pir__I38757 homolog of Drosophila discs large protein, isoform 1 - human >gi_558438 (U13897) homolog of Drosophila discs large protein, isoform 1 [Homo sapiens]

Seq. No.	51914
Seq. ID	uC-gmrominsoy253f10b1
Method	BLASTX
NCBI GI	g3879225
BLAST score	263
E value	5.0e-23
Match length	101
% identity	55
NCBI Description	(Z48809) similar to 1-phosphatidylinositol-4, 5-bisphosphate phosphodiesterase; cDNA EST EMBL:T00496 comes from this gene; cDNA EST EMBL:D36610 comes from this gene; cDNA EST EMBL:T00496 comes from this gene; cDNA EST EMBL:D691

Seq. No.	51915
Seq. ID	uC-gmrominsoy253f11b1
Method	BLASTX
NCBI GI	g3687240
BLAST score	221
E value	4.0e-18
Match length	81
% identity	54
NCBI Description	(AC005169) extensin-like protein [Arabidopsis thaliana]

Seq. No.	51916
Seq. ID	uC-gmrominsoy256c12b1
Method	BLASTX
NCBI GI	g3860275
BLAST score	430
E value	2.0e-42
Match length	107
% identity	76
NCBI Description	(AC005824) putative GTP-binding protein [Arabidopsis thaliana] >gi_4314395_gb_AAD15605_ (AC006232) putative terminal flower 1 (TFL1) [Arabidopsis thaliana] >gi_4521159_dbj_BAA75933.1_ (AB024712) ATC [Arabidopsis thaliana] >gi_4521161_dbj_BAA75931.1_ (AB024714) ATC [Arabidopsis thaliana] >gi_4521163_dbj_BAA75932.1_ (AB024715) ATC [Arabidopsis thaliana]

Seq. No.	51917
Seq. ID	uC-gmrominsoy256h01b1
Method	BLASTX
NCBI GI	g1350976
BLAST score	268
E value	1.0e-23
Match length	66
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_939718 (U30454) ribosomal protein S2 [Urechis caupo]

Seq. No. 51918

Seq. ID	uC-gmrominsoy257f03b1
Method	BLASTX
NCBI GI	g1350783
BLAST score	188
E value	5.0e-14
Match length	138
% identity	48
NCBI Description	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi_282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No.	51919
Seq. ID	uC-gmrominsoy258h10b1
Method	BLASTN
NCBI GI	g439856
BLAST score	223
E value	1.0e-122
Match length	315
% identity	93
NCBI Description	Glycine max Williams 82 lipoxygenase mRNA, complete cds

Seq. No.	51920
Seq. ID	uC-gmrominsoy260a11b1
Method	BLASTX
NCBI GI	g3004556
BLAST score	213
E value	3.0e-17
Match length	77
% identity	52
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51921
Seq. ID	uC-gmrominsoy260b04b1
Method	BLASTX
NCBI GI	g4455240
BLAST score	346
E value	1.0e-32
Match length	102
% identity	64
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	51922
Seq. ID	uC-gmrominsoy260g02b1
Method	BLASTX
NCBI GI	g113695
BLAST score	211
E value	8.0e-17
Match length	92
% identity	46
NCBI Description	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE I PRECURSOR (PEPTIDE C-TERMINAL ALPHA-AMIDATING ENZYME I) (AE-I) >gi_66350_pir__URXLA1 peptidylglycine monooxygenase (EC 1.14.17.3) I precursor - African clawed frog >gi_213936 (M18134) amidating enzyme precursor [Xenopus laevis]

Seq. No.	51923
Seq. ID	uC-gmrominsoy261a05b1
Method	BLASTX
NCBI GI	g4218535
BLAST score	418
E value	4.0e-41
Match length	96
% identity	73
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	51924
Seq. ID	uC-gmrominsoy261a08b1
Method	BLASTX
NCBI GI	g1825731
BLAST score	415
E value	5.0e-58
Match length	126
% identity	89
NCBI Description	(U88308) C32E8.10 gene product [Caenorhabditis elegans]

Seq. No.	51925
Seq. ID	uC-gmrominsoy261a12b1
Method	BLASTX
NCBI GI	g2982303
BLAST score	451
E value	4.0e-45
Match length	111
% identity	85
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	51926
Seq. ID	uC-gmrominsoy261e06b1
Method	BLASTX
NCBI GI	g284076
BLAST score	434
E value	6.0e-43
Match length	128
% identity	64
NCBI Description	ERD-2-like protein, ELP-1 - human

Seq. No.	51927
Seq. ID	uC-gmrominsoy261g05b1
Method	BLASTX
NCBI GI	g1235974
BLAST score	351
E value	3.0e-33
Match length	92
% identity	68
NCBI Description	(X96713) collagen [Globodera pallida]

Seq. No.	51928
Seq. ID	uC-gmrominsoy262a09b1
Method	BLASTX
NCBI GI	g2500130
BLAST score	381
E value	5.0e-37

Match length	84
% identity	83
NCBI Description	THIOREDOXIN REDUCTASE 2 (NADPH-DEPENDENT THIOREDOXIN REDUCTASE 2) (NTR 2) >gi_1076358_pir__S44026 thioredoxin reductase (NADPH) (EC 1.6.4.5) A - Arabidopsis thaliana (fragment) >gi_468524_emb_CAA80655_ (Z23108) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	51929
Seq. ID	uC-gmrominsoy262c01b1
Method	BLASTX
NCBI GI	g2315153
BLAST score	295
E value	8.0e-27
Match length	74
% identity	78
NCBI Description	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]

Seq. No.	51930
Seq. ID	uC-gmrominsoy262e10b1
Method	BLASTX
NCBI GI	g3702352
BLAST score	146
E value	1.0e-09
Match length	59
% identity	53
NCBI Description	(AC005397) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	51931
Seq. ID	uC-gmrominsoy262g06b1
Method	BLASTX
NCBI GI	g2944180
BLAST score	195
E value	5.0e-15
Match length	49
% identity	73
NCBI Description	(AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	51932
Seq. ID	uC-gmrominsoy263g07b1
Method	BLASTX
NCBI GI	g2738248
BLAST score	245
E value	5.0e-21
Match length	55
% identity	89
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	51933
Seq. ID	uC-gmrominsoy263h11b1
Method	BLASTX
NCBI GI	g3745803
BLAST score	184
E value	1.0e-13

Match length	42
% identity	86
NCBI Description	Chain B, Rat Liver F1-Atpase

Seq. No.	51934
Seq. ID	uC-gmrominsoy264d09b1
Method	BLASTX
NCBI GI	g2809232
BLAST score	454
E value	2.0e-45
Match length	101
% identity	84
NCBI Description	(AC002560) F21B7.1 [Arabidopsis thaliana]

Seq. No.	51935
Seq. ID	uC-gmrominsoy264e03b1
Method	BLASTX
NCBI GI	g3878996
BLAST score	483
E value	1.0e-48
Match length	127
% identity	65
NCBI Description	(Z75955) similar to alpha-N-acetylgalactosaminidase; cDNA EST EMBL:M92935 comes from this gene; cDNA EST CEMSA04R comes from this gene [Caenorhabditis elegans]

Seq. No.	51936
Seq. ID	uC-gmrominsoy264f02b1
Method	BLASTN
NCBI GI	g169980
BLAST score	257
E value	1.0e-142
Match length	368
% identity	93
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	51937
Seq. ID	uC-gmrominsoy264f04b1
Method	BLASTX
NCBI GI	g1805249
BLAST score	166
E value	1.0e-11
Match length	112
% identity	43
NCBI Description	(U51990) hPrp18 [Homo sapiens] >gi_4506123_ref_NP_003666.1_pPRP18_ pre-mRNA splicing factor similar to S. cerevisiae Prp18

Seq. No.	51938
Seq. ID	uC-gmrominsoy265a10b1
Method	BLASTX
NCBI GI	g461735
BLAST score	286
E value	1.0e-25
Match length	98
% identity	67
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR

>gi_478785_pir__S29315 chaperonin 60 - cucurbit
>gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita sp.]

Seq. No.	51939
Seq. ID	uC-gmrominsoy265b11b1
Method	BLASTX
NCBI GI	g4388726
BLAST score	475
E value	3.0e-48
Match length	127
% identity	72
NCBI Description	(AC006413) putative 12-oxophytodienoate-10,11-reductase [Arabidopsis thaliana]

Seq. No.	51940
Seq. ID	uC-gmrominsoy265d02b1
Method	BLASTX
NCBI GI	g547766
BLAST score	305
E value	2.0e-44
Match length	108
% identity	86
NCBI Description	CASEIN KINASE I, DELTA ISOFORM (CKI-DELTA) >gi_423795_pir__A46002 casein kinase I (EC 2.7.1.-) delta, 49K isoform - rat >gi_294525 (L07578) casein kinase I delta [Rattus norvegicus]

Seq. No.	51941
Seq. ID	uC-gmrominsoy265d11b1
Method	BLASTX
NCBI GI	g4006878
BLAST score	175
E value	1.0e-12
Match length	62
% identity	52
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	51942
Seq. ID	uC-gmrominsoy265f07b1
Method	BLASTX
NCBI GI	g2982458
BLAST score	147
E value	3.0e-09
Match length	80
% identity	53
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	51943
Seq. ID	uC-gmrominsoy265g04b1
Method	BLASTX
NCBI GI	g2055454
BLAST score	343
E value	3.0e-32
Match length	84
% identity	77
NCBI Description	(U97204) prohibitin-like molecule TC-PRO-1 [Toxocara canis]

Seq. No.	51944
Seq. ID	uC-gmrominsoy265h11b1
Method	BLASTX
NCBI GI	g1125808
BLAST score	531
E value	2.0e-54
Match length	109
% identity	92
NCBI Description	(U42845) coded for by C. elegans cDNA yk63a8.5; coded for by C. elegans cDNA yk83a12.5; coded for by C. elegans cDNA yk74b10.5; coded for by C. elegans cDNA yk64a6.5; coded for by C. elegans cDNA yk108g8.5; coded for by C. elegans cDNA yk90b

Seq. No.	51945
Seq. ID	uC-gmrominsoy268d09b1
Method	BLASTX
NCBI GI	g1169546
BLAST score	381
E value	8.0e-37
Match length	117
% identity	60
NCBI Description	PUTATIVE ER LUMEN PROTEIN RETAINING RECEPTOR C28H8.4 >gi_669010 (U20861) similar to endoplasmic reticulum lumen protein retaining receptor [Caenorhabditis elegans]

Seq. No.	51946
Seq. ID	uC-gmrominsoy268g05b1
Method	BLASTX
NCBI GI	g3242708
BLAST score	178
E value	5.0e-13
Match length	124
% identity	35
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	51947
Seq. ID	uC-gmrominsoy270a08b1
Method	BLASTX
NCBI GI	g1174718
BLAST score	312
E value	1.0e-28
Match length	100
% identity	62
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	51948
Seq. ID	uC-gmrominsoy270e07b1
Method	BLASTX
NCBI GI	g485131
BLAST score	218
E value	1.0e-17

Match length	81
% identity	56
NCBI Description	(U00052) similar to ADP, ATP carrier proteins [Caenorhabditis elegans]

Seq. No.	51949
Seq. ID	uC-gmrominsoy270g02b1
Method	BLASTX
NCBI GI	g1706681
BLAST score	178
E value	4.0e-13
Match length	84
% identity	45
NCBI Description	DIPHOSPHOMEVALONATE DECARBOXYLASE (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) >gi_1235682 (U49260) mevalonate pyrophosphate decarboxylase [Homo sapiens] >gi_4505289_ref_NP_002452.1_pMVD_ mevalonate (diphospho) decarboxylase

Seq. No.	51950
Seq. ID	uC-gmrominsoy271d02b1
Method	BLASTX
NCBI GI	g2828296
BLAST score	313
E value	7.0e-54
Match length	116
% identity	90
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	51951
Seq. ID	uC-gmrominsoy273b03b1
Method	BLASTX
NCBI GI	g1350996
BLAST score	560
E value	1.0e-57
Match length	145
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_453574_dbj_BAA05485_ (D26473) Ribosomal Protein [Cricetulus griseus]

Seq. No.	51952
Seq. ID	uC-gmrominsoy273g02b1
Method	BLASTX
NCBI GI	g3319342
BLAST score	141
E value	1.0e-08
Match length	33
% identity	67
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No.	51953
Seq. ID	uC-gmrominsoy274e02b1
Method	BLASTX
NCBI GI	g2088838
BLAST score	226

E value	7.0e-19
Match length	79
% identity	53
NCBI Description	(AF003386) F59E12.4 gene product [Caenorhabditis elegans]

Seq. No.	51954
Seq. ID	uC-gmrominsoy276a02b1
Method	BLASTX
NCBI GI	g1946371
BLAST score	389
E value	1.0e-37
Match length	143
% identity	54
NCBI Description	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No.	51955
Seq. ID	uC-gmrominsoy276e11b1
Method	BLASTX
NCBI GI	g3877856
BLAST score	169
E value	6.0e-12
Match length	97
% identity	29
NCBI Description	(Z34801) similar to Nucleoporin; cDNA EST EMBL:M88930 comes from this gene; cDNA EST EMBL:D27619 comes from this gene; cDNA EST EMBL:T00612 comes from this gene; cDNA EST EMBL:T01203 comes from this gene; cDNA EST EMBL:T01511 c

Seq. No.	51956
Seq. ID	uC-gmrominsoy276h11b1
Method	BLASTX
NCBI GI	g3928150
BLAST score	403
E value	2.0e-39
Match length	105
% identity	70
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	51957
Seq. ID	uC-gmrominsoy277a08b1
Method	BLASTX
NCBI GI	g138364
BLAST score	143
E value	2.0e-09
Match length	50
% identity	56
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	51958
Seq. ID	uC-gmrominsoy277b08b1
Method	BLASTX
NCBI GI	g4097880
BLAST score	254

E value	3.0e-22
Match length	84
% identity	65
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	51959
Seq. ID	uC-gmrominsoy277f09b1
Method	BLASTN
NCBI GI	g169980
BLAST score	217
E value	1.0e-118
Match length	377
% identity	93
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	51960
Seq. ID	uC-gmrominsoy280c12b1
Method	BLASTX
NCBI GI	g3894164
BLAST score	177
E value	1.0e-12
Match length	139
% identity	30
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	51961
Seq. ID	uC-gmrominsoy280h12b1
Method	BLASTX
NCBI GI	g4559396
BLAST score	223
E value	3.0e-18
Match length	76
% identity	54
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	51962
Seq. ID	uC-gmrominsoy283c11b1
Method	BLASTX
NCBI GI	g3128216
BLAST score	196
E value	4.0e-15
Match length	69
% identity	54
NCBI Description	(AC004077) putative GA4 protein [Arabidopsis thaliana]

Seq. No.	51963
Seq. ID	uC-gmrominsoy284a06b1
Method	BLASTN
NCBI GI	g1399306
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	Glycine max phosphoinositide-specific phospholipase C P25 mRNA, complete cds

Seq. No.	51964
Seq. ID	uC-gmrominsoy284b07b1
Method	BLASTX
NCBI GI	g3080367
BLAST score	246
E value	8.0e-21
Match length	126
% identity	40
NCBI Description	(AL022580) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51965
Seq. ID	uC-gmrominsoy284e08b1
Method	BLASTX
NCBI GI	g2583118
BLAST score	282
E value	1.0e-29
Match length	119
% identity	63
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	51966
Seq. ID	uC-gmrominsoy285c08b1
Method	BLASTX
NCBI GI	g3309084
BLAST score	248
E value	2.0e-31
Match length	94
% identity	56
NCBI Description	(AF076252) calcineurin B-like protein 2 [Arabidopsis thaliana]

Seq. No.	51967
Seq. ID	uC-gmrominsoy285f01b1
Method	BLASTX
NCBI GI	g2582971
BLAST score	268
E value	4.0e-24
Match length	81
% identity	68
NCBI Description	(D83711) TKRP125 [Nicotiana tabacum]

Seq. No.	51968
Seq. ID	uC-gmrominsoy287a11b1
Method	BLASTN
NCBI GI	g4097879
BLAST score	95
E value	2.0e-46
Match length	155
% identity	90
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	51969
Seq. ID	uC-gmrominsoy287c03b1
Method	BLASTX
NCBI GI	g4467096
BLAST score	192

E value 6.0e-15
Match length 85
% identity 52
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 51970
Seq. ID uC-gmrominsoy287c12b1
Method BLASTX
NCBI GI g4249386
BLAST score 593
E value 1.0e-61
Match length 132
% identity 83
NCBI Description (AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No. 51971
Seq. ID uC-gmrominsoy287d03b1
Method BLASTX
NCBI GI g3885328
BLAST score 168
E value 7.0e-12
Match length 87
% identity 40
NCBI Description (AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 51972
Seq. ID uC-gmrominsoy287e05b1
Method BLASTX
NCBI GI g138364
BLAST score 164
E value 7.0e-12
Match length 48
% identity 62
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 51973
Seq. ID uC-gmrominsoy287g09b1
Method BLASTX
NCBI GI g138364
BLAST score 156
E value 6.0e-11
Match length 37
% identity 81
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 51974
Seq. ID uC-gmrominsoy287h03b1
Method BLASTX

NCBI GI	g1853970
BLAST score	175
E value	9.0e-13
Match length	109
% identity	34
NCBI Description	(D88122) CPRD46 protein [Vigna unguiculata]

Seq. No.	51975
Seq. ID	uC-gmrominsoy293d03b1
Method	BLASTX
NCBI GI	g115402
BLAST score	324
E value	4.0e-30
Match length	92
% identity	65
NCBI Description	CUTICLE COLLAGEN 6 >gi_84433_pir__JS0167 collagen col-6 - Caenorhabditis elegans >gi_156264 (M25477) collagen [Caenorhabditis elegans]

Seq. No.	51976
Seq. ID	uC-gmrominsoy294b09b1
Method	BLASTX
NCBI GI	g138364
BLAST score	152
E value	2.0e-10
Match length	47
% identity	66
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	51977
Seq. ID	uC-gmrominsoy298a08b1
Method	BLASTN
NCBI GI	g1808591
BLAST score	107
E value	3.0e-53
Match length	215
% identity	87
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	51978
Seq. ID	uC-gmrominsoy298a10b1
Method	BLASTX
NCBI GI	g2980761
BLAST score	302
E value	8.0e-28
Match length	87
% identity	62
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	51979
Seq. ID	uC-gmrominsoy299b05b1
Method	BLASTX
NCBI GI	g1654140
BLAST score	315

E value 3.0e-29
Match length 102
% identity 54
NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No. 51980
Seq. ID uC-gmrominsoy299e03b1
Method BLASTX
NCBI GI g1531758
BLAST score 214
E value 3.0e-17
Match length 61
% identity 64
NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 51981
Seq. ID uC-gmrominsoy299h09b1
Method BLASTX
NCBI GI g3874907
BLAST score 187
E value 3.0e-14
Match length 91
% identity 43
NCBI Description (Z81048) cDNA EST EMBL:T00064 comes from this gene; cDNA EST EMBL:T01650 comes from this gene; cDNA EST EMBL:C07343 comes from this gene; cDNA EST EMBL:C08680 comes from this gene; cDNA EST yk491h1.3 comes from this gene; cDNA

Seq. No. 51982
Seq. ID uC-gmrominsoy300b08b1
Method BLASTN
NCBI GI g938299
BLAST score 194
E value 1.0e-105
Match length 448
% identity 91
NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)

Seq. No. 51983
Seq. ID uC-gmrominsoy300e10b1
Method BLASTX
NCBI GI g3878494
BLAST score 300
E value 3.0e-27
Match length 126
% identity 49
NCBI Description (Z79602) predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2 (SW:YAE2_YEAST); cDNA EST EMBL:T01631 comes from this gene; cDNA EST EMBL:M88949 comes from this gene [Caenorhabditis elegans]

Seq. No. 51984
Seq. ID uC-gmrominsoy300g08b1
Method BLASTX
NCBI GI g3142300
BLAST score 307

E value	5.0e-28
Match length	94
% identity	62
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	51985
Seq. ID	uC-gmrominsoy300g12b1
Method	BLASTX
NCBI GI	g2943789
BLAST score	160
E value	6.0e-11
Match length	84
% identity	43
NCBI Description	(AB000875) RD22BP1 [Arabidopsis thaliana]

Seq. No.	51986
Seq. ID	uC-gmrominsoy302e02b1
Method	BLASTX
NCBI GI	g3643598
BLAST score	512
E value	4.0e-52
Match length	138
% identity	70
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	51987
Seq. ID	uC-gmrominsoy302g02b1
Method	BLASTX
NCBI GI	g1176059
BLAST score	317
E value	3.0e-29
Match length	127
% identity	55
NCBI Description	HYPOTHETICAL 45.2 KD GTP-BINDING PROTEIN IN TRX1-RTA1 INTERGENIC REGION >gi_1077194_pir__S53933 probable membrane protein YGR210c - yeast (Saccharomyces cerevisiae) >gi_790501_emb_CAA89003_ (Z49133) unknown [Saccharomyces cerevisiae] >gi_1165215 (U40843) ORFS7; Method: conceptual translation supplied by author. [Saccharomyces cerevisiae] >gi_1323377_emb_CAA97237_ (Z72995) ORF YGR210c [Saccharomyces cerevisiae]

Seq. No.	51988
Seq. ID	uC-gmrominsoy303a05b1
Method	BLASTX
NCBI GI	g3123025
BLAST score	154
E value	5.0e-10
Match length	89
% identity	36
NCBI Description	VITELLOGENIN 6 PRECURSOR >gi_1515337 (U35449) vitellogenin [Oscheius sp. 'CEW1']

Seq. No.	51989
Seq. ID	uC-gmrominsoy303a07b1
Method	BLASTN
NCBI GI	g2062705
BLAST score	33
E value	6.0e-09
Match length	35
% identity	59
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	51990
Seq. ID	uC-gmrominsoy303b03b1
Method	BLASTX
NCBI GI	g1076821
BLAST score	188
E value	3.0e-14
Match length	92
% identity	42
NCBI Description	probable 1-acyl-glycerol-3-phosphate acyltransferase - maize >gi_575960_emb_CAA82638_ (Z29518) 1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea mays]

Seq. No.	51991
Seq. ID	uC-gmrominsoy303d04b1
Method	BLASTX
NCBI GI	g3874892
BLAST score	137
E value	1.0e-08
Match length	42
% identity	62
NCBI Description	(Z48045) similar to P97 protein; cDNA EST EMBL:M89239 comes from this gene; cDNA EST EMBL:D28083 comes from this gene; cDNA EST EMBL:D28082 comes from this gene; cDNA EST EMBL:T00671 comes from this gene; cDNA EST EMBL:D32722 c... >gi_3875715_emb_CAA88314_ (Z48334) similar to P97 protein; cDNA EST EMBL:M89239 comes from this gene; cDNA EST EMBL:D28083 comes from this gene; cDNA EST EMBL:D28082 comes from this gene; cDNA EST EMBL:T00671 comes from this gene; cDNA EST EMBL:D32722 c

Seq. No.	51992
Seq. ID	uC-gmrominsoy304h02b1
Method	BLASTN
NCBI GI	g166873
BLAST score	60
E value	3.0e-25
Match length	168
% identity	84
NCBI Description	A.thaliana S-adenosylmethionine synthetase 2 (sam-2) gene, complete cds

Seq. No.	51993
Seq. ID	uC-gmrominsoy304h05b1
Method	BLASTX
NCBI GI	g2194128
BLAST score	221

E value	4.0e-18
Match length	125
% identity	38
NCBI Description	(AC002062) Strong similarity to Arabidopsis receptor-like kinase (gb_ATLECGENE) and F20P5.15. [Arabidopsis thaliana]

Seq. No.	51994
Seq. ID	uC-gmrominsoy305a01b1
Method	BLASTX
NCBI GI	g4454467
BLAST score	360
E value	2.0e-34
Match length	126
% identity	52
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	51995
Seq. ID	uC-gmrominsoy305e03b1
Method	BLASTN
NCBI GI	g169964
BLAST score	49
E value	1.0e-18
Match length	168
% identity	89
NCBI Description	Soybean glutathione reductase (GR) mRNA, complete cds

Seq. No.	51996
Seq. ID	uC-gmrominsoy305e07b1
Method	BLASTN
NCBI GI	g4210834
BLAST score	82
E value	3.0e-38
Match length	179
% identity	85
NCBI Description	Pisum sativum mRNA for ketol-acid reductoisomerase

Seq. No.	51997
Seq. ID	uC-gmrominsoy305h11b1
Method	BLASTX
NCBI GI	g4220521
BLAST score	151
E value	7.0e-11
Match length	63
% identity	65
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	51998
Seq. ID	uC-gmrominsoy306g01b1
Method	BLASTX
NCBI GI	g2245020
BLAST score	156
E value	2.0e-10
Match length	46
% identity	63
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	51999

Seq. ID	uC-gmrominsoy306h02b1
Method	BLASTN
NCBI GI	g347458
BLAST score	278
E value	1.0e-155
Match length	314
% identity	97
NCBI Description	Glycine max brassinosteroid-regulated protein mRNA, complete cds

Seq. No.	52000
Seq. ID	uC-gmrominsoy306h12b1
Method	BLASTX
NCBI GI	g3297813
BLAST score	328
E value	2.0e-30
Match length	158
% identity	53
NCBI Description	(AL031032) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52001
Seq. ID	uC-gmrominsoy307b04b1
Method	BLASTX
NCBI GI	g3881332
BLAST score	590
E value	3.0e-61
Match length	151
% identity	70
NCBI Description	(AL032658) predicted using Genefinder; similar to AMP-binding enzyme; cDNA EST yk315d1.5 comes from this gene; cDNA EST EMBL:D33594 comes from this gene; cDNA EST EMBL:D36453 comes from this gene; cDNA EST EMBL:D71491 comes fro

Seq. No.	52002
Seq. ID	uC-gmrominsoy308b06b1
Method	BLASTX
NCBI GI	g3915601
BLAST score	341
E value	3.0e-32
Match length	113
% identity	56
NCBI Description	ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38) >gi_1498259 (L07541) replication factor C, 38-kDa subunit [Homo sapiens] >gi_4506489_ref_NP_002906.1_pRFC3_ replication factor C (activator 1) 3 (38kD)

Seq. No.	52003
Seq. ID	uC-gmrominsoy308b12b1
Method	BLASTX
NCBI GI	g4455155
BLAST score	185
E value	6.0e-14
Match length	54
% identity	65
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment)

[Arabidopsis thaliana]

Seq. No.	52004
Seq. ID	uC-gmrominsoy308c06b1
Method	BLASTX
NCBI GI	g4263048
BLAST score	219
E value	8.0e-18
Match length	125
% identity	47
NCBI Description	(AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No.	52005
Seq. ID	uC-gmrominsoy308f06b1
Method	BLASTX
NCBI GI	g4455179
BLAST score	256
E value	3.0e-22
Match length	119
% identity	46
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52006
Seq. ID	uC-gmrominsoy308f09b1
Method	BLASTX
NCBI GI	g133980
BLAST score	257
E value	2.0e-22
Match length	67
% identity	73
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_70934_pir__R3ZP6E ribosomal protein S6.e, cytosolic - fission yeast (Schizosaccharomyces pombe) >gi_173474 (M36382) ribosomal protein S6 (rps6) precursor [Schizosaccharomyces pombe] >gi_1008992_emb_CAA91100_ (Z54308) 40S ribosomal protein [Schizosaccharomyces pombe]

Seq. No.	52007
Seq. ID	uC-gmrominsoy308h08b1
Method	BLASTX
NCBI GI	g3892045
BLAST score	277
E value	3.0e-25
Match length	55
% identity	87
NCBI Description	(AC002330) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	52008
Seq. ID	uC-gmrominsoy309f02b1
Method	BLASTX
NCBI GI	g3599491
BLAST score	188
E value	3.0e-14
Match length	42
% identity	86
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	52009
Seq. ID	uC-gmrominsoy309h11b1
Method	BLASTN
NCBI GI	g2952109
BLAST score	125
E value	7.0e-64
Match length	245
% identity	98
NCBI Description	Fusarium oxysporum f. sp. cubense NRRL 25603 translation elongation factor gene, partial cds >gi_2952111_gb_AF008488_ Fusarium oxysporum f. sp. cubense NRRL 25605 translation elongation factor gene, partial cds >gi_2952147_gb_AF008506_AF008506 Fusarium oxysporum f. sp. perniciosum NRRL 22550 translation elongation factor gene, partial cds

Seq. No.	52010
Seq. ID	uC-gmrominsoy310h07b1
Method	BLASTX
NCBI GI	g3337356
BLAST score	326
E value	3.0e-30
Match length	64
% identity	97
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	52011
Seq. ID	uC-gmrominsoy311b03b1
Method	BLASTX
NCBI GI	g3292829
BLAST score	356
E value	1.0e-33
Match length	163
% identity	48
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	52012
Seq. ID	uC-gmrominsoy311d12b1
Method	BLASTN
NCBI GI	g1808591
BLAST score	101
E value	1.0e-49
Match length	217
% identity	87
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	52013
Seq. ID	uC-gmrominsoy311f09b1
Method	BLASTX
NCBI GI	g4544412
BLAST score	215
E value	2.0e-17
Match length	75
% identity	47
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52014
Seq. ID	uC-gmrominsoy311f10b1
Method	BLASTN
NCBI GI	g3193221
BLAST score	312
E value	1.0e-175
Match length	446
% identity	97
NCBI Description	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

Seq. No.	52015
Seq. ID	uC-gmrominsoy313c01b1
Method	BLASTX
NCBI GI	g1055107
BLAST score	253
E value	9.0e-22
Match length	106
% identity	50
NCBI Description	(U39995) No definition line found [Caenorhabditis elegans]

Seq. No.	52016
Seq. ID	uC-gmrominsoy313e07b1
Method	BLASTX
NCBI GI	g4321715
BLAST score	213
E value	2.0e-17
Match length	76
% identity	50
NCBI Description	(AF058326) GMP synthase [Lactococcus lactis]

Seq. No.	52017
Seq. ID	uC-gmrominsoy313f09b1
Method	BLASTX
NCBI GI	g4432846
BLAST score	452
E value	3.0e-45
Match length	114
% identity	71
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	52018
Seq. ID	uC-gmrominsoy313g08b1
Method	BLASTX
NCBI GI	g3157943
BLAST score	213
E value	6.0e-17
Match length	95
% identity	45
NCBI Description	(AC002131) Contains similarity to BAP31 protein gb_X81816 from Mus musculus. [Arabidopsis thaliana]

Seq. No.	52019
Seq. ID	uC-gmrominsoy314a12b1
Method	BLASTX
NCBI GI	g4106970

BLAST score	183
E value	1.0e-13
Match length	120
% identity	10
NCBI Description	(AF113948) resistance protein candidate RGC2B [Lactuca sativa]

Seq. No.	52020
Seq. ID	uC-gmrominsoy314c05b1
Method	BLASTX
NCBI GI	g2313769
BLAST score	143
E value	7.0e-09
Match length	81
% identity	8
NCBI Description	(AE000578) fucosyltransferase [Helicobacter pylori 26695]

Seq. No.	52021
Seq. ID	uC-gmrominsoy314e03b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	156
E value	1.0e-10
Match length	78
% identity	50
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	52022
Seq. ID	uC-gmrominsoy314f04b1
Method	BLASTX
NCBI GI	g4218535
BLAST score	197
E value	3.0e-15
Match length	70
% identity	70
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	52023
Seq. ID	uC-gmrominsoy314f09b1
Method	BLASTX
NCBI GI	g3875207
BLAST score	331
E value	5.0e-31
Match length	77
% identity	77
NCBI Description	(Z81486) Similarity to Human muscarinic acetylcholine receptor (SW:P20309); cDNA EST EMBL:D28081 comes from this gene; cDNA EST EMBL:D28080 comes from this gene [Caenorhabditis elegans]

Seq. No.	52024
Seq. ID	uC-gmrominsoy314g09b1
Method	BLASTN
NCBI GI	g1296533
BLAST score	167
E value	6.0e-89

Match length	311
% identity	88
NCBI Description	H.armigera actA3b gene

Seq. No.	52025
Seq. ID	uC-gmrominsoy315b07b1
Method	BLASTX
NCBI GI	g4006816
BLAST score	182
E value	2.0e-13
Match length	137
% identity	39
NCBI Description	(AC005970) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	52026
Seq. ID	uC-gmrominsoy315f07b1
Method	BLASTX
NCBI GI	g2245378
BLAST score	193
E value	9.0e-15
Match length	41
% identity	80
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	52027
Seq. ID	uC-gmrominsoy315f10b1
Method	BLASTX
NCBI GI	g127737
BLAST score	366
E value	5.0e-35
Match length	111
% identity	24
NCBI Description	MYOSIN HEAVY CHAIN A (MHC A) >gi_84468_pir__S02771 myosin heavy chain A - Caenorhabditis elegans >gi_6799_emb_CAA30856_ (X08067) myosin heavy chain 3 [Caenorhabditis elegans]

Seq. No.	52028
Seq. ID	uC-gmrominsoy317b12b1
Method	BLASTX
NCBI GI	g1703082
BLAST score	315
E value	4.0e-29
Match length	124
% identity	48
NCBI Description	PROBABLE ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi_1326262 (U58727) coded for by C. elegans cDNA yk133b7.5; coded for by C. elegans cDNA yk133b7.3; coded for by C. elegans cDNA CEESE58F; strong similarity to ATP citrate lyase and the alpha chain of succinyl-coa synthases [Caenorhabditis elegans]

Seq. No.	52029
Seq. ID	uC-gmrominsoy318a03b1
Method	BLASTX
NCBI GI	g4204271

BLAST score	386
E value	2.0e-37
Match length	97
% identity	74
NCBI Description	(AC005223) Unknown protein [Arabidopsis thaliana]

Seq. No.	52030
Seq. ID	uC-gmrominsoy318a05b1
Method	BLASTN
NCBI GI	g4432793
BLAST score	157
E value	6.0e-83
Match length	381
% identity	72
NCBI Description	Arabidopsis thaliana chromosome II BAC T19K21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52031
Seq. ID	uC-gmrominsoy318a08b1
Method	BLASTN
NCBI GI	g343517
BLAST score	77
E value	5.0e-35
Match length	204
% identity	87
NCBI Description	Tobacco (N.tabacum) chloroplast Met-tRNA, Val-tRNA-uac and flanks

Seq. No.	52032
Seq. ID	uC-gmrominsoy318b04b1
Method	BLASTN
NCBI GI	g2264305
BLAST score	205
E value	1.0e-111
Match length	425
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	52033
Seq. ID	uC-gmrominsoy318b05b1
Method	BLASTN
NCBI GI	g3869075
BLAST score	378
E value	0.0e+00
Match length	425
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	52034
Seq. ID	uC-gmrominsoy318b06b1
Method	BLASTN
NCBI GI	g2160155
BLAST score	110
E value	3.0e-55
Match length	193

% identity	90
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	52035
Seq. ID	uC-gmrominsoy318b09b1
Method	BLASTN
NCBI GI	g3063438
BLAST score	334
E value	0.0e+00
Match length	367
% identity	97
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	52036
Seq. ID	uC-gmrominsoy318b10b1
Method	BLASTN
NCBI GI	g4092472
BLAST score	509
E value	0.0e+00
Match length	589
% identity	45
NCBI Description	Arabidopsis thaliana BAC F1K3 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	52037
Seq. ID	uC-gmrominsoy318b11b1
Method	BLASTN
NCBI GI	g3201608
BLAST score	198
E value	1.0e-107
Match length	373
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52038
Seq. ID	uC-gmrominsoy318c05b1
Method	BLASTN
NCBI GI	g4580400
BLAST score	369
E value	0.0e+00
Match length	504
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T16I21 genomic sequence, complete sequence

Seq. No.	52039
Seq. ID	uC-gmrominsoy318c09b1
Method	BLASTN
NCBI GI	g343354
BLAST score	227
E value	1.0e-124
Match length	431
% identity	88
NCBI Description	Spinach (S.oleracea) cp coupling factor complex (ATPase);

beta & epsilon subunit genes

Seq. No.	52040
Seq. ID	uC-gmrominsoy318d03b1
Method	BLASTN
NCBI GI	g3695394
BLAST score	197
E value	1.0e-107
Match length	308
% identity	93
NCBI Description	Arabidopsis thaliana BAC T5H22

Seq. No.	52041
Seq. ID	uC-gmrominsoy318d04b1
Method	BLASTN
NCBI GI	g16169
BLAST score	131
E value	2.0e-67
Match length	370
% identity	89
NCBI Description	A.thaliana tandemly repeated sequence AR21

Seq. No.	52042
Seq. ID	uC-gmrominsoy318d06b1
Method	BLASTN
NCBI GI	g3327388
BLAST score	214
E value	1.0e-117
Match length	394
% identity	5
NCBI Description	Arabidopsis thaliana chromosome II BAC T12J2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52043
Seq. ID	uC-gmrominsoy318d08b1
Method	BLASTN
NCBI GI	g2924257
BLAST score	107
E value	2.0e-53
Match length	179
% identity	45
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	52044
Seq. ID	uC-gmrominsoy318d11b1
Method	BLASTN
NCBI GI	g3184270
BLAST score	169
E value	4.0e-90
Match length	233
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52045
Seq. ID	uC-gmrominsoy318d12b1
Method	BLASTX

NCBI GI	g1899058
BLAST score	207
E value	1.0e-16
Match length	72
% identity	61
NCBI Description	(U77378) transcriptional activator CBF1 [Arabidopsis thaliana] >gi_4091982_gb_AAC99369_ (AF076155) CRT/CRE binding factor 1 [Arabidopsis thaliana]

Seq. No.	52046
Seq. ID	uC-gmrominsoy318e01b1
Method	BLASTN
NCBI GI	g12283
BLAST score	225
E value	1.0e-123
Match length	408
% identity	89
NCBI Description	Spinach plastid psbB operon with genes for 10 kD phosphoprotein associated with photosystem II (psbH), apocytochrome b6 and subunit 4 (petD) of cytochrome b6f complex

Seq. No.	52047
Seq. ID	uC-gmrominsoy318e02b1
Method	BLASTX
NCBI GI	g2827520
BLAST score	199
E value	1.0e-15
Match length	92
% identity	42
NCBI Description	(AL021633) receptor kinase - like protein [Arabidopsis thaliana]

Seq. No.	52048
Seq. ID	uC-gmrominsoy318e03b1
Method	BLASTX
NCBI GI	g2924279
BLAST score	210
E value	3.0e-17
Match length	46
% identity	87
NCBI Description	(Z00044) NADH dehydrogenase ND4 subunit [Nicotiana tabacum]

Seq. No.	52049
Seq. ID	uC-gmrominsoy318e04b1
Method	BLASTN
NCBI GI	g2160155
BLAST score	500
E value	0.0e+00
Match length	524
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	52050
Seq. ID	uC-gmrominsoy318e08b1
Method	BLASTN

NCBI GI	g3869062
BLAST score	468
E value	0.0e+00
Match length	495
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	52051
Seq. ID	uC-gmrominsoy318e10b1
Method	BLASTN
NCBI GI	g2924257
BLAST score	143
E value	1.0e-74
Match length	381
% identity	83
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	52052
Seq. ID	uC-gmrominsoy318f02b1
Method	BLASTN
NCBI GI	g4220642
BLAST score	163
E value	1.0e-86
Match length	239
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWC10, complete sequence [Arabidopsis thaliana]

Seq. No.	52053
Seq. ID	uC-gmrominsoy318f05b1
Method	BLASTX
NCBI GI	g4539414
BLAST score	167
E value	3.0e-27
Match length	93
% identity	80
NCBI Description	(AL049524) putative subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	52054
Seq. ID	uC-gmrominsoy318f06b1
Method	BLASTN
NCBI GI	g3327388
BLAST score	234
E value	1.0e-129
Match length	450
% identity	5
NCBI Description	Arabidopsis thaliana chromosome II BAC T12J2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52055
Seq. ID	uC-gmrominsoy318f10b1
Method	BLASTN
NCBI GI	g4027862
BLAST score	417
E value	0.0e+00

Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52056
Seq. ID	uC-gmrominsoy318f11b1
Method	BLASTN
NCBI GI	g4115370
BLAST score	264
E value	1.0e-147
Match length	288
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52057
Seq. ID	uC-gmrominsoy318f12b1
Method	BLASTN
NCBI GI	g3869064
BLAST score	270
E value	1.0e-150
Match length	431
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1O13, complete sequence [Arabidopsis thaliana]

Seq. No.	52058
Seq. ID	uC-gmrominsoy318g01b1
Method	BLASTN
NCBI GI	g1197087
BLAST score	56
E value	7.0e-23
Match length	112
% identity	88
NCBI Description	Fagopyrum esculentum chloroplast DNA

Seq. No.	52059
Seq. ID	uC-gmrominsoy318g02b1
Method	BLASTX
NCBI GI	g2506292
BLAST score	544
E value	7.0e-56
Match length	141
% identity	70
NCBI Description	POSSIBLE CITRATE SYNTHASE 2 >gi_1657529 (U73857) similar to E. coli gltA citrate synthase [Escherichia coli] >gi_1786527 (AE000140) putative citrate synthase; propionate metabolism? [Escherichia coli]

Seq. No.	52060
Seq. ID	uC-gmrominsoy318g05b1
Method	BLASTX
NCBI GI	g4432867
BLAST score	381
E value	1.0e-36
Match length	182

% identity	42
NCBI Description	(AC006300) putative dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	52061
Seq. ID	uC-gmrominsoy318g06b1
Method	BLASTN
NCBI GI	g4567290
BLAST score	457
E value	0.0e+00
Match length	528
% identity	46
NCBI Description	Arabidopsis thaliana chromosome II BAC F18P14 genomic sequence, complete sequence

Seq. No.	52062
Seq. ID	uC-gmrominsoy318g07b1
Method	BLASTX
NCBI GI	g3892701
BLAST score	138
E value	7.0e-09
Match length	60
% identity	48
NCBI Description	(AL033545) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52063
Seq. ID	uC-gmrominsoy318g08b1
Method	BLASTN
NCBI GI	g2660661
BLAST score	279
E value	1.0e-156
Match length	319
% identity	97
NCBI Description	Arabidopsis thaliana chromosome V BAC T19K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52064
Seq. ID	uC-gmrominsoy318g11b1
Method	BLASTN
NCBI GI	g2245126
BLAST score	449
E value	0.0e+00
Match length	477
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	52065
Seq. ID	uC-gmrominsoy318g12b1
Method	BLASTN
NCBI GI	g441281
BLAST score	347
E value	0.0e+00
Match length	459
% identity	93
NCBI Description	B.rapa chloroplast petA gene for cytochrome f

Seq. No.	52066
Seq. ID	uC-gmrominsoy318h04b1
Method	BLASTN
NCBI GI	g3983533
BLAST score	397
E value	0.0e+00
Match length	444
% identity	98
NCBI Description	Arabidopsis thaliana BAC T24G3 from chromosome V near 70 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	52067
Seq. ID	uC-gmrominsoy318h05b1
Method	BLASTN
NCBI GI	g4522002
BLAST score	241
E value	1.0e-133
Match length	272
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T23K3 genomic sequence, complete sequence

Seq. No.	52068
Seq. ID	uC-gmrominsoy318h07b1
Method	BLASTN
NCBI GI	g2529657
BLAST score	335
E value	0.0e+00
Match length	409
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52069
Seq. ID	uC-gmrominsoy319b08b1
Method	BLASTX
NCBI GI	g4314378
BLAST score	436
E value	3.0e-43
Match length	142
% identity	56
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	52070
Seq. ID	uC-gmrominsoy319c07b1
Method	BLASTN
NCBI GI	g2055227
BLAST score	38
E value	4.0e-12
Match length	88
% identity	86
NCBI Description	Glycine max mRNA for SRC1, complete cds

Seq. No.	52071
Seq. ID	uC-gmrominsoy319d06b1
Method	BLASTX
NCBI GI	g2055228

BLAST score 193
E value 4.0e-15
Match length 67
% identity 63
NCBI Description (AB000129) SRC1 [Glycine max]

Seq. No. 52072
Seq. ID uC-gmrominsoy319f04b1
Method BLASTN
NCBI GI g459961
BLAST score 336
E value 0.0e+00
Match length 455
% identity 100
NCBI Description Glycine max proplastid omega-6 desaturase mRNA, complete cds

Seq. No. 52073
Seq. ID uC-gmrominsoy319g04b1
Method BLASTX
NCBI GI g3249084
BLAST score 477
E value 5.0e-48
Match length 131
% identity 23
NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 52074
Seq. ID uC-gmrominsoy319g11b1
Method BLASTN
NCBI GI g439856
BLAST score 153
E value 1.0e-80
Match length 261
% identity 90
NCBI Description Glycine max Williams 82 lipoxygenase mRNA, complete cds

Seq. No. 52075
Seq. ID uC-gmrominsoy319h07b1
Method BLASTX
NCBI GI g4008010
BLAST score 186
E value 6.0e-14
Match length 63
% identity 57
NCBI Description (AF084036) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 52076
Seq. ID uC-gmrominsoy319h11b1
Method BLASTX
NCBI GI g3650037
BLAST score 520
E value 5.0e-53
Match length 133

% identity	77
NCBI Description	(AC005396) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	52077
Seq. ID	uC-gmrominsoy320d07b1
Method	BLASTN
NCBI GI	g1431628
BLAST score	201
E value	1.0e-109
Match length	285
% identity	93
NCBI Description	V.radiata mRNA for pectinacetylesterase

Seq. No.	52078
Seq. ID	uC-gmrominsoy320f05b1
Method	BLASTX
NCBI GI	g3511223
BLAST score	554
E value	3.0e-57
Match length	114
% identity	94
NCBI Description	(AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]

Seq. No.	52079
Seq. ID	uC-gmrominsoy320f08b1
Method	BLASTX
NCBI GI	g4510398
BLAST score	395
E value	2.0e-38
Match length	101
% identity	78
NCBI Description	(AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52080
Seq. ID	uC-gmrominsoy320g09b1
Method	BLASTN
NCBI GI	g3789939
BLAST score	98
E value	5.0e-48
Match length	190
% identity	28
NCBI Description	Saccharum hybrid cultivar H32-8560 tetra-ubiquitin (ubi4) gene, complete cds

Seq. No.	52081
Seq. ID	uC-gmrominsoy320h06b1
Method	BLASTX
NCBI GI	g4567266
BLAST score	166
E value	2.0e-11
Match length	73
% identity	42
NCBI Description	(AC006841) putative pol polyprotein [Arabidopsis thaliana]

Seq. No.	52082
Seq. ID	uC-gmronoir0001f05a1

Method	BLASTX
NCBI GI	g2760837
BLAST score	177
E value	6.0e-13
Match length	79
% identity	35
NCBI Description	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	52083
Seq. ID	uC-gmronoir0001g07b1
Method	BLASTX
NCBI GI	g3763917
BLAST score	392
E value	4.0e-38
Match length	127
% identity	60
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana] >gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52084
Seq. ID	uC-gmronoir000a05b1
Method	BLASTN
NCBI GI	g3510341
BLAST score	47
E value	8.0e-18
Match length	119
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	52085
Seq. ID	uC-gmronoir002c06b1
Method	BLASTX
NCBI GI	g3821254
BLAST score	270
E value	4.0e-24
Match length	85
% identity	65
NCBI Description	(AJ007789) geranylgeranyl reductase [Nicotiana tabacum]

Seq. No.	52086
Seq. ID	uC-gmronoir002g01b1
Method	BLASTX
NCBI GI	g3860797
BLAST score	228
E value	5.0e-19
Match length	80
% identity	62
NCBI Description	(AJ235271) 30S RIBOSOMAL PROTEIN S9 (rpsI) [Rickettsia prowazekii]

Seq. No.	52087
Seq. ID	uC-gmronoir004b09b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	33

E value	6.0e-09
Match length	33
% identity	58
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	52088
Seq. ID	uC-gmronoir004f03b1
Method	BLASTX
NCBI GI	g129018
BLAST score	377
E value	2.0e-36
Match length	107
% identity	63
NCBI Description	ORNITHINE AMINOTRANSFERASE PRECURSOR (ORNITHINE--OXO-ACID AMINOTRANSFERASE) >gi_66645_pir__XNHUO ornithine--oxo-acid transaminase (EC 2.6.1.13) precursor - human >gi_3114488_pdb_1OAT_A Chain A, Ornithine Aminotransferase >gi_3114489_pdb_1OAT_B Chain B, Ornithine Aminotransferase >gi_3114490_pdb_1OAT_C Chain C, Ornithine Aminotransferase >gi_4139654_pdb_2OAT_A Chain A, Ornithine Aminotransferase Complexed With 5-Fluoromethylornithine >gi_4139655_pdb_2OAT_B Chain B, Ornithine Aminotransferase Complexed With 5-Fluoromethylornithine >gi_4139656_pdb_2OAT_C Chain C, Ornithine Aminotransferase Complexed With 5-Fluoromethylornithine >gi_34138_emb_CAA68809_ (Y07511) precursor (AA -35 to 404) [Homo sapiens] >gi_189329 (M12267) ornithine aminotransferase [Homo sapiens] >gi_189348 (M23204) ornithine-delta-aminotransferase [Homo sapiens] >gi_189351 (M14963) ornithine aminotransferase [Homo sapiens] >gi_386987 (M29927) ornithine aminotransferase [Homo sapiens] >gi_4557809_ref_NP_000265.1_pOAT_ ornithine aminotransferase precursor

Seq. No.	52089
Seq. ID	uC-gmronoir006a02b1
Method	BLASTX
NCBI GI	g2462925
BLAST score	487
E value	2.0e-49
Match length	108
% identity	86
NCBI Description	(AJ000053) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana]

Seq. No.	52090
Seq. ID	uC-gmronoir006a07b1
Method	BLASTX
NCBI GI	g1730738
BLAST score	141
E value	1.0e-08
Match length	86
% identity	31
NCBI Description	ACTIN-LIKE PROTEIN ARP5 >gi_2133044_pir__S58718 probable nuclear protein YNL059c - yeast (Saccharomyces cerevisiae) >gi_994827 (U12141) Ynl2430p [Saccharomyces cerevisiae]

>gi_1301932_emb_CAA95933_ (Z71335) ORF YNL059c [Saccharomyces cerevisiae]

Seq. No.	52091
Seq. ID	uC-gmronoir006f08b1
Method	BLASTX
NCBI GI	g3056594
BLAST score	180
E value	3.0e-13
Match length	60
% identity	55
NCBI Description	(AC004255) T1F9.15 [Arabidopsis thaliana]

Seq. No.	52092
Seq. ID	uC-gmronoir006g05b1
Method	BLASTX
NCBI GI	g4263795
BLAST score	219
E value	6.0e-18
Match length	48
% identity	79
NCBI Description	(AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	52093
Seq. ID	uC-gmronoir006h08b1
Method	BLASTN
NCBI GI	g170065
BLAST score	348
E value	0.0e+00
Match length	396
% identity	14
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	52094
Seq. ID	uC-gmronoir007a04b1
Method	BLASTX
NCBI GI	g2804278
BLAST score	280
E value	7.0e-25
Match length	95
% identity	75
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	52095
Seq. ID	uC-gmronoir008b10b1
Method	BLASTX
NCBI GI	g479413
BLAST score	260
E value	9.0e-23
Match length	87
% identity	62
NCBI Description	myosin-like protein - Arabidopsis thaliana

Seq. No.	52096
Seq. ID	uC-gmronoir008e09b1

Method	BLASTX
NCBI GI	g2190016
BLAST score	263
E value	6.0e-23
Match length	109
% identity	44
NCBI Description	(AB004269) alliinase [Allium tuberosum]

Seq. No.	52097
Seq. ID	uC-gmronoir009a05b1
Method	BLASTX
NCBI GI	g4006835
BLAST score	289
E value	5.0e-26
Match length	131
% identity	9
NCBI Description	(AC005970) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52098
Seq. ID	uC-gmronoir009c03b1
Method	BLASTX
NCBI GI	g4033469
BLAST score	157
E value	2.0e-10
Match length	34
% identity	79
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	52099
Seq. ID	uC-gmronoir009f06b1
Method	BLASTN
NCBI GI	g18737
BLAST score	307
E value	1.0e-172
Match length	347
% identity	11
NCBI Description	Glycine max RPRP3 gene for repetitive proline-rich protein

Seq. No.	52100
Seq. ID	uC-gmronoir009h07b1
Method	BLASTN
NCBI GI	g515758
BLAST score	145
E value	9.0e-76
Match length	277
% identity	88
NCBI Description	Vitis vinifera (clone pGME1) malate dehydrogenase mRNA, complete cds

Seq. No.	52101
Seq. ID	uC-gmronoir010f12b1
Method	BLASTN
NCBI GI	g1666233
BLAST score	59
E value	1.0e-24

Match length	171
% identity	84
NCBI Description	Pisum sativum actin (PEAc14) mRNA, complete cds >gi_1724142_gb_U81049_PSU81049 Pisum sativum actin (PEAc14) mRNA, complete cds
Seq. No.	52102
Seq. ID	uC-gmronoir012b07b1
Method	BLASTX
NCBI GI	g122068
BLAST score	668
E value	2.0e-70
Match length	135
% identity	99
NCBI Description	HISTONE H3 (H3.2) >gi_86308_pir__JS0690 histones H3.II and H3.III - chicken >gi_102611_pir__S11315 histone H3 - polychaete (Platynereis dumerilii) >gi_103050_pir__S09655 histone H3 - fruit fly (Drosophila hydei) >gi_109978_pir__JH0304 histone H3.2 - mouse >gi_1078925_pir__A56618 histone H3 - spoonworm (Urechis caupo) >gi_1085856_pir__A56654 histone H3 - Tigriopus californicus >gi_2119005_pir__A56580 histone H3 - midge (Chironomus thummi thummi) >gi_2119019_pir__I50460 H3 histone - muscovy duck >gi_2119020_pir__I51448 histone H3 - African clawed frog >gi_2119021_pir__I49397 histone H3.2 protein - shrew mouse >gi_2144743_pir__HSCH3 histone H3 - chicken >gi_7083_emb_CAA39771_ (X56335) histone H3 [Chironomus thummi] >gi_7433_emb_CAA36805_ (X52576) histone H3 [Drosophila hydei] >gi_7439_emb_CAA34919_ (X17072) histone H3 [Drosophila hydei] >gi_9821_emb_CAA37417_ (X53330) H3 protein (AA 1 - 136) [Platynereis dumerilii] >gi_10615_emb_CAA36638_ (X52393) histone H3 [Tigriopus californicus] >gi_10863_emb_CAA41696_ (X58895) H3 histone [Urechis caupo] >gi_51319_emb_CAA25840_ (X01685) histone H3 (H3.2) (aa 1-136) [Mus musculus] >gi_62734_emb_CAA32855_ (X14732) H3 histone (AA 1-136) [Cairina moschata] >gi_62735_emb_CAA32856_ (X14732) H3 histone (AA 1-136) [Cairina moschata] >gi_63474_emb_CAA26138_ (X02218) H3 (aa 1-136) [Gallus gallus] >gi_63482_emb_CAA44180_ (X62291) histone H3-IV [Gallus gallus] >gi_63484_emb_CAA44181_ (X62292) histone H3-V [Gallus gallus] >gi_64326_emb_CAA25529_ (X01064) histone H3 [Oncorhynchus mykiss] >gi_64772_emb_CAA26813_ (X03017) H3 (aa 1-136) [Xenopus laevis] >gi_64778_emb_CAA26818_ (X03018) histone H3 (aa 1-136) [Xenopus laevis] >gi_64781_emb_CAA26890_ (X03104) H3 (aa 1-135) [Xenopus laevis] >gi_161895 (M84797) histone H3 [Tigriopus californicus] >gi_211857 (M61154) histone H3 [Gallus gallus] >gi_214279 (M21286) histone H3 [Xenopus laevis] >gi_297563_emb_CAA51324_ (X72803) histone H3 [Chironomus thummi] >gi_387183 (M33989) histone H3.2 [Mus musculus] >gi_387195 (M32459) histone H3 [Mus musculus] >gi_387197 (M32461) histone H3 [Mus musculus] >gi_455387 (M21287) histone H3 [Xenopus laevis] >gi_515836_emb_CAA56577_ (X80328) histone H3 protein [Mus musculus] >gi_516331_emb_CAA56573_ (X80326) histone H3.2 protein [Mus pahari] >gi_1458128 (U62669) histone H3.2-F [Mus musculus] >gi_1458134 (U62671) histone H3.2-B [Mus

musculus] >gi_1458144 (U62674) histone H3.2-615 [Mus musculus] >gi_1458146 (U62675) histone H3.2-616 [Mus musculus] >gi_1493815 (U37577) histone H3-VI [Gallus gallus] >gi_1493817 (U37578) histone H3-VII [Gallus gallus] >gi_1493819 (U37579) histone H3-VIII [Gallus gallus] >gi_2564107 (AF007904) histone H3 [Chaetopterus variopedatus]

Seq. No.	52103
Seq. ID	uC-gmronoir013c01b1
Method	BLASTX
NCBI GI	g2245394
BLAST score	330
E value	1.0e-34
Match length	110
% identity	70
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No.	52104
Seq. ID	uC-gmronoir014d05b1
Method	BLASTX
NCBI GI	g1072233
BLAST score	226
E value	2.0e-18
Match length	72
% identity	56
NCBI Description	(U40951) Similar to Adenosine A3 receptor. [Caenorhabditis elegans]

Seq. No.	52105
Seq. ID	uC-gmronoir014f11b1
Method	BLASTX
NCBI GI	g3643608
BLAST score	196
E value	4.0e-15
Match length	108
% identity	45
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52106
Seq. ID	uC-gmronoir015e04b1
Method	BLASTX
NCBI GI	g1710557
BLAST score	569
E value	9.0e-59
Match length	130
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_1181129_emb_CAA93269_ (Z69337) ribosomal protein L3 [Caenorhabditis elegans] >gi_1181131_emb_CAA93268_ (Z69336) ribosomal protein L3 [Caenorhabditis elegans] >gi_3874745_emb_CAA91277_ (Z66495) similar to 60S ribosomal protein L3; cDNA EST EMBL:M75754 comes from this gene; cDNA EST EMBL:M88798 comes from this gene; cDNA EST EMBL:M88842 comes from this gene; cDNA EST EMBL:M88845 comes from this gene; cDNA EST ... >gi_3875827_emb_CAA90183_ (Z49936) similar to 60S ribosomal protein L3; cDNA EST EMBL:M75754 comes from this gene; cDNA

EST EMBL:M88798 comes from this gene; cDNA EST EMBL:M88842 comes from this gene; cDNA EST EMBL:M88845 comes from this gene; cDNA EST

Seq. No.	52107
Seq. ID	uC-gmronoir016b04b1
Method	BLASTX
NCBI GI	g2924781
BLAST score	138
E value	8.0e-09
Match length	41
% identity	63
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	52108
Seq. ID	uC-gmronoir018a12b1
Method	BLASTX
NCBI GI	g3785977
BLAST score	575
E value	2.0e-59
Match length	132
% identity	81
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	52109
Seq. ID	uC-gmronoir019a05b1
Method	BLASTX
NCBI GI	g2369766
BLAST score	186
E value	5.0e-14
Match length	76
% identity	51
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	52110
Seq. ID	uC-gmronoir019e08b1
Method	BLASTX
NCBI GI	g1491939
BLAST score	182
E value	2.0e-13
Match length	89
% identity	42
NCBI Description	(U58314) S-linalool synthase [Clarkia breweri]

Seq. No.	52111
Seq. ID	uC-gmronoir020a10b1
Method	BLASTX
NCBI GI	g4006893
BLAST score	286
E value	1.0e-25
Match length	109
% identity	56
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 52112

Seq. ID	uC-gmronoir022a03b1
Method	BLASTX
NCBI GI	g282404
BLAST score	146
E value	8.0e-10
Match length	55
% identity	56
NCBI Description	GMP synthetase - Bacillus subtilis

Seq. No.	52113
Seq. ID	uC-gmronoir023a11b1
Method	BLASTN
NCBI GI	g4097879
BLAST score	39
E value	4.0e-13
Match length	71
% identity	89
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52114
Seq. ID	uC-gmronoir023f02b1
Method	BLASTX
NCBI GI	g1946371
BLAST score	248
E value	2.0e-21
Match length	94
% identity	55
NCBI Description	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No.	52115
Seq. ID	uC-gmronoir023f03b1
Method	BLASTX
NCBI GI	g393707
BLAST score	317
E value	2.0e-29
Match length	82
% identity	79
NCBI Description	(X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No.	52116
Seq. ID	uC-gmronoir023f07b1
Method	BLASTX
NCBI GI	g2245131
BLAST score	155
E value	3.0e-10
Match length	75
% identity	52
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52117
Seq. ID	uC-gmronoir024b06b1
Method	BLASTN
NCBI GI	g1435059
BLAST score	127
E value	3.0e-65

Match length	194
% identity	95
NCBI Description	Soybean mRNA for cytochrome P450 (CYP93A1), complete cds

Seq. No.	52118
Seq. ID	uC-gmronoir024d07b1
Method	BLASTX
NCBI GI	g4530126
BLAST score	153
E value	4.0e-10
Match length	70
% identity	47
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	52119
Seq. ID	uC-gmronoir024e02b1
Method	BLASTX
NCBI GI	g4512685
BLAST score	214
E value	3.0e-17
Match length	52
% identity	65
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52120
Seq. ID	uC-gmronoir024e09b1
Method	BLASTX
NCBI GI	g729775
BLAST score	206
E value	2.0e-16
Match length	79
% identity	52
NCBI Description	HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR) >gi_100264_pir__S25481 heat shock transcription factor 8 - Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock transcription factor 8 [Lycopersicon peruvianum]

Seq. No.	52121
Seq. ID	uC-gmronoir025a11b1
Method	BLASTX
NCBI GI	g4406759
BLAST score	166
E value	1.0e-11
Match length	67
% identity	49
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52122
Seq. ID	uC-gmronoir025e02b1
Method	BLASTX
NCBI GI	g1049350
BLAST score	456
E value	1.0e-45

Match length	126
% identity	67
NCBI Description	(U39645) similar to the small heat shock protein (HSP20) family [Caenorhabditis elegans]

Seq. No.	52123
Seq. ID	uC-gmronoir027c08b1
Method	BLASTN
NCBI GI	g169952
BLAST score	123
E value	4.0e-63
Match length	167
% identity	93
NCBI Description	Glycine max ferritin mRNA, complete cds

Seq. No.	52124
Seq. ID	uC-gmronoir029b03b1
Method	BLASTX
NCBI GI	g1628622
BLAST score	168
E value	8.0e-12
Match length	83
% identity	42
NCBI Description	(U72631) flavonol synthase [Arabidopsis thaliana] >gi_1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi_1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >gi_1805309 (U84260) flavonol synthase [Arabidopsis thaliana]

Seq. No.	52125
Seq. ID	uC-gmronoir029e03b1
Method	BLASTN
NCBI GI	g2062691
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	52126
Seq. ID	uC-gmronoir029g04b1
Method	BLASTN
NCBI GI	g1370199
BLAST score	42
E value	5.0e-15
Match length	82
% identity	88
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAC1

Seq. No.	52127
Seq. ID	uC-gmronoir030a04b1
Method	BLASTX
NCBI GI	g3122288
BLAST score	635
E value	1.0e-66
Match length	137

% identity	34
NCBI Description	IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) (KAP ALPHA) >gi_1568635 (U69533) AtKAP alpha [Arabidopsis thaliana]

Seq. No.	52128
Seq. ID	uC-gmronoir030c05b1
Method	BLASTX
NCBI GI	g3152595
BLAST score	385
E value	3.0e-37
Match length	99
% identity	71
NCBI Description	(AC002986) Similar to D. melanogaster sno gene gb_U95760. EST gb_N97148 and gb_Z26221 come from this gene. [Arabidopsis thaliana]

Seq. No.	52129
Seq. ID	uC-gmronoir030c11b1
Method	BLASTX
NCBI GI	g2191168
BLAST score	175
E value	1.0e-12
Match length	76
% identity	49
NCBI Description	(AF007270) contains similarity to myosin heavy chain [Arabidopsis thaliana]

Seq. No.	52130
Seq. ID	uC-gmronoir030e10b1
Method	BLASTX
NCBI GI	g1118007
BLAST score	350
E value	3.0e-33
Match length	88
% identity	83
NCBI Description	(U40858) serine/threonine kinase [Caenorhabditis elegans]

Seq. No.	52131
Seq. ID	uC-gmronoir031d09b1
Method	BLASTX
NCBI GI	g3776567
BLAST score	267
E value	2.0e-23
Match length	130
% identity	41
NCBI Description	(AC005388) Strong similarity to F21B7.33 gi_2809264 from A. thaliana BAC gb_AC002560. EST gb_N65119 comes from this gene. [Arabidopsis thaliana]

Seq. No.	52132
Seq. ID	uC-gmronoir033d09b1
Method	BLASTN
NCBI GI	g257815
BLAST score	85
E value	1.0e-40
Match length	93

% identity	98
NCBI Description	chalcone synthase [soybeans, mRNA, 1119 nt]

Seq. No.	52133
Seq. ID	uC-gmronoir034d03b1
Method	BLASTX
NCBI GI	g2529677
BLAST score	719
E value	3.0e-76
Match length	158
% identity	89
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]

Seq. No.	52134
Seq. ID	uC-gmronoir035d05b1
Method	BLASTX
NCBI GI	g2498343
BLAST score	430
E value	2.0e-42
Match length	123
% identity	67
NCBI Description	PROBABLE ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (ETF-QO) (ETF-UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING-FLAVOPROTEIN DEHYDROGENASE) >gi_1216303 (U00048) similar to E. coli YAAS gene and nitrogen fixation protein FIXC [Caenorhabditis elegans]

Seq. No.	52135
Seq. ID	uC-gmronoir036c09b1
Method	BLASTX
NCBI GI	g3150407
BLAST score	278
E value	1.0e-24
Match length	107
% identity	54
NCBI Description	(AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52136
Seq. ID	uC-gmronoir038d04b1
Method	BLASTX
NCBI GI	g3876548
BLAST score	452
E value	5.0e-45
Match length	148
% identity	64
NCBI Description	(Z81072) predicted using Genefinder; Similarity to Human erythrocyte band 7 integral membrane protein (SW:BAN7_HUMAN) [Caenorhabditis elegans]

Seq. No.	52137
Seq. ID	uC-gmronoir038h06b1
Method	BLASTX
NCBI GI	g4097880
BLAST score	172
E value	2.0e-12

Match length	47
% identity	70
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	52138
Seq. ID	uC-gmronoir039d02b1
Method	BLASTX
NCBI GI	g4455155
BLAST score	324
E value	4.0e-30
Match length	129
% identity	67
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No.	52139
Seq. ID	uC-gmronoir039f03b1
Method	BLASTX
NCBI GI	g4249410
BLAST score	236
E value	8.0e-20
Match length	84
% identity	57
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	52140
Seq. ID	uC-gmronoir040g05b1
Method	BLASTN
NCBI GI	g408791
BLAST score	113
E value	1.0e-56
Match length	207
% identity	96
NCBI Description	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds

Seq. No.	52141
Seq. ID	uC-gmronoir041f02b1
Method	BLASTX
NCBI GI	g4206194
BLAST score	309
E value	8.0e-29
Match length	75
% identity	76
NCBI Description	(AF071527) GH3-like protein [Arabidopsis thaliana] >gi_4262168_gb_AAD14468_ (AC005275) putative GH3-like protein [Arabidopsis thaliana]

Seq. No.	52142
Seq. ID	uC-gmronoir041h05b1
Method	BLASTX
NCBI GI	g1432058
BLAST score	214
E value	3.0e-17
Match length	106
% identity	58
NCBI Description	(U58540) WRKY2 [Petroselinum crispum]

Seq. No.	52143
Seq. ID	uC-gmronoir042f06b1
Method	BLASTX
NCBI GI	g2462265
BLAST score	418
E value	6.0e-41
Match length	146
% identity	54
NCBI Description	(Y12793) patatin-like protein [Cucumis sativus]

Seq. No.	52144
Seq. ID	uC-gmronoir042h06b1
Method	BLASTX
NCBI GI	g3914359
BLAST score	123
E value	3.0e-16
Match length	88
% identity	59
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1928979 (U92656) phospholipase D [Vigna unguiculata]

Seq. No.	52145
Seq. ID	uC-gmronoir043a05b1
Method	BLASTX
NCBI GI	g3096947
BLAST score	301
E value	2.0e-27
Match length	127
% identity	42
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	52146
Seq. ID	uC-gmronoir043b01b1
Method	BLASTX
NCBI GI	g2894612
BLAST score	201
E value	3.0e-16
Match length	69
% identity	57
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	52147
Seq. ID	uC-gmronoir043d12b1
Method	BLASTX
NCBI GI	g2501735
BLAST score	305
E value	6.0e-28
Match length	67
% identity	75
NCBI Description	HYPOTHETICAL 24.9 KD PROTEIN C16C10.7 IN CHROMOSOME III >gi_3874385_emb_CAA86745_ (Z46787) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk237a6.3 comes from this gene; cDNA EST yk237a6.5 comes from this gene; cDNA EST yk390f8.3 comes from this gene; cDNA EST yk390f8.5

comes from this gene [Caen

Seq. No.	52148
Seq. ID	uC-gmronoir043e09b1
Method	BLASTX
NCBI GI	g3377851
BLAST score	223
E value	1.0e-18
Match length	88
% identity	56
NCBI Description	(AF076274) contains similarity to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 155.05) [Arabidopsis thaliana]

Seq. No.	52149
Seq. ID	uC-gmronoir044e11b1
Method	BLASTN
NCBI GI	g887570
BLAST score	166
E value	2.0e-88
Match length	290
% identity	89
NCBI Description	P.sativum mRNA for starch synthase (2035 bp)

Seq. No.	52150
Seq. ID	uC-gmronoir044g09b1
Method	BLASTX
NCBI GI	g2828293
BLAST score	178
E value	3.0e-13
Match length	72
% identity	53
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	52151
Seq. ID	uC-gmronoir045c10b1
Method	BLASTX
NCBI GI	g2104422
BLAST score	143
E value	5.0e-09
Match length	89
% identity	30
NCBI Description	(Z95395) putative membrane transport protein [Schizosaccharomyces pombe]

Seq. No.	52152
Seq. ID	uC-gmronoir046a12b1
Method	BLASTX
NCBI GI	g3947733
BLAST score	207
E value	1.0e-16
Match length	83
% identity	49
NCBI Description	(AJ009719) NL25 [Solanum tuberosum]

Seq. No.	52153
Seq. ID	uC-gmronoir046b05b1

Method	BLASTX
NCBI GI	g4104931
BLAST score	663
E value	8.0e-70
Match length	129
% identity	93
NCBI Description	(AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No.	52154
Seq. ID	uC-gmronoir046h03b1
Method	BLASTX
NCBI GI	g4204912
BLAST score	463
E value	2.0e-46
Match length	130
% identity	69
NCBI Description	(U58918) MEK kinase [Arabidopsis thaliana]

Seq. No.	52155
Seq. ID	uC-gmronoir047c11b1
Method	BLASTX
NCBI GI	g1086263
BLAST score	252
E value	7.0e-22
Match length	97
% identity	53
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	52156
Seq. ID	uC-gmronoir048g02b1
Method	BLASTN
NCBI GI	g347454
BLAST score	153
E value	2.0e-80
Match length	299
% identity	54
NCBI Description	Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3' end

Seq. No.	52157
Seq. ID	uC-gmronoir048h08b1
Method	BLASTN
NCBI GI	g938299
BLAST score	86
E value	8.0e-41
Match length	238
% identity	85
NCBI Description	V.ungiculata mRNA for unknown protein (A3 gene)

Seq. No.	52158
Seq. ID	uC-gmronoir049a01b1
Method	BLASTX
NCBI GI	g3461814
BLAST score	229
E value	2.0e-19
Match length	52

% identity	83
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52159
Seq. ID	uC-gmronoir050b09b1
Method	BLASTN
NCBI GI	g18703
BLAST score	38
E value	6.0e-12
Match length	86
% identity	86
NCBI Description	G.max mRNA for nodulin

Seq. No.	52160
Seq. ID	uC-gmronoir052h03b1
Method	BLASTX
NCBI GI	g862499
BLAST score	210
E value	6.0e-17
Match length	74
% identity	53
NCBI Description	(U29244) similar to human (TRE) transforming protein (PIR:S22157) [Caenorhabditis elegans]

Seq. No.	52161
Seq. ID	uC-gmronoir053h11b1
Method	BLASTX
NCBI GI	g3913981
BLAST score	197
E value	2.0e-15
Match length	76
% identity	49
NCBI Description	PUTATIVE STEROID DEHYDROGENASE LET-767 >gi_726418 (U23177) similar to estradiol 17 beta-dehydrogenase 3 (SP:DHB3_HUMAN, P37058) [Caenorhabditis elegans]

Seq. No.	52162
Seq. ID	uC-gmronoir055c01b1
Method	BLASTX
NCBI GI	g2842727
BLAST score	389
E value	6.0e-38
Match length	98
% identity	82
NCBI Description	PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) >gi_3877109_emb_CAB02111_ (Z79755) predicted using Genefinder; Similarity to Bovine isocitrate dehydrogenase (SW:IDH3_BOVIN); cDNA EST EMBL:Z14736 comes from this gene; cDNA EST EMBL:M75988 comes from this gene; cDNA EST EMBL:D69472 comes from this gene

Seq. No.	52163
Seq. ID	uC-gmronoir055c06b1
Method	BLASTX
NCBI GI	g1514643
BLAST score	523

E value	2.0e-53
Match length	121
% identity	47
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	52164
Seq. ID	uC-gmronoir055f05b1
Method	BLASTN
NCBI GI	g408791
BLAST score	133
E value	7.0e-69
Match length	164
% identity	96
NCBI Description	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds

Seq. No.	52165
Seq. ID	uC-gmronoir056a09b1
Method	BLASTX
NCBI GI	g100099
BLAST score	147
E value	2.0e-10
Match length	77
% identity	58
NCBI Description	DNA-binding protein VBP1 - fava bean >gi_1372966 (M81827) CREB-like protein [Vicia faba]

Seq. No.	52166
Seq. ID	uC-gmronoir057c03b1
Method	BLASTX
NCBI GI	g3874497
BLAST score	294
E value	1.0e-26
Match length	100
% identity	53
NCBI Description	(Z92826) predicted using Genefinder; cDNA EST EMBL:D75104 comes from this gene; cDNA EST EMBL:T00707 comes from this gene; cDNA EST CEMSB73F comes from this gene [Caenorhabditis elegans]

Seq. No.	52167
Seq. ID	uC-gmronoir058a10b1
Method	BLASTX
NCBI GI	g2829926
BLAST score	157
E value	2.0e-10
Match length	61
% identity	56
NCBI Description	(AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	52168
Seq. ID	uC-gmronoir060a10b1
Method	BLASTX
NCBI GI	g4512698
BLAST score	585
E value	8.0e-61
Match length	118

% identity	89
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52169
Seq. ID	uC-gmronoir060c10b1
Method	BLASTN
NCBI GI	g3293200
BLAST score	152
E value	6.0e-80
Match length	326
% identity	87
NCBI Description	Pisum sativum GTP-binding protein (IAP34) mRNA, complete cds

Seq. No.	52170
Seq. ID	uC-gmronoir062b12b1
Method	BLASTX
NCBI GI	g2739386
BLAST score	208
E value	1.0e-16
Match length	68
% identity	57
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	52171
Seq. ID	uC-gmronoir062d08b1
Method	BLASTX
NCBI GI	g4426611
BLAST score	142
E value	1.0e-08
Match length	113
% identity	33
NCBI Description	(AF096897) pushover [Drosophila melanogaster]

Seq. No.	52172
Seq. ID	uC-gmronoir063f07b1
Method	BLASTX
NCBI GI	g2642165
BLAST score	179
E value	3.0e-13
Match length	92
% identity	39
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52173
Seq. ID	uC-gmronoir063f11b1
Method	BLASTX
NCBI GI	g2500404
BLAST score	436
E value	3.0e-43
Match length	106
% identity	81
NCBI Description	PROBABLE 40S RIBOSOMAL PROTEIN S9 >gi_3876944_emb_CAA93262_ (Z69302) predicted using Genefinder; Similarity to Rat 40S ribosomal S9 (SW:RS9_RAT); cDNA EST EMBL:D71695 comes from this gene; cDNA EST EMBL:D71722 comes from this gene; cDNA EST EMBL:D72327 comes from this gene; cDNA EST EMB

Seq. No.	52174
Seq. ID	uC-gmronoir063g08b1
Method	BLASTX
NCBI GI	g3122301
BLAST score	321
E value	9.0e-30
Match length	121
% identity	50
NCBI Description	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (CAM KINASE I) >gi_1362763_pir__S57347 cam kinase I - human >gi_790790 (L41816) cam kinase I [Homo sapiens] >gi_4502553_ref_NP_003647.1_pCAMK1_ calcium/calmodulin-dependent protein kinase I

Seq. No.	52175
Seq. ID	uC-gmronoir063g10b1
Method	BLASTN
NCBI GI	g1173641
BLAST score	364
E value	0.0e+00
Match length	415
% identity	97
NCBI Description	Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No.	52176
Seq. ID	uC-gmronoir063h01b1
Method	BLASTX
NCBI GI	g4097880
BLAST score	247
E value	1.0e-21
Match length	58
% identity	81
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	52177
Seq. ID	uC-gmronoir063h11b1
Method	BLASTN
NCBI GI	g18764
BLAST score	150
E value	6.0e-79
Match length	250
% identity	90
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	52178
Seq. ID	uC-gmronoir064b04b1
Method	BLASTX
NCBI GI	g1915974
BLAST score	356
E value	6.0e-34
Match length	84
% identity	87
NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi_2102693 (U64818) fructokinase [Lycopersicon esculentum]

Seq. No. 52179

Seq. ID	uC-gmronoir064b05b1
Method	BLASTX
NCBI GI	g4432841
BLAST score	353
E value	2.0e-33
Match length	95
% identity	71
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52180
Seq. ID	uC-gmronoir065f10b1
Method	BLASTX
NCBI GI	g3695393
BLAST score	301
E value	2.0e-27
Match length	124
% identity	51
NCBI Description	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]

Seq. No.	52181
Seq. ID	uC-gmronoir065h07b1
Method	BLASTN
NCBI GI	g3452136
BLAST score	66
E value	6.0e-29
Match length	98
% identity	92
NCBI Description	Glycine max mRNA for glucose-6-phosphate-dehydrogenase, partial

Seq. No.	52182
Seq. ID	uC-gmronoir065h09b1
Method	BLASTX
NCBI GI	g3176723
BLAST score	269
E value	6.0e-24
Match length	92
% identity	54
NCBI Description	(AC002392) putative protein kinase [Arabidopsis thaliana]

Seq. No.	52183
Seq. ID	uC-gmronoir068a03b1
Method	BLASTN
NCBI GI	g1778369
BLAST score	103
E value	4.0e-51
Match length	175
% identity	90
NCBI Description	Glycine max asparagine synthetase 2 (AS2) mRNA, complete cds

Seq. No.	52184
Seq. ID	uC-gmronoir068a12b1
Method	BLASTN
NCBI GI	g4115338

BLAST score	106
E value	1.0e-52
Match length	298
% identity	31
NCBI Description	Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

Seq. No.	52185
Seq. ID	uC-gmronoir068f07b1
Method	BLASTX
NCBI GI	g1931640
BLAST score	284
E value	1.0e-25
Match length	85
% identity	59
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	52186
Seq. ID	uC-gmronoir071b03b1
Method	BLASTX
NCBI GI	g2244834
BLAST score	150
E value	1.0e-09
Match length	99
% identity	39
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52187
Seq. ID	uC-gmronoir071h04b1
Method	BLASTX
NCBI GI	g2443810
BLAST score	535
E value	6.0e-55
Match length	114
% identity	89
NCBI Description	(AF020432) eukaryotic translation initiation factor XeIF-4AIII [Xenopus laevis]

Seq. No.	52188
Seq. ID	uC-gmronoir073c01b1
Method	BLASTX
NCBI GI	g2160173
BLAST score	318
E value	3.0e-29
Match length	165
% identity	5
NCBI Description	(AC000132) Similar to N. tabacum salt-inducible protein (gb_U08285). [Arabidopsis thaliana]

Seq. No.	52189
Seq. ID	uC-gmronoir073g08b1
Method	BLASTX
NCBI GI	g4325344
BLAST score	508
E value	2.0e-51
Match length	126
% identity	76

NCBI Description	(AF128393) similar to beta-transducins (Pfam: PF00400, Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]

Seq. No.	52190
Seq. ID	uC-gmronoir073h01b1
Method	BLASTN
NCBI GI	g2062691
BLAST score	33
E value	5.0e-09
Match length	48
% identity	43
NCBI Description	Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	52191
Seq. ID	uC-gmronoir076b02b1
Method	BLASTX
NCBI GI	g3881593
BLAST score	249
E value	3.0e-21
Match length	132
% identity	39
NCBI Description	(Z99288) ZK262.3 [Caenorhabditis elegans]

Seq. No.	52192
Seq. ID	uC-gmropic0001a09a1
Method	BLASTN
NCBI GI	g3290021
BLAST score	48
E value	7.0e-18
Match length	104
% identity	87
NCBI Description	Solanum tuberosum cysteine synthase mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	52193
Seq. ID	uC-gmropic0001c06a1
Method	BLASTN
NCBI GI	g2463568
BLAST score	216
E value	1.0e-118
Match length	234
% identity	99
NCBI Description	Glycine max mRNA for squalene synthase, complete cds

Seq. No.	52194
Seq. ID	uC-gmropic0001c07a1
Method	BLASTN
NCBI GI	g1336081
BLAST score	94
E value	2.0e-45
Match length	198
% identity	87
NCBI Description	Glycine max var. Century ascorbate peroxidase 2 (APx2) mRNA, complete cds

Seq. No.	52195

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Seq. ID	uC-gmropic0001c08b1
Method	BLASTX
NCBI GI	g2494130
BLAST score	275
E value	2.0e-24
Match length	91
% identity	68
NCBI Description	(AC002376) Contains similarity to Glycine SRC2 (gb_AB000130). [Arabidopsis thaliana]

Seq. No.	52196
Seq. ID	uC-gmropic0001e07b1
Method	BLASTN
NCBI GI	g2970653
BLAST score	105
E value	5.0e-52
Match length	146
% identity	97
NCBI Description	Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	52197
Seq. ID	uC-gmropic004c03b1
Method	BLASTX
NCBI GI	g2444180
BLAST score	469
E value	4.0e-47
Match length	118
% identity	72
NCBI Description	(U94785) unconventional myosin [Helianthus annuus]

Seq. No.	52198
Seq. ID	uC-gmropic004d06b1
Method	BLASTX
NCBI GI	g2149640
BLAST score	139
E value	6.0e-09
Match length	32
% identity	84
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	52199
Seq. ID	uC-gmropic004d09b1
Method	BLASTX
NCBI GI	g4415921
BLAST score	173
E value	6.0e-13
Match length	44
% identity	70
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	52200
Seq. ID	uC-gmropic004h11b1
Method	BLASTX
NCBI GI	g543905
BLAST score	276

E value	8.0e-25
Match length	57
% identity	81
NCBI Description	BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162) brassinosteroid-regulated protein [Glycine max]

Seq. No.	52201
Seq. ID	uC-gmropic005b05b1
Method	BLASTN
NCBI GI	g758249
BLAST score	142
E value	5.0e-74
Match length	205
% identity	97
NCBI Description	P.vulgaris mRNA for plasma membrane H+ ATPase

Seq. No.	52202
Seq. ID	uC-gmropic005c08b1
Method	BLASTX
NCBI GI	g4204290
BLAST score	291
E value	2.0e-45
Match length	131
% identity	68
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	52203
Seq. ID	uC-gmropic005d08b1
Method	BLASTN
NCBI GI	g303900
BLAST score	236
E value	1.0e-130
Match length	337
% identity	30
NCBI Description	Soybean gene for ubiquitin, complete cds

Seq. No.	52204
Seq. ID	uC-gmropic005h08b1
Method	BLASTX
NCBI GI	g3876865
BLAST score	145
E value	4.0e-09
Match length	80
% identity	35
NCBI Description	(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No.	52205
Seq. ID	uC-gmropic005h09b1
Method	BLASTX
NCBI GI	g4102600
BLAST score	357
E value	3.0e-34
Match length	81

% identity	84
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	52206
Seq. ID	uC-gmropic006d11b1
Method	BLASTN
NCBI GI	g467551
BLAST score	244
E value	1.0e-135
Match length	418
% identity	96
NCBI Description	Soybean mRNA for phosphoenolpyruvate carboxylase

Seq. No.	52207
Seq. ID	uC-gmropic006e08b1
Method	BLASTX
NCBI GI	g3135251
BLAST score	157
E value	1.0e-10
Match length	43
% identity	63
NCBI Description	(AC003058) putative receptor protein kinase [Arabidopsis thaliana] >gi_3176719 (AC002392) putative protein kinase [Arabidopsis thaliana]

Seq. No.	52208
Seq. ID	uC-gmropic006f08b1
Method	BLASTX
NCBI GI	g2760830
BLAST score	181
E value	1.0e-13
Match length	38
% identity	89
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	52209
Seq. ID	uC-gmropic007a05b1
Method	BLASTN
NCBI GI	g18764
BLAST score	260
E value	1.0e-144
Match length	344
% identity	94
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	52210
Seq. ID	uC-gmropic007c01b1
Method	BLASTX
NCBI GI	g2980770
BLAST score	509
E value	8.0e-52
Match length	123
% identity	77
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	52211

Seq. ID	uC-gmropic007c05b1
Method	BLASTN
NCBI GI	g1675195
BLAST score	41
E value	8.0e-14
Match length	45
% identity	98
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	52212
Seq. ID	uC-gmropic007c06b1
Method	BLASTN
NCBI GI	g4039114
BLAST score	50
E value	2.0e-19
Match length	141
% identity	88
NCBI Description	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds

Seq. No.	52213
Seq. ID	uC-gmropic007g06b1
Method	BLASTN
NCBI GI	g2315210
BLAST score	48
E value	2.0e-18
Match length	124
% identity	85
NCBI Description	Lycopersicon esculentum mRNA for proteasome, alpha subunit

Seq. No.	52214
Seq. ID	uC-gmropic008a09b1
Method	BLASTX
NCBI GI	g3805764
BLAST score	211
E value	7.0e-17
Match length	132
% identity	38
NCBI Description	(AC005693) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52215
Seq. ID	uC-gmropic008c06b1
Method	BLASTN
NCBI GI	g2920665
BLAST score	216
E value	1.0e-118
Match length	311
% identity	99
NCBI Description	Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No.	52216
Seq. ID	uC-gmropic008f02b1
Method	BLASTX
NCBI GI	g1086263
BLAST score	119
E value	3.0e-10

Match length 124
% identity 36
NCBI Description TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No. 52217
Seq. ID uC-gmropic008g07b1
Method BLASTX
NCBI GI g3183088
BLAST score 260
E value 1.0e-22
Match length 68
% identity 66
NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No. 52218
Seq. ID uC-gmropic009b01b1
Method BLASTX
NCBI GI g2935342
BLAST score 148
E value 2.0e-09
Match length 85
% identity 33
NCBI Description (AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]

Seq. No. 52219
Seq. ID uC-gmropic009b09b1
Method BLASTX
NCBI GI g1946361
BLAST score 249
E value 3.0e-21
Match length 60
% identity 67
NCBI Description (U93215) C3HC4 zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 52220
Seq. ID uC-gmropic009c02b1
Method BLASTX
NCBI GI g2827643
BLAST score 173
E value 6.0e-13
Match length 48
% identity 71
NCBI Description (AL021636) predicted protein [Arabidopsis thaliana] >gi_3549641_emb_CAA06432_ (AJ005195) receiver-like protein 4 [Arabidopsis thaliana]

Seq. No. 52221
Seq. ID uC-gmropic009c08b1
Method BLASTX
NCBI GI g3033389
BLAST score 211

E value	8.0e-17
Match length	139
% identity	11
NCBI Description	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No.	52222
Seq. ID	uC-gmropic009g01b1
Method	BLASTX
NCBI GI	g4314356
BLAST score	261
E value	7.0e-23
Match length	97
% identity	47
NCBI Description	(AC006340) putative anthocyanidin-3-glucoside rhamnosyltransferase [Arabidopsis thaliana]

Seq. No.	52223
Seq. ID	uC-gmropic009g05b1
Method	BLASTX
NCBI GI	g3033377
BLAST score	262
E value	8.0e-23
Match length	111
% identity	50
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	52224
Seq. ID	uC-gmropic010b03b1
Method	BLASTX
NCBI GI	g3201615
BLAST score	289
E value	6.0e-26
Match length	142
% identity	47
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	52225
Seq. ID	uC-gmropic010d05b1
Method	BLASTN
NCBI GI	g1006804
BLAST score	132
E value	5.0e-68
Match length	228
% identity	91
NCBI Description	Vigna radiata 1-aminocyclopropane-1-carboxylic acid synthase (VRACS6) mRNA, complete cds

Seq. No.	52226
Seq. ID	uC-gmropic010g10b1
Method	BLASTN
NCBI GI	g1405560
BLAST score	37
E value	2.0e-11
Match length	77
% identity	87
NCBI Description	F.sylvatica mRNA for GTP1 protein

Seq. No.	52227
Seq. ID	uC-gmropic011a05b1
Method	BLASTX
NCBI GI	g3785974
BLAST score	276
E value	2.0e-24
Match length	133
% identity	66
NCBI Description	(AC005560) putative DNA recombinase [Arabidopsis thaliana]

Seq. No.	52228
Seq. ID	uC-gmropic011d02b1
Method	BLASTX
NCBI GI	g4510376
BLAST score	415
E value	8.0e-41
Match length	106
% identity	73
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	52229
Seq. ID	uC-gmropic011d05b1
Method	BLASTX
NCBI GI	g4455296
BLAST score	181
E value	1.0e-13
Match length	93
% identity	49
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52230
Seq. ID	uC-gmropic011e01b1
Method	BLASTX
NCBI GI	g1518540
BLAST score	144
E value	1.0e-09
Match length	41
% identity	71
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	52231
Seq. ID	uC-gmropic012a01b1
Method	BLASTX
NCBI GI	g2245060
BLAST score	239
E value	4.0e-20
Match length	73
% identity	63
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No.	52232
Seq. ID	uC-gmropic012a02b1
Method	BLASTX
NCBI GI	g2505870
BLAST score	237
E value	8.0e-20

Match length	58
% identity	74
NCBI Description	(Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52233
Seq. ID	uC-gmropic012a05b1
Method	BLASTN
NCBI GI	g1917018
BLAST score	36
E value	8.0e-11
Match length	68
% identity	88
NCBI Description	Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA, complete cds

Seq. No.	52234
Seq. ID	uC-gmropic012b04b1
Method	BLASTX
NCBI GI	g3184098
BLAST score	169
E value	2.0e-12
Match length	50
% identity	60
NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No.	52235
Seq. ID	uC-gmropic012g10b1
Method	BLASTX
NCBI GI	g3859696
BLAST score	123
E value	7.0e-10
Match length	93
% identity	39
NCBI Description	(AL033497) unknown hypothetical protein [Candida albicans]

Seq. No.	52236
Seq. ID	uC-gmropic012h08b1
Method	BLASTN
NCBI GI	g4324966
BLAST score	198
E value	1.0e-107
Match length	198
% identity	100
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No.	52237
Seq. ID	uC-gmropic013b10b1
Method	BLASTX
NCBI GI	g3033389
BLAST score	159
E value	4.0e-11
Match length	73
% identity	8
NCBI Description	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No.	52238

Seq. ID	uC-gmropic013e04b1
Method	BLASTX
NCBI GI	g2947059
BLAST score	254
E value	6.0e-22
Match length	55
% identity	82
NCBI Description	(AC002521) similar to myb transforming protein [Arabidopsis thaliana]

Seq. No.	52239
Seq. ID	uC-gmropic014b05b1
Method	BLASTX
NCBI GI	g3702331
BLAST score	138
E value	7.0e-09
Match length	65
% identity	42
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52240
Seq. ID	uC-gmropic014h07b1
Method	BLASTX
NCBI GI	g4454039
BLAST score	457
E value	8.0e-46
Match length	111
% identity	81
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	52241
Seq. ID	uC-gmropic015e01b1
Method	BLASTX
NCBI GI	g2443280
BLAST score	144
E value	1.0e-09
Match length	68
% identity	44
NCBI Description	(AB001432) motor domain of KIF15 [Mus musculus]

Seq. No.	52242
Seq. ID	uC-gmropic015g02b1
Method	BLASTN
NCBI GI	g1262165
BLAST score	278
E value	1.0e-155
Match length	366
% identity	96
NCBI Description	Soybean nitrate reductase (INR1) mRNA, complete cds

Seq. No.	52243
Seq. ID	uC-gmropic016d01b1
Method	BLASTX
NCBI GI	g3717965
BLAST score	152
E value	3.0e-10

Match length 87
% identity 38
NCBI Description (AL031640) 1-evidence=predicted by content; 1-method=genefinder;084; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SPTREMBL:O60878; 2-match_description=DIA-12C PROTEIN.; 2-match_species=HOMO SAPIENS (HUMAN).;

Seq. No. 52244
Seq. ID uC-gmropic016e08b1
Method BLASTX
NCBI GI g4079639
BLAST score 254
E value 6.0e-22
Match length 89
% identity 56
NCBI Description (AJ131635) beta-galactosidase [psychrophilic bacterium TAE 79]

Seq. No. 52245
Seq. ID uC-gmropic016h10b1
Method BLASTX
NCBI GI g3947733
BLAST score 173
E value 9.0e-13
Match length 59
% identity 56
NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 52246
Seq. ID uC-gmropic017c03b1
Method BLASTX
NCBI GI g2854158
BLAST score 145
E value 3.0e-09
Match length 108
% identity 30
NCBI Description (AF045641) No definition line found [Caenorhabditis elegans]

Seq. No. 52247
Seq. ID uC-gmropic018a02b1
Method BLASTX
NCBI GI g3643603
BLAST score 537
E value 5.0e-55
Match length 139
% identity 73
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 52248
Seq. ID uC-gmropic018b09b1
Method BLASTN
NCBI GI g170065
BLAST score 161
E value 1.0e-85

Match length	185
% identity	18
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	52249
Seq. ID	uC-gmropic018d09b1
Method	BLASTX
NCBI GI	g282963
BLAST score	158
E value	5.0e-11
Match length	76
% identity	51
NCBI Description	transforming protein (myb) homolog (clone myb.Ph2) - garden petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia x hybrida]

Seq. No.	52250
Seq. ID	uC-gmropic018h09b1
Method	BLASTN
NCBI GI	g2921511
BLAST score	69
E value	1.0e-30
Match length	69
% identity	100
NCBI Description	Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds

Seq. No.	52251
Seq. ID	uC-gmropic019b11b1
Method	BLASTX
NCBI GI	g2129597
BLAST score	245
E value	7.0e-21
Match length	52
% identity	94
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	52252
Seq. ID	uC-gmropic019h03b1
Method	BLASTX
NCBI GI	g4558497
BLAST score	207
E value	2.0e-16
Match length	91
% identity	43
NCBI Description	(AF121951) CAAX prenyl protein protease RCE1 [Homo sapiens]

Seq. No.	52253
Seq. ID	uC-gmropic020a07b1
Method	BLASTX
NCBI GI	g4371285
BLAST score	502
E value	6.0e-51
Match length	118

% identity	79
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52254
Seq. ID	uC-gmropic020b05b1
Method	BLASTN
NCBI GI	g20680
BLAST score	90
E value	6.0e-43
Match length	122
% identity	93
NCBI Description	P.sativum mRNA of cDNA clone 26g

Seq. No.	52255
Seq. ID	uC-gmropic020d02b1
Method	BLASTX
NCBI GI	g4105772
BLAST score	203
E value	4.0e-16
Match length	43
% identity	41
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	52256
Seq. ID	uC-gmropic020d06b1
Method	BLASTX
NCBI GI	g2213598
BLAST score	196
E value	3.0e-15
Match length	111
% identity	35
NCBI Description	(AC000348) T7N9.18 [Arabidopsis thaliana]

Seq. No.	52257
Seq. ID	uC-gmropic020f02b1
Method	BLASTN
NCBI GI	g3982595
BLAST score	136
E value	1.0e-70
Match length	226
% identity	90
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	52258
Seq. ID	uC-gmropic020f04b1
Method	BLASTX
NCBI GI	g4572671
BLAST score	403
E value	3.0e-39
Match length	137
% identity	55
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	52259
Seq. ID	uC-gmropic020g11b1
Method	BLASTX

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NCBI GI	g4467125
BLAST score	462
E value	2.0e-46
Match length	110
% identity	77
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	52260
Seq. ID	uC-gmropic021b03b1
Method	BLASTX
NCBI GI	g2959767
BLAST score	556
E value	3.0e-57
Match length	161
% identity	68
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	52261
Seq. ID	uC-gmropic021b09b1
Method	BLASTX
NCBI GI	g125722
BLAST score	228
E value	8.0e-19
Match length	109
% identity	53
NCBI Description	KUNITZ-TYPE TRYPSIN INHIBITOR KTI1 PRECURSOR >gi_81814_pir__JQ1091 trypsin inhibitor KTi1 (Kunitz) - soybean >gi_256635_bbs_115028 (S45035) Kunitz trypsin inhibitor KTi1 [soybeans, Peptide, 203 aa] [Glycine max]

Seq. No.	52262
Seq. ID	uC-gmropic021f01b1
Method	BLASTN
NCBI GI	g18764
BLAST score	437
E value	0.0e+00
Match length	441
% identity	100
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	52263
Seq. ID	uC-gmropic021g07b1
Method	BLASTN
NCBI GI	g218276
BLAST score	35
E value	4.0e-10
Match length	51
% identity	92
NCBI Description	Spinach mRNA for O-acetylserine(thiol)-lyase, complete cds

Seq. No.	52264
Seq. ID	uC-gmropic021g08b1
Method	BLASTX
NCBI GI	g4309731
BLAST score	240

E value	3.0e-20
Match length	142
% identity	36
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52265
Seq. ID	uC-gmropic021h02b1
Method	BLASTX
NCBI GI	g3702343
BLAST score	483
E value	7.0e-49
Match length	116
% identity	82
NCBI Description	(AC005397) putative homeotic gene regulator [Arabidopsis thaliana]

Seq. No.	52266
Seq. ID	uC-gmropic022a01b1
Method	BLASTN
NCBI GI	g1431628
BLAST score	221
E value	1.0e-121
Match length	404
% identity	91
NCBI Description	V.radiata mRNA for pectinacetylesterase

Seq. No.	52267
Seq. ID	uC-gmropic022a03b1
Method	BLASTN
NCBI GI	g1438878
BLAST score	55
E value	4.0e-22
Match length	108
% identity	99
NCBI Description	Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No.	52268
Seq. ID	uC-gmropic022a07b1
Method	BLASTX
NCBI GI	g1931655
BLAST score	527
E value	5.0e-54
Match length	113
% identity	84
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	52269
Seq. ID	uC-gmropic022c10b1
Method	BLASTX
NCBI GI	g2317912
BLAST score	470
E value	3.0e-47
Match length	107
% identity	78
NCBI Description	(U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana]

Seq. No.	52270
Seq. ID	uC-gmropic022d11b1
Method	BLASTN
NCBI GI	g2970653
BLAST score	115
E value	8.0e-58
Match length	299
% identity	84
NCBI Description	Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	52271
Seq. ID	uC-gmropic022e10b1
Method	BLASTX
NCBI GI	g2288985
BLAST score	346
E value	1.0e-32
Match length	101
% identity	61
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52272
Seq. ID	uC-gmropic022e12b1
Method	BLASTX
NCBI GI	g129060
BLAST score	279
E value	8.0e-25
Match length	130
% identity	47
NCBI Description	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX PRECURSOR (E2) (PDC-E2) >gi_82982_pir__A30198 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) precursor - yeast (Saccharomyces cerevisiae) >gi_170972 (J04096) dihydrolipoamide acetyltransferase precursor (EC 2.3.1.12) [Saccharomyces cerevisiae] >gi_791115_emb_CAA60189_ (X86470) dihydrolipoamide S-acetyltransferase [Saccharomyces cerevisiae] >gi_1301955_emb_CAA95945_ (Z71347) ORF YNL071w [Saccharomyces cerevisiae]

Seq. No.	52273
Seq. ID	uC-gmropic022h05b1
Method	BLASTX
NCBI GI	g4512667
BLAST score	538
E value	3.0e-55
Match length	111
% identity	87
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	52274
Seq. ID	uC-gmropic023e09b1
Method	BLASTX
NCBI GI	g445612
BLAST score	454
E value	3.0e-45
Match length	92

% identity	92
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	52275
Seq. ID	uC-gmropic023f10b1
Method	BLASTX
NCBI GI	g3513738
BLAST score	378
E value	2.0e-36
Match length	125
% identity	62
NCBI Description	(AF080118) similar to the GDSL family of lipolytic enzymes [Arabidopsis thaliana]

Seq. No.	52276
Seq. ID	uC-gmropic023g09b1
Method	BLASTX
NCBI GI	g1872521
BLAST score	298
E value	5.0e-27
Match length	77
% identity	49
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	52277
Seq. ID	uC-gmropic023g11b1
Method	BLASTX
NCBI GI	g4262226
BLAST score	304
E value	9.0e-28
Match length	74
% identity	77
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	52278
Seq. ID	uC-gmropic023h06b1
Method	BLASTX
NCBI GI	g99755
BLAST score	352
E value	2.0e-33
Match length	147
% identity	44
NCBI Description	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) >gi_16356_emb_CAA37917_ (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq. No.	52279
Seq. ID	uC-gmropic023h10b1
Method	BLASTN
NCBI GI	g18764
BLAST score	308
E value	1.0e-173
Match length	411
% identity	94

NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	52280
Seq. ID	uC-gmropic024c09b1
Method	BLASTN
NCBI GI	g170048
BLAST score	467
E value	0.0e+00
Match length	467
% identity	12
NCBI Description	Glycine max SbPRP1 gene encoding a proline-rich protein, complete cds

Seq. No.	52281
Seq. ID	uC-gmropic024f11b1
Method	BLASTX
NCBI GI	g4406773
BLAST score	340
E value	2.0e-32
Match length	78
% identity	47
NCBI Description	(AC006836) putative cell division control protein 48 [Arabidopsis thaliana]

Seq. No.	52282
Seq. ID	uC-gmropic024g12b1
Method	BLASTX
NCBI GI	g1346113
BLAST score	534
E value	8.0e-55
Match length	107
% identity	94
NCBI Description	GTP CYCLOHYDROLASE II >gi_1084339_pir__JC4209 GTP cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana >gi_940383_dbj_BAA08113_ (D45165) GTP cyclohydrolase II [Arabidopsis thaliana]

Seq. No.	52283
Seq. ID	uC-gmropic024h11b1
Method	BLASTX
NCBI GI	g3461835
BLAST score	361
E value	1.0e-34
Match length	113
% identity	65
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	52284
Seq. ID	uC-gmropic025e01b1
Method	BLASTX
NCBI GI	g4539301
BLAST score	232
E value	6.0e-20
Match length	78
% identity	62

NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	52285
Seq. ID	uC-gmropic025e06b1
Method	BLASTX
NCBI GI	g4455176
BLAST score	284
E value	2.0e-25
Match length	134
% identity	45
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52286
Seq. ID	uC-gmropic025f02b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	2.0e-11
Match length	49
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	52287
Seq. ID	uC-gmropic026a02b1
Method	BLASTX
NCBI GI	g2979554
BLAST score	301
E value	4.0e-37
Match length	105
% identity	75
NCBI Description	(AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No.	52288
Seq. ID	uC-gmropic026b06b1
Method	BLASTN
NCBI GI	g1877396
BLAST score	45
E value	2.0e-16
Match length	124
% identity	84
NCBI Description	R.communis mRNA for shaggy-like kinase, partial

Seq. No.	52289
Seq. ID	uC-gmropic026b10b1
Method	BLASTX
NCBI GI	g2262159
BLAST score	226
E value	7.0e-19
Match length	51
% identity	75
NCBI Description	(AC002329) predicted protein similar to S.pombe protein C5H10.03 [Arabidopsis thaliana]

Seq. No.	52290
Seq. ID	uC-gmropic026f05b1
Method	BLASTX

NCBI GI	g3201625
BLAST score	142
E value	7.0e-09
Match length	79
% identity	47
NCBI Description	(AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52291
Seq. ID	uC-gmropic027a10b1
Method	BLASTX
NCBI GI	g3337352
BLAST score	542
E value	1.0e-55
Match length	137
% identity	76
NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	52292
Seq. ID	uC-gmropic027b08b1
Method	BLASTX
NCBI GI	g3292829
BLAST score	172
E value	2.0e-12
Match length	46
% identity	70
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	52293
Seq. ID	uC-gmropic027d10b1
Method	BLASTX
NCBI GI	g4432841
BLAST score	434
E value	6.0e-43
Match length	125
% identity	75
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52294
Seq. ID	uC-gmropic027e06b1
Method	BLASTX
NCBI GI	g1351856
BLAST score	356
E value	4.0e-34
Match length	82
% identity	76
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	52295
Seq. ID	uC-gmropic027g09b1
Method	BLASTX
NCBI GI	g1235680
BLAST score	399
E value	7.0e-39
Match length	135

% identity	61
NCBI Description	(U48698) receptor serine/threonine kinase PR5K [Arabidopsis thaliana] >gi_1589714_prf__2211427A receptor protein kinase [Arabidopsis thaliana]

Seq. No.	52296
Seq. ID	uC-gmropic027g12b1
Method	BLASTX
NCBI GI	g4580460
BLAST score	631
E value	4.0e-66
Match length	129
% identity	96
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	52297
Seq. ID	uC-gmropic028e07b1
Method	BLASTX
NCBI GI	g1654140
BLAST score	176
E value	3.0e-13
Match length	36
% identity	89
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	52298
Seq. ID	uC-gmropic028f03b1
Method	BLASTX
NCBI GI	g421955
BLAST score	106
E value	1.0e-17
Match length	131
% identity	50
NCBI Description	hypothetical protein 4 - potato transposon Tst1 >gi_21434_emb_CAA36616_ (X52387) ORF4 [Solanum tuberosum]

Seq. No.	52299
Seq. ID	uC-gmropic029a05b1
Method	BLASTX
NCBI GI	g2832623
BLAST score	200
E value	1.0e-15
Match length	66
% identity	58
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	52300
Seq. ID	uC-gmropic029b03b1
Method	BLASTX
NCBI GI	g2911058
BLAST score	394
E value	3.0e-38
Match length	133
% identity	64
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	52301
Seq. ID	uC-gmropic029c12b1
Method	BLASTX
NCBI GI	g4204314
BLAST score	163
E value	2.0e-11
Match length	92
% identity	45
NCBI Description	(AC003027) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	52302
Seq. ID	uC-gmropic029e12b1
Method	BLASTX
NCBI GI	g4539320
BLAST score	305
E value	7.0e-28
Match length	108
% identity	68
NCBI Description	(AL035679) putative endo-1, 4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	52303
Seq. ID	uC-gmropic029f05b1
Method	BLASTX
NCBI GI	g1561774
BLAST score	247
E value	6.0e-35
Match length	91
% identity	85
NCBI Description	(U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.	52304
Seq. ID	uC-gmropic029g06b1
Method	BLASTX
NCBI GI	g2887500
BLAST score	144
E value	4.0e-09
Match length	28
% identity	79
NCBI Description	(AC002339) putative AP2 domain-containing protein [Arabidopsis thaliana]

Seq. No.	52305
Seq. ID	uC-gmropic030b11b1
Method	BLASTX
NCBI GI	g1885383
BLAST score	206
E value	2.0e-16
Match length	90
% identity	57
NCBI Description	(U84568) phospholipase D [Arabidopsis thaliana]

Seq. No.	52306
Seq. ID	uC-gmropic030c06b1
Method	BLASTX
NCBI GI	g4406780

BLAST score 350
E value 3.0e-33
Match length 111
% identity 53
NCBI Description (AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No. 52307
Seq. ID uC-gmropic030e11b1
Method BLASTX
NCBI GI g2191134
BLAST score 175
E value 1.0e-12
Match length 98
% identity 39
NCBI Description (AF007269) contains weak similarity to Galectin-3 binding protein [Arabidopsis thaliana]

Seq. No. 52308
Seq. ID uC-gmropic031d09b1
Method BLASTX
NCBI GI g2055228
BLAST score 181
E value 1.0e-13
Match length 77
% identity 51
NCBI Description (AB000129) SRC1 [Glycine max]

Seq. No. 52309
Seq. ID uC-gmropic031g05b1
Method BLASTX
NCBI GI g3776578
BLAST score 204
E value 3.0e-16
Match length 62
% identity 55
NCBI Description (AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No. 52310
Seq. ID uC-gmropic032a04b1
Method BLASTX
NCBI GI g3947733
BLAST score 338
E value 1.0e-31
Match length 133
% identity 47
NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 52311
Seq. ID uC-gmropic032f05b1
Method BLASTX
NCBI GI g122772
BLAST score 493
E value 2.0e-51
Match length 139
% identity 72

NCBI Description	TRANSCRIPTION FACTOR HBP-1B >gi_100809_pir__S15347 transcription factor HBP-1b - wheat >gi_21635_emb_CAA40102_ (X56782) HBP-1b [Triticum aestivum]

Seq. No.	52312
Seq. ID	uC-gmropic033a04b1
Method	BLASTN
NCBI GI	g170073
BLAST score	223
E value	1.0e-122
Match length	274
% identity	96
NCBI Description	Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No.	52313
Seq. ID	uC-gmropic033b01b1
Method	BLASTX
NCBI GI	g4468812
BLAST score	365
E value	7.0e-35
Match length	108
% identity	66
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	52314
Seq. ID	uC-gmropic033d10b1
Method	BLASTX
NCBI GI	g4063751
BLAST score	181
E value	2.0e-13
Match length	72
% identity	56
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	52315
Seq. ID	uC-gmropic033e01b1
Method	BLASTX
NCBI GI	g3378208
BLAST score	282
E value	2.0e-25
Match length	74
% identity	48
NCBI Description	(AF079232) annexin p34 [Lycopersicon esculentum]

Seq. No.	52316
Seq. ID	uC-gmropic033e02b1
Method	BLASTX
NCBI GI	g3080395
BLAST score	218
E value	1.0e-17
Match length	114
% identity	48
NCBI Description	(AL022603) hypothetical protein [Arabidopsis thaliana]

Seq. No. 52317

Seq. ID	uC-gmropic033e03b1
Method	BLASTX
NCBI GI	g479356
BLAST score	495
E value	4.0e-50
Match length	142
% identity	61
NCBI Description	protein kinase PK1 (EC 2.7.1.-), receptor-like - maize

Seq. No.	52318
Seq. ID	uC-gmropic033e09b1
Method	BLASTX
NCBI GI	g4008010
BLAST score	569
E value	1.0e-58
Match length	158
% identity	66
NCBI Description	(AF084036) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	52319
Seq. ID	uC-gmropic033g12b1
Method	BLASTX
NCBI GI	g3337366
BLAST score	465
E value	1.0e-46
Match length	144
% identity	62
NCBI Description	(AC004481) unknown protein [Arabidopsis thaliana]

Seq. No.	52320
Seq. ID	uC-gmropic033h08b1
Method	BLASTX
NCBI GI	g3738298
BLAST score	307
E value	6.0e-28
Match length	92
% identity	68
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	52321
Seq. ID	uC-gmropic034a10b1
Method	BLASTX
NCBI GI	g445612
BLAST score	386
E value	2.0e-37
Match length	79
% identity	92
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	52322
Seq. ID	uC-gmropic034e12b1
Method	BLASTX
NCBI GI	g4455259
BLAST score	179

E value	4.0e-13
Match length	94
% identity	40
NCBI Description	(AL035523) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	52323
Seq. ID	uC-gmropic034f02b1
Method	BLASTN
NCBI GI	g3172156
BLAST score	98
E value	1.0e-47
Match length	226
% identity	86
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52324
Seq. ID	uC-gmropic035b07b1
Method	BLASTX
NCBI GI	g1352186
BLAST score	371
E value	1.0e-35
Match length	104
% identity	64
NCBI Description	ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No.	52325
Seq. ID	uC-gmropic035e03b1
Method	BLASTX
NCBI GI	g4335717
BLAST score	143
E value	8.0e-09
Match length	140
% identity	32
NCBI Description	(AC006248) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	52326
Seq. ID	uC-gmropic035h03b1
Method	BLASTN
NCBI GI	g388206
BLAST score	37
E value	2.0e-11
Match length	69
% identity	88
NCBI Description	Lycopersicon esculentum ubiquitin carrier protein (Ubc) mRNA, complete cds. >gi_2086269_gb_I38279_I38279 Sequence 109 from patent US

Seq. No.	52327
Seq. ID	uC-gmropic036b11b1
Method	BLASTX
NCBI GI	g2335096
BLAST score	356

E value	7.0e-34
Match length	89
% identity	75
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52328
Seq. ID	uC-gmropic036c10b1
Method	BLASTX
NCBI GI	g3283996
BLAST score	149
E value	2.0e-09
Match length	113
% identity	39
NCBI Description	(AF072908) calcium-dependent protein kinase [Nicotiana tabacum]

Seq. No.	52329
Seq. ID	uC-gmropic036d11b1
Method	BLASTX
NCBI GI	g3876559
BLAST score	330
E value	1.0e-30
Match length	105
% identity	57
NCBI Description	(Z81072) Similarity to Human cyclin A/CDK2-associatd protein P19 (RNA polymerase elongation factor) (SW:SKP1_HUMAN); cDNA EST EMBL:T00114 comes from this gene; cDNA EST yk390f11.5 comes from this gene; cDNA EST yk402e11.5 comes... >gi_3877216_emb_CAB03110_ (Z81084) Similarity to Human cyclin A/CDK2-associatd protein P19 (RNA polymerase elongation factor) (SW:SKP1_HUMAN); cDNA EST EMBL:T00114 comes from this gene; cDNA EST yk390f11.5 comes from this gene; cDNA EST yk402e11.5 comes

Seq. No.	52330
Seq. ID	uC-gmropic036e01b1
Method	BLASTX
NCBI GI	g2827141
BLAST score	345
E value	9.0e-33
Match length	98
% identity	65
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	52331
Seq. ID	uC-gmropic036e09b1
Method	BLASTX
NCBI GI	g3482967
BLAST score	478
E value	4.0e-48
Match length	112
% identity	79
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	52332
Seq. ID	uC-gmropic036g06b1
Method	BLASTX
NCBI GI	g2739004
BLAST score	193
E value	5.0e-15
Match length	87
% identity	46
NCBI Description	(AF022461) CYP82C1p [Glycine max]

Seq. No.	52333
Seq. ID	uC-gmropic037b04b1
Method	BLASTX
NCBI GI	g1653767
BLAST score	220
E value	3.0e-18
Match length	81
% identity	56
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	52334
Seq. ID	uC-gmropic037d10b1
Method	BLASTX
NCBI GI	g4090935
BLAST score	166
E value	1.0e-11
Match length	126
% identity	33
NCBI Description	(AF028719) DNA polymerase type I [Rhodothermus sp. 'ITI 518']

Seq. No.	52335
Seq. ID	uC-gmropic037f10b1
Method	BLASTX
NCBI GI	g3021272
BLAST score	138
E value	2.0e-18
Match length	74
% identity	69
NCBI Description	(AL022347) serine /threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	52336
Seq. ID	uC-gmropic037g01b1
Method	BLASTX
NCBI GI	g2160144
BLAST score	182
E value	1.0e-13
Match length	95
% identity	40
NCBI Description	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No.	52337
Seq. ID	uC-gmropic037g10b1
Method	BLASTX
NCBI GI	g1663549

BLAST score 268
E value 6.0e-24
Match length 79
% identity 63
NCBI Description (U55809) disease resistance protein homolog [Glycine max]

Seq. No. 52338
Seq. ID uC-gmropic038b12b1
Method BLASTX
NCBI GI g2654868
BLAST score 307
E value 2.0e-28
Match length 79
% identity 70
NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No. 52339
Seq. ID uC-gmropic038d03b1
Method BLASTN
NCBI GI g515750
BLAST score 320
E value 1.0e-180
Match length 433
% identity 95
NCBI Description Soybean phytochrome A (phyA) mRNA, complete cds

Seq. No. 52340
Seq. ID uC-gmropic038d09b1
Method BLASTX
NCBI GI g4510377
BLAST score 228
E value 5.0e-23
Match length 85
% identity 68
NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 52341
Seq. ID uC-gmropic038h03b1
Method BLASTX
NCBI GI g4539324
BLAST score 173
E value 2.0e-12
Match length 64
% identity 55
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 52342
Seq. ID uC-gmropic039a06b1
Method BLASTN
NCBI GI g21981
BLAST score 60
E value 1.0e-25
Match length 96
% identity 91
NCBI Description V.angustifolia 25S/18S rRNA intergenic spacer DNA

Seq. No. 52343

Seq. ID	uC-gmropic039b03b1
Method	BLASTX
NCBI GI	g4249410
BLAST score	290
E value	4.0e-26
Match length	115
% identity	61
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	52344
Seq. ID	uC-gmropic039c09b1
Method	BLASTX
NCBI GI	g4063700
BLAST score	142
E value	9.0e-09
Match length	58
% identity	45
NCBI Description	(AF099053) phosphatidylserine synthase-2 [Mus musculus]

Seq. No.	52345
Seq. ID	uC-gmropic039d04b1
Method	BLASTX
NCBI GI	g3250695
BLAST score	222
E value	3.0e-18
Match length	107
% identity	46
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	52346
Seq. ID	uC-gmropic039h12b1
Method	BLASTN
NCBI GI	g862479
BLAST score	93
E value	9.0e-45
Match length	187
% identity	93
NCBI Description	Glycine max valosin-containing protein mRNA, complete cds

Seq. No.	52347
Seq. ID	uC-gmropic040a02b1
Method	BLASTX
NCBI GI	g124369
BLAST score	280
E value	4.0e-25
Match length	113
% identity	58
NCBI Description	ACETOLACTATE SYNTHASE II PRECURSOR (ACETOHYDROXY-ACID SYNTHASE II) (ALS II) >gi_68239_pir__YCNT2 acetolactate synthase (EC 4.1.3.18) class II precursor - common tobacco >gi_19779_emb_CAA30485_ (X07645) ALS SuRB gene (AA 1-664) [Nicotiana tabacum]

Seq. No.	52348
Seq. ID	uC-gmropic040a05b1
Method	BLASTN
NCBI GI	g3452086

BLAST score	163
E value	1.0e-86
Match length	191
% identity	92
NCBI Description	Glycine max mRNA for 14-3-3 protein, partial

Seq. No.	52349
Seq. ID	uC-gmropic040b05b1
Method	BLASTN
NCBI GI	g1277163
BLAST score	289
E value	1.0e-161
Match length	375
% identity	94
NCBI Description	Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No.	52350
Seq. ID	uC-gmropic040d02b1
Method	BLASTX
NCBI GI	g461498
BLAST score	177
E value	8.0e-13
Match length	71
% identity	83
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]

Seq. No.	52351
Seq. ID	uC-gmropic040g04b1
Method	BLASTN
NCBI GI	g255407
BLAST score	61
E value	3.0e-26
Match length	93
% identity	91
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	52352
Seq. ID	uC-gmropic040g06b1
Method	BLASTX
NCBI GI	g2191166
BLAST score	157
E value	2.0e-10
Match length	117
% identity	36
NCBI Description	(AF007270) A_IG002P16.15 gene product [Arabidopsis thaliana]

Seq. No.	52353
Seq. ID	uC-gmropic041a08b1
Method	BLASTX
NCBI GI	g3687237

BLAST score	140
E value	9.0e-09
Match length	83
% identity	41
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	52354
Seq. ID	uC-gmropic041c12b1
Method	BLASTN
NCBI GI	g2653445
BLAST score	105
E value	6.0e-52
Match length	189
% identity	89
NCBI Description	Vigna radiata mRNA for proton pyrophosphatase, complete cds

Seq. No.	52355
Seq. ID	uC-gmropic041d02b1
Method	BLASTN
NCBI GI	g310575
BLAST score	146
E value	2.0e-76
Match length	230
% identity	91
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	52356
Seq. ID	uC-gmropic041d09b1
Method	BLASTX
NCBI GI	g3341693
BLAST score	140
E value	1.0e-08
Match length	63
% identity	46
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	52357
Seq. ID	uC-gmropic041g06b1
Method	BLASTX
NCBI GI	g2213600
BLAST score	190
E value	3.0e-14
Match length	79
% identity	43
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	52358
Seq. ID	uC-gmropic041h03b1
Method	BLASTX
NCBI GI	g1168536
BLAST score	238
E value	5.0e-20
Match length	55
% identity	78
NCBI Description	PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE) >gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-)

precursor - barley >gi_18904_emb_CAA39602_ (X56136) aspartic proteinase [Hordeum vulgare]

Seq. No.	52359
Seq. ID	uC-gmropic042b10b1
Method	BLASTX
NCBI GI	g3080393
BLAST score	318
E value	3.0e-29
Match length	101
% identity	62
NCBI Description	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	52360
Seq. ID	uC-gmropic042b11b1
Method	BLASTN
NCBI GI	g3204107
BLAST score	147
E value	6.0e-77
Match length	247
% identity	90
NCBI Description	Cicer arietinum mRNA for putative cytidine or deoxycytidylate deaminase, partial

Seq. No.	52361
Seq. ID	uC-gmropic042c08b1
Method	BLASTX
NCBI GI	g4559331
BLAST score	584
E value	2.0e-60
Match length	122
% identity	84
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	52362
Seq. ID	uC-gmropic042d06b1
Method	BLASTN
NCBI GI	g2661018
BLAST score	357
E value	0.0e+00
Match length	401
% identity	97
NCBI Description	Glycine max catalase (cat3) mRNA, complete cds

Seq. No.	52363
Seq. ID	uC-gmropic042f05b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	45
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	52364
Seq. ID	uC-gmropic043b02b1

Method	BLASTN
NCBI GI	g347454
BLAST score	198
E value	1.0e-107
Match length	311
% identity	93
NCBI Description	Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3' end

Seq. No.	52365
Seq. ID	uC-gmropic043b05b1
Method	BLASTX
NCBI GI	g4263714
BLAST score	525
E value	1.0e-53
Match length	123
% identity	84
NCBI Description	(AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	52366
Seq. ID	uC-gmropic043d06b1
Method	BLASTX
NCBI GI	g4105772
BLAST score	349
E value	5.0e-33
Match length	89
% identity	39
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	52367
Seq. ID	uC-gmropic043e02b1
Method	BLASTX
NCBI GI	g3021265
BLAST score	191
E value	8.0e-15
Match length	93
% identity	44
NCBI Description	(AL022347) protein kinase - like protein [Arabidopsis thaliana] >gi_3292839_emb_CAA19829_ (AL031018) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	52368
Seq. ID	uC-gmropic043f03b1
Method	BLASTX
NCBI GI	g4467096
BLAST score	299
E value	3.0e-27
Match length	91
% identity	63
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	52369
Seq. ID	uC-gmropic043f06b1
Method	BLASTX
NCBI GI	g2275219
BLAST score	269

E value 3.0e-24
Match length 67
% identity 73
NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]

Seq. No. 52370
Seq. ID uC-gmropic043g08b1
Method BLASTX
NCBI GI g2104446
BLAST score 372
E value 7.0e-36
Match length 108
% identity 62
NCBI Description (Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No. 52371
Seq. ID uC-gmropic043h01b1
Method BLASTX
NCBI GI g2160179
BLAST score 223
E value 3.0e-18
Match length 84
% identity 58
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 52372
Seq. ID uC-gmropic043h07b1
Method BLASTX
NCBI GI g2654868
BLAST score 557
E value 2.0e-57
Match length 127
% identity 83
NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No. 52373
Seq. ID uC-gmropic044a03b1
Method BLASTX
NCBI GI g4210449
BLAST score 442
E value 5.0e-44
Match length 110
% identity 79
NCBI Description (AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No. 52374
Seq. ID uC-gmropic044e04b1
Method BLASTX
NCBI GI g4263818
BLAST score 179
E value 4.0e-13
Match length 73
% identity 49
NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]

Seq. No. 52375
Seq. ID uC-gmropic044e05b1

Method	BLASTX
NCBI GI	g3608154
BLAST score	165
E value	2.0e-11
Match length	60
% identity	60
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	52376
Seq. ID	uC-gmropic044e08b1
Method	BLASTN
NCBI GI	g780371
BLAST score	38
E value	6.0e-12
Match length	128
% identity	87
NCBI Description	Oryza sativa enolase mRNA, complete cds

Seq. No.	52377
Seq. ID	uC-gmropic045c04b1
Method	BLASTX
NCBI GI	g2959781
BLAST score	295
E value	3.0e-27
Match length	75
% identity	76
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	52378
Seq. ID	uC-gmropic045c09b1
Method	BLASTN
NCBI GI	g762878
BLAST score	38
E value	3.0e-12
Match length	118
% identity	83
NCBI Description	Psophocarpus tetragonolobus mRNA for chitinase, complete cds

Seq. No.	52379
Seq. ID	uC-gmropic046d02b1
Method	BLASTX
NCBI GI	g2558938
BLAST score	361
E value	2.0e-34
Match length	144
% identity	54
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	52380
Seq. ID	uC-gmropic046f08b1
Method	BLASTX
NCBI GI	g4185142
BLAST score	233
E value	9.0e-20
Match length	72
% identity	67

NCBI Description	(AC005724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana]

Seq. No.	52381
Seq. ID	uC-gmropic047a11b1
Method	BLASTX
NCBI GI	g4049353
BLAST score	551
E value	1.0e-56
Match length	144
% identity	69
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	52382
Seq. ID	uC-gmropic047b06b1
Method	BLASTN
NCBI GI	g310575
BLAST score	164
E value	3.0e-87
Match length	278
% identity	92
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	52383
Seq. ID	uC-gmropic047c03b1
Method	BLASTX
NCBI GI	g3298437
BLAST score	308
E value	2.0e-28
Match length	68
% identity	87
NCBI Description	(AB010877) chloroplast ribosomal protein L3 [Nicotiana tabacum]

Seq. No.	52384
Seq. ID	uC-gmropic049a02b1
Method	BLASTX
NCBI GI	g4512660
BLAST score	327
E value	1.0e-30
Match length	114
% identity	61
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544467_gb_AAD22374.1_AC006580_6 (AC006580) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52385
Seq. ID	uC-gmropic049a03b1
Method	BLASTX
NCBI GI	g1176658
BLAST score	198
E value	3.0e-15
Match length	76
% identity	49
NCBI Description	HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II >gi_726363 (U23168) No definition line found [Caenorhabditis elegans]

Seq. No.	52386
Seq. ID	uC-gmropic049b10b1
Method	BLASTN
NCBI GI	g3982595
BLAST score	288
E value	1.0e-161
Match length	390
% identity	93
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	52387
Seq. ID	uC-gmropic049c07b1
Method	BLASTX
NCBI GI	g1616787
BLAST score	303
E value	9.0e-28
Match length	89
% identity	69
NCBI Description	(U71122) pyruvate decarboxylase [Arabidopsis thaliana]

Seq. No.	52388
Seq. ID	uC-gmropic049c10b1
Method	BLASTX
NCBI GI	g2642217
BLAST score	192
E value	3.0e-15
Match length	43
% identity	81
NCBI Description	(AF030387) NOI protein [Oryza sativa]

Seq. No.	52389
Seq. ID	uC-gmropic049c12b1
Method	BLASTX
NCBI GI	g3193290
BLAST score	262
E value	6.0e-23
Match length	104
% identity	50
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido

Seq. No.	52390
Seq. ID	uC-gmropic049d07b1
Method	BLASTX
NCBI GI	g3688186
BLAST score	307
E value	4.0e-28
Match length	118
% identity	68
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	52391
Seq. ID	uC-gmropic050a01b1

Method	BLASTX
NCBI GI	g4455338
BLAST score	538
E value	3.0e-55
Match length	132
% identity	73
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	52392
Seq. ID	uC-gmropic050b10b1
Method	BLASTX
NCBI GI	g1364059
BLAST score	290
E value	5.0e-26
Match length	130
% identity	46
NCBI Description	dioscorin class A precursor - Dioscorea cayenensis >gi_433463_emb_CAA53781_ (X76187) storage protein [Dioscorea cayenensis]

Seq. No.	52393
Seq. ID	uC-gmropic050c07b1
Method	BLASTX
NCBI GI	g4566614
BLAST score	488
E value	3.0e-49
Match length	111
% identity	83
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	52394
Seq. ID	uC-gmropic050d01b1
Method	BLASTX
NCBI GI	g2500542
BLAST score	155
E value	2.0e-10
Match length	92
% identity	40
NCBI Description	PUTATIVE ATP-DEPENDENT RNA HELICASE YMR128W >gi_1078577_pir__S53058 probable membrane protein YMR128w - yeast (Saccharomyces cerevisiae) >gi_728667_emb_CAA88553_ (Z48622) unknown [Saccharomyces cerevisiae]

Seq. No.	52395
Seq. ID	uC-gmropic050d03b1
Method	BLASTX
NCBI GI	g4263522
BLAST score	369
E value	2.0e-35
Match length	130
% identity	10
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52396
Seq. ID	uC-gmropic050e01b1
Method	BLASTX

NCBI GI	g4455285
BLAST score	175
E value	1.0e-12
Match length	124
% identity	41
NCBI Description	(AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52397
Seq. ID	uC-gmropic054a10b1
Method	BLASTX
NCBI GI	g4262149
BLAST score	142
E value	9.0e-09
Match length	35
% identity	77
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	52398
Seq. ID	uC-gmropic054f10b1
Method	BLASTX
NCBI GI	g4263714
BLAST score	252
E value	7.0e-22
Match length	54
% identity	89
NCBI Description	(AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	52399
Seq. ID	uC-gmropic054g10b1
Method	BLASTX
NCBI GI	g4200122
BLAST score	224
E value	3.0e-18
Match length	116
% identity	41
NCBI Description	(AJ009555) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52400
Seq. ID	uC-gmropic055a02b1
Method	BLASTX
NCBI GI	g2961377
BLAST score	496
E value	3.0e-50
Match length	148
% identity	4
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	52401
Seq. ID	uC-gmropic055f06b1
Method	BLASTN
NCBI GI	g1498052
BLAST score	124
E value	3.0e-63
Match length	380

% identity	83
NCBI Description	Zea mays ribosomal protein S8 mRNA, complete cds

Seq. No.	52402
Seq. ID	uC-gmropic055f12b1
Method	BLASTN
NCBI GI	g4324966
BLAST score	49
E value	1.0e-18
Match length	49
% identity	100
NCBI Description	Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No.	52403
Seq. ID	uC-gmropic055g06b1
Method	BLASTX
NCBI GI	g2853073
BLAST score	282
E value	2.0e-25
Match length	96
% identity	54
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	52404
Seq. ID	uC-gmropic055h06b1
Method	BLASTX
NCBI GI	g2244904
BLAST score	348
E value	3.0e-33
Match length	90
% identity	12
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	52405
Seq. ID	uC-gmropic056a03b1
Method	BLASTX
NCBI GI	g2346974
BLAST score	282
E value	3.0e-25
Match length	104
% identity	54
NCBI Description	(AB006599) ZPT2-12 [Petunia x hybrida]

Seq. No.	52406
Seq. ID	uC-gmropic056b08b1
Method	BLASTN
NCBI GI	g456713
BLAST score	321
E value	0.0e+00
Match length	353
% identity	26
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	52407
Seq. ID	uC-gmropic056d10b1
Method	BLASTN

NCBI GI	g1196896
BLAST score	97
E value	3.0e-47
Match length	234
% identity	89
NCBI Description	Glycine max acidic ribosomal protein P0 mRNA, complete cds

Seq. No.	52408
Seq. ID	uC-gmropic056f07b1
Method	BLASTX
NCBI GI	g4467128
BLAST score	424
E value	1.0e-41
Match length	137
% identity	55
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	52409
Seq. ID	uC-gmropic056g09b1
Method	BLASTN
NCBI GI	g170065
BLAST score	389
E value	0.0e+00
Match length	425
% identity	15
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	52410
Seq. ID	uC-gmropic057b05b1
Method	BLASTX
NCBI GI	g4335745
BLAST score	248
E value	4.0e-21
Match length	100
% identity	49
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	52411
Seq. ID	uC-gmropic057c08b1
Method	BLASTX
NCBI GI	g3080450
BLAST score	341
E value	5.0e-32
Match length	147
% identity	48
NCBI Description	(AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52412
Seq. ID	uC-gmropic057e02b1
Method	BLASTX
NCBI GI	g4469015
BLAST score	292
E value	2.0e-26
Match length	109

% identity	91
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	52413
Seq. ID	uC-gmropic057g11b1
Method	BLASTX
NCBI GI	g2598589
BLAST score	283
E value	2.0e-25
Match length	88
% identity	60
NCBI Description	(Y15367) MtN19 [Medicago truncatula]

Seq. No.	52414
Seq. ID	uC-gmropic057h08b1
Method	BLASTX
NCBI GI	g3402722
BLAST score	195
E value	4.0e-15
Match length	80
% identity	50
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]

Seq. No.	52415
Seq. ID	uC-gmropic058f05b1
Method	BLASTX
NCBI GI	g3763921
BLAST score	304
E value	1.0e-27
Match length	95
% identity	57
NCBI Description	(AC004450) putative pirin protein [Arabidopsis thaliana]

Seq. No.	52416
Seq. ID	uC-gmropic061b04b1
Method	BLASTX
NCBI GI	g4309698
BLAST score	580
E value	5.0e-60
Match length	154
% identity	79
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	52417
Seq. ID	uC-gmropic061b05b1
Method	BLASTX
NCBI GI	g3935168
BLAST score	230
E value	1.0e-36
Match length	137
% identity	65
NCBI Description	(AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No.	52418
Seq. ID	uC-gmropic061c09b1
Method	BLASTX

NCBI GI	g3927831
BLAST score	309
E value	2.0e-28
Match length	121
% identity	25
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	52419
Seq. ID	uC-gmropic061f01b1
Method	BLASTX
NCBI GI	g3152577
BLAST score	187
E value	4.0e-14
Match length	115
% identity	50
NCBI Description	(AC002986) Contains similarity to Kinesin-like protein C gb_D21138 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	52420
Seq. ID	uC-gmropic061f03b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	6.0e-11
Match length	49
% identity	49
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	52421
Seq. ID	uC-gmropic061f06b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	48
% identity	65
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	52422
Seq. ID	uC-gmropic061g02b1
Method	BLASTX
NCBI GI	g2780192
BLAST score	134
E value	4.0e-18
Match length	91
% identity	52
NCBI Description	(AJ222713) unnamed protein product [Arabidopsis thaliana]

Seq. No.	52423
Seq. ID	uC-gmropic061h10b1
Method	BLASTN
NCBI GI	g2317899
BLAST score	64
E value	8.0e-28
Match length	144
% identity	86

NCBI Description	Glycine max Sali3-2 mRNA, complete cds
Seq. No.	52424
Seq. ID	uC-gmropic062e05b1
Method	BLASTX
NCBI GI	g3202042
BLAST score	232
E value	1.0e-19
Match length	61
% identity	84
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]
Seq. No.	52425
Seq. ID	uC-gmropic062g04b1
Method	BLASTN
NCBI GI	g169930
BLAST score	34
E value	8.0e-10
Match length	112
% identity	84
NCBI Description	Glycine max calcium dependent protein kinase mRNA
Seq. No.	52426
Seq. ID	uC-gmropic063a06b1
Method	BLASTX
NCBI GI	g4539344
BLAST score	191
E value	4.0e-15
Match length	55
% identity	62
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	52427
Seq. ID	uC-gmropic063f04b1
Method	BLASTX
NCBI GI	g2465923
BLAST score	159
E value	1.0e-10
Match length	64
% identity	50
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
Seq. No.	52428
Seq. ID	uC-gmropic063f07b1
Method	BLASTN
NCBI GI	g18737
BLAST score	302
E value	1.0e-169
Match length	350
% identity	11
NCBI Description	Glycine max RPRP3 gene for repetitive proline-rich protein
Seq. No.	52429
Seq. ID	uC-gmropic063h04b1
Method	BLASTX

NCBI GI	g399505
BLAST score	194
E value	8.0e-15
Match length	104
% identity	44
NCBI Description	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) >gi_105847_pir__A40876 dimethylaniline monooxygenase (N-oxide-forming) (EC 1.14.13.8), hepatic 1 - human >gi_182671 (M64082) flavin-containing monooxygenase [Homo sapiens] >gi_4503755_ref_NP_002012.1_pFMO1_ flavin containing monooxygenase

Seq. No.	52430
Seq. ID	uC-gmropic064a02b1
Method	BLASTX
NCBI GI	g3786011
BLAST score	378
E value	2.0e-36
Match length	134
% identity	59
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	52431
Seq. ID	uC-gmropic064a05b1
Method	BLASTX
NCBI GI	g2961377
BLAST score	222
E value	4.0e-18
Match length	142
% identity	3
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	52432
Seq. ID	uC-gmropic064a11b1
Method	BLASTN
NCBI GI	g18761
BLAST score	440
E value	0.0e+00
Match length	440
% identity	100
NCBI Description	Soybean stem mRNA for 31 kD glycoprotein

Seq. No.	52433
Seq. ID	uC-gmropic064g01b1
Method	BLASTX
NCBI GI	g3322609
BLAST score	392
E value	4.0e-38
Match length	107
% identity	73
NCBI Description	(AE001213) phosphogluconate dehydrogenase (gnd) [Treponema pallidum]

09602.P005.SEQ.ST25

Seq. No.	52434
Seq. ID	uC-gmropic064g10b1
Method	BLASTN
NCBI GI	g4098966
BLAST score	82
E value	3.0e-38
Match length	211
% identity	93
NCBI Description	Glycine max putative reistance gene analog genomic sequence

Seq. No.	52435
Seq. ID	uC-gmropic065b03b1
Method	BLASTX
NCBI GI	g2224927
BLAST score	264
E value	1.0e-23
Match length	62
% identity	77
NCBI Description	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]

Seq. No.	52436
Seq. ID	uC-gmropic065c08b1
Method	BLASTX
NCBI GI	g2244807
BLAST score	422
E value	1.0e-41
Match length	139
% identity	58
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52437
Seq. ID	uC-gmropic065d07b1
Method	BLASTX
NCBI GI	g4454012
BLAST score	225
E value	1.0e-18
Match length	64
% identity	70
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	52438
Seq. ID	uC-gmropic065e01b1
Method	BLASTX
NCBI GI	g2766715
BLAST score	311
E value	1.0e-28
Match length	119
% identity	46
NCBI Description	(AF039365) chromomethylase [Arabidopsis arenosa] >gi_2865435 (AF039375) chromomethylase [Arabidopsis arenosa]

Seq. No.	52439
Seq. ID	uC-gmropic065e09b1
Method	BLASTN

09604769.1 09604769

NCBI GI	g4159707
BLAST score	63
E value	8.0e-27
Match length	167
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence [Arabidopsis thaliana]

Seq. No.	52440
Seq. ID	uC-gmropic065h01b1
Method	BLASTX
NCBI GI	g1350783
BLAST score	208
E value	2.0e-16
Match length	101
% identity	5
NCBI Description	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi_282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No.	52441
Seq. ID	uC-gmropic066b05b1
Method	BLASTX
NCBI GI	g2335097
BLAST score	239
E value	3.0e-20
Match length	123
% identity	45
NCBI Description	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	52442
Seq. ID	uC-gmropic067h06b1
Method	BLASTX
NCBI GI	g1346524
BLAST score	516
E value	2.0e-58
Match length	126
% identity	87
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_497900 (M73430) S-adenosyl methionine synthetase [Populus deltoides]

Seq. No.	52443
Seq. ID	uC-gmropic068b08b1
Method	BLASTN
NCBI GI	g2791833
BLAST score	77
E value	2.0e-35
Match length	149
% identity	88
NCBI Description	Manihot esculenta elongation factor 1-alpha (MeEF1) gene, complete cds

Seq. No.	52444
Seq. ID	uC-gmropic068c07b1
Method	BLASTX
NCBI GI	g2244792
BLAST score	464
E value	9.0e-47
Match length	95
% identity	92
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	52445
Seq. ID	uC-gmropic068e02b1
Method	BLASTX
NCBI GI	g3413719
BLAST score	138
E value	4.0e-09
Match length	38
% identity	87
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643592 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	52446
Seq. ID	uC-gmropic068g11b1
Method	BLASTX
NCBI GI	g2827714
BLAST score	296
E value	8.0e-27
Match length	134
% identity	9
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	52447
Seq. ID	uC-gmropic069e11b1
Method	BLASTN
NCBI GI	g1498337
BLAST score	329
E value	0.0e+00
Match length	365
% identity	98
NCBI Description	Glycine max actin (Soy119) gene, partial cds

Seq. No.	52448
Seq. ID	uC-gmropic070f12b1
Method	BLASTN
NCBI GI	g22382
BLAST score	46
E value	9.0e-17
Match length	78
% identity	90
NCBI Description	Z.mays mRNA for U5snRNA (U53)

Seq. No.	52449
Seq. ID	uC-gmropic070g01b1
Method	BLASTX

NCBI GI	g3482980
BLAST score	141
E value	8.0e-09
Match length	101
% identity	39
NCBI Description	(AL031369) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52450
Seq. ID	uC-gmropic071d04b1
Method	BLASTX
NCBI GI	g3850108
BLAST score	306
E value	6.0e-28
Match length	133
% identity	45
NCBI Description	(AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]

Seq. No.	52451
Seq. ID	uC-gmropic071e08b1
Method	BLASTX
NCBI GI	g4490756
BLAST score	212
E value	1.0e-17
Match length	70
% identity	57
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52452
Seq. ID	uC-gmropic071g01b1
Method	BLASTX
NCBI GI	g2781347
BLAST score	355
E value	6.0e-34
Match length	91
% identity	71
NCBI Description	(AC003113) F24O1.3 [Arabidopsis thaliana]

Seq. No.	52453
Seq. ID	uC-gmropic071h09b1
Method	BLASTX
NCBI GI	g3193300
BLAST score	144
E value	4.0e-09
Match length	106
% identity	38
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	52454
Seq. ID	uC-gmropic072a10b1
Method	BLASTX
NCBI GI	g3047111
BLAST score	432
E value	1.0e-42
Match length	170
% identity	54
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	52455
Seq. ID	uC-gmropic072e10b1
Method	BLASTX
NCBI GI	g3935184
BLAST score	342
E value	3.0e-32
Match length	99
% identity	71
NCBI Description	(AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No.	52456
Seq. ID	uC-gmropic072g12b1
Method	BLASTX
NCBI GI	g3935167
BLAST score	187
E value	5.0e-14
Match length	65
% identity	83
NCBI Description	(AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No.	52457
Seq. ID	uC-gmropic073a02b1
Method	BLASTX
NCBI GI	g2496789
BLAST score	191
E value	2.0e-14
Match length	64
% identity	59
NCBI Description	1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP REDUCTOISOMERASE) >gi_1001556_dbj_BAA10183_ (D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	52458
Seq. ID	uC-gmropic073a10b1
Method	BLASTX
NCBI GI	g719291
BLAST score	462
E value	4.0e-46
Match length	129
% identity	77
NCBI Description	(U19134) unknown [Arabidopsis thaliana] >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]

Seq. No.	52459
Seq. ID	uC-gmropic073d08b1
Method	BLASTN
NCBI GI	g1165321
BLAST score	178
E value	1.0e-95
Match length	257
% identity	17
NCBI Description	Glycine max extensin (SbHRGP3) gene, complete cds

Seq. No.	52460
Seq. ID	uC-gmropic073g04b1
Method	BLASTX

NCBI GI	g4493885
BLAST score	211
E value	5.0e-17
Match length	102
% identity	54
NCBI Description	(AL034558) predicted using hexExon; MAL3P2.7 (PFC0190c), PAST homolog, len: 526 aa; Similarity to PAST proteins from H.sapiens and D.melanogaster. H.sapiens HPAST protein (TR:O14611) BLAST Score: 1245, sum P(1) = 5.1e-127, 47

Seq. No.	52461
Seq. ID	uC-gmropic073h01b1
Method	BLASTX
NCBI GI	g2323344
BLAST score	466
E value	1.0e-46
Match length	147
% identity	60
NCBI Description	(AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]

Seq. No.	52462
Seq. ID	uC-gmropic074a06b1
Method	BLASTX
NCBI GI	g2894599
BLAST score	193
E value	8.0e-15
Match length	104
% identity	45
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	52463
Seq. ID	uC-gmropic074b03b1
Method	BLASTX
NCBI GI	g134892
BLAST score	403
E value	3.0e-39
Match length	146
% identity	57
NCBI Description	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi_88607_pir__A29440 signal recognition particle receptor - human >gi_30866_emb_CAA29608_ (X06272) docking protein [Homo sapiens] >gi_4507223_ref_NP_003130.1_pSRPR_ signal recognition particle receptor ('docking protein')

Seq. No.	52464
Seq. ID	uC-gmropic074d01b1
Method	BLASTX
NCBI GI	g3201627
BLAST score	159
E value	2.0e-17
Match length	91
% identity	56
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	52465
Seq. ID	uC-gmropic074d12b1

Method	BLASTX
NCBI GI	g2832658
BLAST score	196
E value	1.0e-15
Match length	47
% identity	77
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	52466
Seq. ID	uC-gmropic074e10b1
Method	BLASTN
NCBI GI	g170065
BLAST score	279
E value	1.0e-156
Match length	311
% identity	9
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	52467
Seq. ID	uC-gmropic074f08b1
Method	BLASTN
NCBI GI	g1907370
BLAST score	43
E value	6.0e-15
Match length	51
% identity	96
NCBI Description	Cryptomeria japonica 28S ribosomal RNA gene, partial sequence

Seq. No.	52468
Seq. ID	uC-gmropic074h03b1
Method	BLASTX
NCBI GI	g833835
BLAST score	464
E value	1.0e-46
Match length	110
% identity	73
NCBI Description	(U26025) amygdalin hydrolase isoform AH I precursor [Prunus serotina]

Seq. No.	52469
Seq. ID	uC-gmropic074h08b1
Method	BLASTX
NCBI GI	g3327196
BLAST score	294
E value	1.0e-26
Match length	90
% identity	67
NCBI Description	(AB014591) KIAA0691 protein [Homo sapiens]

Seq. No.	52470
Seq. ID	uC-gmropic074h10b1
Method	BLASTX
NCBI GI	g2795805
BLAST score	258
E value	8.0e-23

Match length	76
% identity	59
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]

Seq. No.	52471
Seq. ID	uC-gmropic075b07b1
Method	BLASTX
NCBI GI	g4559384
BLAST score	423
E value	9.0e-42
Match length	123
% identity	67
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	52472
Seq. ID	uC-gmropic075d03b1
Method	BLASTX
NCBI GI	g3138972
BLAST score	206
E value	2.0e-16
Match length	122
% identity	43
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	52473
Seq. ID	uC-gmropic075d09b1
Method	BLASTX
NCBI GI	g4567281
BLAST score	177
E value	1.0e-12
Match length	60
% identity	57
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	52474
Seq. ID	uC-gmropic075e01b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	45
% identity	48
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	52475
Seq. ID	uC-gmropic075e04b1
Method	BLASTX
NCBI GI	g4539348
BLAST score	182
E value	6.0e-14
Match length	53
% identity	62
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	52476
Seq. ID	uC-gmropic075g08b1
Method	BLASTX
NCBI GI	g3451075
BLAST score	241
E value	3.0e-20
Match length	75
% identity	55
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	52477
Seq. ID	uC-gmropic078c11b1
Method	BLASTX
NCBI GI	g1750403
BLAST score	222
E value	2.0e-18
Match length	87
% identity	51
NCBI Description	(U80953) weakly similar in serine repeat region to rat thyroxine-binding globulin (PIR:A39567) and to D. melanogaster ecdysone-inducible protein E75-C (SP:E75C_DROME,P13055) [Caenorhabditis elegans]

Seq. No.	52478
Seq. ID	uC-gmropic080a08b1
Method	BLASTX
NCBI GI	g4490719
BLAST score	221
E value	5.0e-18
Match length	48
% identity	81
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	52479
Seq. ID	uC-gmropic080c08b1
Method	BLASTX
NCBI GI	g4185142
BLAST score	548
E value	2.0e-56
Match length	137
% identity	74
NCBI Description	(AC005724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana]

Seq. No.	52480
Seq. ID	uC-gmropic080d11b1
Method	BLASTX
NCBI GI	g4455278
BLAST score	210
E value	9.0e-17
Match length	82
% identity	50
NCBI Description	(AL035527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52481
Seq. ID	uC-gmropic083c03b1

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Method	BLASTX
NCBI GI	g4033446
BLAST score	220
E value	6.0e-18
Match length	111
% identity	45
NCBI Description	AGGLUTININ II PRECURSOR (CLAII) (LECCLAII) >gi_2147661_pir__S72502 mannose/glucose-binding lectin CLAII precursor - Cladrastis lutea >gi_1141759 (U21959) lectin precursor [Cladrastis lutea]

Seq. No.	52482
Seq. ID	uC-gmropic083f03b1
Method	BLASTN
NCBI GI	g927504
BLAST score	37
E value	5.0e-12
Match length	53
% identity	92
NCBI Description	P.sativum mRNA for fructose-1, 6-biphosphate aldolase (clone aldcyt2)

Seq. No.	52483
Seq. ID	uC-gmropic083h03b1
Method	BLASTX
NCBI GI	g2921406
BLAST score	454
E value	2.0e-45
Match length	102
% identity	87
NCBI Description	(AF036234) vacuolar protein sorting homolog [Arabidopsis thaliana]

Seq. No.	52484
Seq. ID	uC-gmropic087d10b1
Method	BLASTX
NCBI GI	g3758833
BLAST score	238
E value	5.0e-20
Match length	90
% identity	57
NCBI Description	(Y18225) MtN6 [Medicago truncatula]

Seq. No.	52485
Seq. ID	uC-gmropic087h10b1
Method	BLASTX
NCBI GI	g2462837
BLAST score	367
E value	2.0e-35
Match length	89
% identity	82
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52486
Seq. ID	uC-gmropic088a09b1
Method	BLASTX
NCBI GI	g3080452

BLAST score	210
E value	6.0e-17
Match length	62
% identity	69
NCBI Description	(AL022605) putative L-ascorbate oxidase [Arabidopsis thaliana]

Seq. No.	52487
Seq. ID	uC-gmropic088b12b1
Method	BLASTX
NCBI GI	g4220462
BLAST score	460
E value	5.0e-46
Match length	103
% identity	85
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	52488
Seq. ID	uC-gmropic088d02b1
Method	BLASTX
NCBI GI	g3046696
BLAST score	325
E value	8.0e-31
Match length	66
% identity	91
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	52489
Seq. ID	uC-gmropic088h12b1
Method	BLASTX
NCBI GI	g4455177
BLAST score	365
E value	7.0e-35
Match length	141
% identity	53
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	52490
Seq. ID	uC-gmropic089a10b1
Method	BLASTN
NCBI GI	g4115338
BLAST score	169
E value	3.0e-90
Match length	305
% identity	23
NCBI Description	Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

Seq. No.	52491
Seq. ID	uC-gmropic089d02b1
Method	BLASTX
NCBI GI	g2384675
BLAST score	309
E value	2.0e-28
Match length	86
% identity	67

NCBI Description	(AF012659) putative potassium transporter AtKT4p [Arabidopsis thaliana]

Seq. No.	52492
Seq. ID	uC-gmropic089d05b1
Method	BLASTX
NCBI GI	g3367574
BLAST score	300
E value	3.0e-27
Match length	137
% identity	47
NCBI Description	(AL031135) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52493
Seq. ID	uC-gmropic089g06b1
Method	BLASTN
NCBI GI	g1808591
BLAST score	86
E value	1.0e-40
Match length	272
% identity	86
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	52494
Seq. ID	uC-gmropic090b01b1
Method	BLASTX
NCBI GI	g2130082
BLAST score	158
E value	8.0e-11
Match length	78
% identity	13
NCBI Description	protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] >gi_1586408_prf__2203451A receptor kinase-like protein [Oryza sativa]

Seq. No.	52495
Seq. ID	uC-gmropic090f10b1
Method	BLASTX
NCBI GI	g2642165
BLAST score	129
E value	9.0e-13
Match length	55
% identity	56
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52496
Seq. ID	uC-gmropic090g08b1
Method	BLASTX
NCBI GI	g3096935
BLAST score	206
E value	7.0e-17
Match length	77
% identity	56
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	52497
Seq. ID	uC-gmropic091b03b1
Method	BLASTX
NCBI GI	g1663549
BLAST score	153
E value	2.0e-10
Match length	78
% identity	45
NCBI Description	(U55809) disease resistance protein homolog [Glycine max]

Seq. No.	52498
Seq. ID	uC-gmropic091c10b1
Method	BLASTN
NCBI GI	g3449322
BLAST score	34
E value	2.0e-09
Match length	77
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	52499
Seq. ID	uC-gmropic091d05b1
Method	BLASTX
NCBI GI	g1297187
BLAST score	265
E value	2.0e-23
Match length	69
% identity	65
NCBI Description	(U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No.	52500
Seq. ID	uC-gmropic093a12b1
Method	BLASTX
NCBI GI	g3292823
BLAST score	263
E value	6.0e-23
Match length	102
% identity	49
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	52501
Seq. ID	uC-gmropic093e11b1
Method	BLASTX
NCBI GI	g4406778
BLAST score	554
E value	5.0e-57
Match length	153
% identity	20
NCBI Description	(AC006532) putative brassinosteroid insensitive protein [Arabidopsis thaliana]

Seq. No.	52502
Seq. ID	uC-gmropic094g01b1
Method	BLASTN
NCBI GI	g218266

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BLAST score	334
E value	0.0e+00
Match length	410
% identity	98
NCBI Description	Glycine max mRNA for phosphoenolpyruvate carboxylase, complete cds >gi_2175011_dbj_E06829_E06829 cDNA encoding phosphoenolpyruvate carboxylase >gi_2176575_dbj_E08459_E08459 cDNA encoding phosphoenol pyruvate carboxylase

Seq. No.	52503
Seq. ID	uC-gmropic094h02b1
Method	BLASTX
NCBI GI	g4049353
BLAST score	155
E value	2.0e-10
Match length	81
% identity	48
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	52504
Seq. ID	uC-gmropic094h05b1
Method	BLASTX
NCBI GI	g1763230
BLAST score	166
E value	7.0e-12
Match length	45
% identity	69
NCBI Description	(U72145) 3-hydroxy-3-methylglutaryl coenzyme a reductase [Camptotheca acuminata]

Seq. No.	52505
Seq. ID	uC-gmropic096a09b1
Method	BLASTN
NCBI GI	g1326160
BLAST score	59
E value	2.0e-24
Match length	161
% identity	96
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	52506
Seq. ID	uC-gmropic096c06b1
Method	BLASTX
NCBI GI	g2494119
BLAST score	299
E value	4.0e-27
Match length	95
% identity	59
NCBI Description	(AC002376) EST gb_T04104 comes from this gene. [Arabidopsis thaliana]

Seq. No.	52507
Seq. ID	uC-gmropic096d04b1
Method	BLASTX
NCBI GI	g3850579
BLAST score	281

E value	4.0e-25
Match length	130
% identity	48
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an

Seq. No.	52508
Seq. ID	uC-gmropic096d05b1
Method	BLASTN
NCBI GI	g1125103
BLAST score	165
E value	9.0e-88
Match length	234
% identity	96
NCBI Description	Glycine max seed coat peroxidase isozyme (SPOD4.1) mRNA, partial cds

Seq. No.	52509
Seq. ID	uC-gmropic096d08b1
Method	BLASTX
NCBI GI	g4558664
BLAST score	191
E value	1.0e-14
Match length	118
% identity	11
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52510
Seq. ID	uC-gmropic096g01b1
Method	BLASTX
NCBI GI	g2191191
BLAST score	228
E value	8.0e-19
Match length	97
% identity	57
NCBI Description	(AF007271) A_TM021B04.14 gene product [Arabidopsis thaliana]

Seq. No.	52511
Seq. ID	uC-gmropic096h09b1
Method	BLASTX
NCBI GI	g3914361
BLAST score	146
E value	2.0e-09
Match length	111
% identity	33
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_2281951_emb_CAB06620_ (Z84822) phospholipase D [Nicotiana tabacum]

Seq. No.	52512
Seq. ID	uC-gmropic097c05b1
Method	BLASTX

NCBI GI	g478409
BLAST score	222
E value	2.0e-18
Match length	79
% identity	61
NCBI Description	peroxidase (EC 1.11.1.7), cationic - adzuki bean >gi_218328_dbj_BAA01950_ (D11337) peroxidase [Vigna angularis]

Seq. No.	52513
Seq. ID	uC-gmropic097e06b1
Method	BLASTX
NCBI GI	g2129771
BLAST score	238
E value	1.0e-20
Match length	72
% identity	65
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	52514
Seq. ID	uC-gmropic097e07b1
Method	BLASTX
NCBI GI	g2501494
BLAST score	411
E value	2.0e-40
Match length	117
% identity	64
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 5) >gi_542015_pir__S41951 UTP-glucose glucosyltransferase - cassava >gi_453249_emb_CAA54612_ (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	52515
Seq. ID	uC-gmropic097f06b1
Method	BLASTN
NCBI GI	g170065
BLAST score	205
E value	1.0e-112
Match length	264
% identity	18
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	52516
Seq. ID	uC-gmropic098b02b1
Method	BLASTX
NCBI GI	g1809127
BLAST score	345
E value	1.0e-32
Match length	88
% identity	72
NCBI Description	(U77674) terminal flower 1 [Arabidopsis thaliana]

>gi_2208929_dbj_BAA20483_ (D86932) terminal flower1 [Arabidopsis thaliana] >gi_2208931_dbj_BAA20484_ (D87130) terminal flower1 [Arabidopsis thaliana] >gi_2208933_dbj_BAA20485_ (D87519) terminal flower1 [Arabidopsis thaliana]

Seq. No.	52517
Seq. ID	uC-gmropic098d11b1
Method	BLASTX
NCBI GI	g1077378
BLAST score	346
E value	1.0e-32
Match length	135
% identity	22
NCBI Description	probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae) >gi_609371 (U19027) Ylr222cp [Saccharomyces cerevisiae]

Seq. No.	52518
Seq. ID	uC-gmropic098f09b1
Method	BLASTX
NCBI GI	g2795807
BLAST score	378
E value	3.0e-36
Match length	159
% identity	49
NCBI Description	(AC003674) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52519
Seq. ID	uC-gmropic099c04b1
Method	BLASTX
NCBI GI	g3176673
BLAST score	194
E value	8.0e-15
Match length	72
% identity	54
NCBI Description	(AC003671) Similar to serine/threonine kinase gb_Y12531 from Brassica oleracea. [Arabidopsis thaliana]

Seq. No.	52520
Seq. ID	uC-gmropic100c10b1
Method	BLASTX
NCBI GI	g2811029
BLAST score	526
E value	9.0e-54
Match length	136
% identity	77
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	52521
Seq. ID	uC-gmropic100e08b1
Method	BLASTX
NCBI GI	g4335735
BLAST score	326

E value 2.0e-30
Match length 97
% identity 62
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 52522
Seq. ID uC-gmropic100f11b1
Method BLASTX
NCBI GI g2344896
BLAST score 385
E value 3.0e-37
Match length 123
% identity 59
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No. 52523
Seq. ID uC-gmropic100g01b1
Method BLASTX
NCBI GI g2506139
BLAST score 391
E value 5.0e-38
Match length 118
% identity 60
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No. 52524
Seq. ID uC-gmropic101b05b1
Method BLASTX
NCBI GI g2895758
BLAST score 190
E value 2.0e-14
Match length 104
% identity 44
NCBI Description (AF045022) phosphatidic acid-preferring phospholipase A1 [Bos taurus]

Seq. No. 52525
Seq. ID uC-gmropic101c10b1
Method BLASTX
NCBI GI g4538926
BLAST score 519
E value 6.0e-53
Match length 125
% identity 77
NCBI Description (AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]

Seq. No. 52526
Seq. ID uC-gmropic102a02b1
Method BLASTX
NCBI GI g4559339
BLAST score 241
E value 4.0e-25
Match length 75
% identity 81

NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	52527
Seq. ID	uC-gmropic102f03b1
Method	BLASTX
NCBI GI	g3668089
BLAST score	311
E value	5.0e-29
Match length	81
% identity	75
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	52528
Seq. ID	uC-gmropic102g06b1
Method	BLASTX
NCBI GI	g3860247
BLAST score	274
E value	8.0e-25
Match length	64
% identity	80
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	52529
Seq. ID	uC-gmropic103a03b1
Method	BLASTX
NCBI GI	g3738306
BLAST score	257
E value	2.0e-22
Match length	89
% identity	56
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	52530
Seq. ID	uC-gmropic103b01b1
Method	BLASTX
NCBI GI	g2462822
BLAST score	277
E value	2.0e-24
Match length	142
% identity	19
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52531
Seq. ID	uC-gmropic103b03b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	286
E value	1.0e-25
Match length	84
% identity	63
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	52532
Seq. ID	uC-gmropic103e01b1
Method	BLASTN
NCBI GI	g255407

BLAST score	236
E value	1.0e-130
Match length	292
% identity	15
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	52533
Seq. ID	uC-gmropic103e04b1
Method	BLASTX
NCBI GI	g1617270
BLAST score	174
E value	4.0e-13
Match length	65
% identity	51
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	52534
Seq. ID	uC-gmropic103h05b1
Method	BLASTX
NCBI GI	g1362583
BLAST score	624
E value	2.0e-65
Match length	118
% identity	96
NCBI Description	beta-tubulin isotype I - nematode (Haemonchus contortus) >gi_897749_emb_CAA56353_ (X80047) tub1_cds [Haemonchus contortus]

Seq. No.	52535
Seq. ID	uC-gmropic104b12b1
Method	BLASTX
NCBI GI	g2342685
BLAST score	327
E value	1.0e-30
Match length	100
% identity	64
NCBI Description	(AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No.	52536
Seq. ID	uC-gmropic104f08b1
Method	BLASTX
NCBI GI	g2258317
BLAST score	183
E value	2.0e-13
Match length	135
% identity	47
NCBI Description	(AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]

Seq. No.	52537
Seq. ID	uC-gmropic104g01b1
Method	BLASTX
NCBI GI	g543959

BLAST score	245
E value	5.0e-21
Match length	74
% identity	62
NCBI Description	CYSTATHIONINE BETA-SYNTHASE (SERINE SULFHYDRASE) (BETA-THIONASE) >gi_388716 (L19501) cystathionine beta-synthase [Homo sapiens] >gi_558582_emb_CAA57656_ (X82166) cystathionine beta-synthase [Homo sapiens] >gi_1289362 (L14577) cystathionine beta-synthase [Homo sapiens] >gi_3776242 (AF042836) cystathionine beta-synthase major isoform [Homo sapiens] >gi_4557415_ref_NP_000062.1_pCBS_ cystathionine-beta-synthase

Seq. No.	52538
Seq. ID	uC-gmropic104g08b1
Method	BLASTN
NCBI GI	g255407
BLAST score	247
E value	1.0e-137
Match length	291
% identity	15
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	52539
Seq. ID	uC-gmropic104h08b1
Method	BLASTX
NCBI GI	g3885341
BLAST score	251
E value	2.0e-21
Match length	118
% identity	47
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	52540
Seq. ID	uC-gmropic105b01b1
Method	BLASTN
NCBI GI	g170065
BLAST score	235
E value	1.0e-129
Match length	299
% identity	19
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	52541
Seq. ID	uC-gmropic105d04b1
Method	BLASTX
NCBI GI	g3776559
BLAST score	358
E value	4.0e-34
Match length	125
% identity	58
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	52542
Seq. ID	uC-gmropic105e12b1
Method	BLASTX
NCBI GI	g2244907
BLAST score	177
E value	2.0e-13
Match length	68
% identity	51
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	52543
Seq. ID	uC-gmropic105g07b1
Method	BLASTX
NCBI GI	g3980413
BLAST score	169
E value	5.0e-12
Match length	111
% identity	41
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	52544
Seq. ID	uC-gmropic105h11b1
Method	BLASTX
NCBI GI	g3158476
BLAST score	254
E value	3.0e-22
Match length	57
% identity	88
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	52545
Seq. ID	uC-gmropic106c04b1
Method	BLASTX
NCBI GI	g2058454
BLAST score	533
E value	2.0e-54
Match length	128
% identity	80
NCBI Description	(U65390) CaMB-channel protein [Nicotiana tabacum]

Seq. No.	52546
Seq. ID	uC-gmropic106e07b1
Method	BLASTX
NCBI GI	g3242709
BLAST score	547
E value	4.0e-56
Match length	153
% identity	65
NCBI Description	(AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]

Seq. No.	52547
Seq. ID	uC-gmropic106g03b1

Method	BLASTX
NCBI GI	g3395432
BLAST score	241
E value	2.0e-20
Match length	56
% identity	77
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	52548
Seq. ID	uC-gmropic106g06b1
Method	BLASTN
NCBI GI	g18588
BLAST score	234
E value	1.0e-129
Match length	284
% identity	98
NCBI Description	Soybean gene 3 for chalcone synthetase protein

Seq. No.	52549
Seq. ID	uC-gmropic106h11b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	50
% identity	51
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	52550
Seq. ID	uC-gmropic107a06b1
Method	BLASTX
NCBI GI	g3522943
BLAST score	435
E value	4.0e-43
Match length	111
% identity	43
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	52551
Seq. ID	uC-gmropic107b02b1
Method	BLASTX
NCBI GI	g4115373
BLAST score	244
E value	1.0e-20
Match length	140
% identity	9
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	52552
Seq. ID	uC-gmropic107c12b1
Method	BLASTN
NCBI GI	g255407
BLAST score	109
E value	1.0e-54
Match length	153
% identity	31

NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	52553
Seq. ID	uC-gmropic107e04b1
Method	BLASTX
NCBI GI	g4432832
BLAST score	234
E value	1.0e-19
Match length	111
% identity	48
NCBI Description	(AC006283) similar to protein Htf9C [Arabidopsis thaliana]

Seq. No.	52554
Seq. ID	uC-gmropic107f12b1
Method	BLASTN
NCBI GI	g4220641
BLAST score	38
E value	4.0e-12
Match length	82
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	52555
Seq. ID	uC-gmropic107h02b1
Method	BLASTX
NCBI GI	g4099833
BLAST score	397
E value	1.0e-38
Match length	136
% identity	55
NCBI Description	(U90265) bifunctional nuclease [Zinnia elegans]

Seq. No.	52556
Seq. ID	uC-gmropic108c06b1
Method	BLASTX
NCBI GI	g3395431
BLAST score	215
E value	3.0e-17
Match length	73
% identity	55
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	52557
Seq. ID	uC-gmropic108d03b1
Method	BLASTX
NCBI GI	g2827556
BLAST score	272
E value	3.0e-24
Match length	88
% identity	60
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	52558
Seq. ID	uC-gmropic108g07b1

Method	BLASTX
NCBI GI	g3445212
BLAST score	258
E value	3.0e-22
Match length	78
% identity	67
NCBI Description	(AC004786) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	52559
Seq. ID	uC-gmropic109g10b1
Method	BLASTX
NCBI GI	g4378659
BLAST score	345
E value	2.0e-32
Match length	142
% identity	46
NCBI Description	(AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]

Seq. No.	52560
Seq. ID	uC-gmropic109h12b1
Method	BLASTX
NCBI GI	g4519673
BLAST score	476
E value	5.0e-48
Match length	116
% identity	26
NCBI Description	(AB017694) WREBP-2 [Nicotiana tabacum]

Seq. No.	52561
Seq. ID	uC-gmropic110b02b1
Method	BLASTN
NCBI GI	g255407
BLAST score	348
E value	0.0e+00
Match length	364
% identity	15
NCBI Description	repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No.	52562
Seq. ID	uC-gmropic110b04b1
Method	BLASTN
NCBI GI	g3982595
BLAST score	286
E value	1.0e-160
Match length	380
% identity	94
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	52563
Seq. ID	uC-gmropic110b06b1
Method	BLASTX
NCBI GI	g2960364
BLAST score	466

E value 1.0e-46
Match length 122
% identity 74
NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No. 52564
Seq. ID uC-gmropic110d02b1
Method BLASTN
NCBI GI g255407
BLAST score 376
E value 0.0e+00
Match length 384
% identity 14
NCBI Description repetitive proline-rich protein {cDNA clone 1A10-2} [Glycine max=soybeans, axes germinated for 31 hours, mRNA, 943 nt]

Seq. No. 52565
Seq. ID uC-gmropic111b04b1
Method BLASTX
NCBI GI g2136107
BLAST score 186
E value 6.0e-14
Match length 98
% identity 43
NCBI Description retinoblastoma protein binding protein RBQ-3 - human >gi_755750_emb_CAA59446_ (X85134) RB protein binding protein [Homo sapiens]

Seq. No. 52566
Seq. ID uC-gmropic111d08b1
Method BLASTX
NCBI GI g4335739
BLAST score 223
E value 4.0e-18
Match length 52
% identity 79
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 52567
Seq. ID uC-gmropic111e11b1
Method BLASTN
NCBI GI g18764
BLAST score 206
E value 1.0e-112
Match length 386
% identity 88
NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 52568
Seq. ID uC-gmropic111g03b1
Method BLASTX
NCBI GI g2623296
BLAST score 355
E value 1.0e-33
Match length 120

% identity	63
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52569
Seq. ID	uC-gmropic112a11b1
Method	BLASTN
NCBI GI	g170065
BLAST score	272
E value	1.0e-151
Match length	296
% identity	11
NCBI Description	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds

Seq. No.	52570
Seq. ID	uC-gmropic112d09b1
Method	BLASTX
NCBI GI	g3688187
BLAST score	330
E value	1.0e-30
Match length	70
% identity	81
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	52571
Seq. ID	uC-gmropic112g09b1
Method	BLASTX
NCBI GI	g3056593
BLAST score	260
E value	1.0e-22
Match length	107
% identity	48
NCBI Description	(AC004255) T1F9.14 [Arabidopsis thaliana]

Seq. No.	52572
Seq. ID	uC-gmropic113e12b1
Method	BLASTN
NCBI GI	g3982595
BLAST score	40
E value	9.0e-14
Match length	108
% identity	84
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	52573
Seq. ID	uC-gmropic114b01b1
Method	BLASTN
NCBI GI	g1675195
BLAST score	91
E value	1.0e-43
Match length	215
% identity	86
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	52574
Seq. ID	uC-gmropic115a07b1

Method	BLASTX
NCBI GI	g4455155
BLAST score	196
E value	3.0e-15
Match length	115
% identity	37
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No.	52575
Seq. ID	uC-gmropic115a10b1
Method	BLASTX
NCBI GI	g3021272
BLAST score	200
E value	2.0e-15
Match length	149
% identity	40
NCBI Description	(AL022347) serine /threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	52576
Seq. ID	uC-gmropic115b02b1
Method	BLASTX
NCBI GI	g3461844
BLAST score	331
E value	7.0e-31
Match length	131
% identity	51
NCBI Description	(AC005315) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52577
Seq. ID	uC-gmropic115d02b1
Method	BLASTX
NCBI GI	g2500354
BLAST score	155
E value	8.0e-11
Match length	27
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_ (AB001891) QM family protein [Solanum melongena]

Seq. No.	52578
Seq. ID	uC-gmropic117d11b1
Method	BLASTX
NCBI GI	g2392772
BLAST score	223
E value	8.0e-19
Match length	51
% identity	80
NCBI Description	(AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	52579
Seq. ID	uC-gmropic120d11b1
Method	BLASTX
NCBI GI	g2462762
BLAST score	339

E value	7.0e-32
Match length	121
% identity	57
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	52580
Seq. ID	uC-gmropic120h12b1
Method	BLASTN
NCBI GI	g170048
BLAST score	362
E value	0.0e+00
Match length	414
% identity	13
NCBI Description	Glycine max SbPRP1 gene encoding a proline-rich protein, complete cds

Seq. No.	52581
Seq. ID	uaw700660746.h1
Method	BLASTN
NCBI GI	g2282583
BLAST score	97
E value	2.0e-47
Match length	228
% identity	86
NCBI Description	Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds

Seq. No.	52582
Seq. ID	uaw700660755.h1
Method	BLASTX
NCBI GI	g2129626
BLAST score	146
E value	2.0e-09
Match length	93
% identity	49
NCBI Description	J-domain protein - Arabidopsis thaliana >gi_928936_emb_CAA89204_ (Z49238) J-domain protein [Arabidopsis thaliana] >gi_1585434_prf__2124427A diamide resistance gene [Arabidopsis thaliana]

Seq. No.	52583
Seq. ID	uaw700660787.h1
Method	BLASTX
NCBI GI	g2501612
BLAST score	157
E value	2.0e-22
Match length	91
% identity	52
NCBI Description	HYPOTHETICAL 89.8 KD PROTEIN YPL207W >gi_2133000_pir__S65226 probable membrane protein YPL207w - yeast (Saccharomyces cerevisiae) >gi_1370430_emb_CAA97922_ (Z73563) ORF YPL207w [Saccharomyces cerevisiae]

Seq. No.	52584
Seq. ID	uaw700660811.h1
Method	BLASTX

NCBI GI	g421960
BLAST score	187
E value	2.0e-28
Match length	90
% identity	76
NCBI Description	small nuclear ribonucleoprotein U2B'' - potato >gi_169589 (M72892) spliceosomal protein [Solanum tuberosum]

Seq. No.	52585
Seq. ID	uaw700660833.h1
Method	BLASTX
NCBI GI	g1168863
BLAST score	249
E value	2.0e-21
Match length	84
% identity	56
NCBI Description	CADMIUM INDUCED PROTEIN AS8 >gi_629507_pir__S47247 cadmium-induced protein - Arabidopsis thaliana >gi_534902_emb_CAA85363_ (Z36896) cadmium induced protein [Arabidopsis thaliana] >gi_2828282_emb_CAA16696.1_ (AL021687) cadmium-induced protein [Arabidopsis thaliana] >gi_2832634_emb_CAA16763_ (AL021711) cadmium-induced protein [Arabidopsis thaliana]

Seq. No.	52586
Seq. ID	uaw700660837.h1
Method	BLASTX
NCBI GI	g4049345
BLAST score	348
E value	4.0e-33
Match length	107
% identity	20
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	52587
Seq. ID	uaw700660840.h1
Method	BLASTX
NCBI GI	g130720
BLAST score	202
E value	6.0e-16
Match length	87
% identity	47
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi_500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	52588
Seq. ID	uaw700660851.h1
Method	BLASTN
NCBI GI	g18737
BLAST score	285
E value	1.0e-159
Match length	333
% identity	21

NCBI Description	Glycine max RPRP3 gene for repetitive proline-rich protein

Seq. No.	52589
Seq. ID	uaw700660868.h1
Method	BLASTX
NCBI GI	g731758
BLAST score	170
E value	3.0e-12
Match length	106
% identity	41
NCBI Description	HYPOTHETICAL 67.8 KD PROTEIN IN IKI1-ERG9 INTERGENIC REGION >gi_626691_pir__S46687 hypothetical protein YHR188c - yeast (Saccharomyces cerevisiae) >gi_458939 (U00030) Yhr188cp [Saccharomyces cerevisiae]

Seq. No.	52590
Seq. ID	uaw700660911.h1
Method	BLASTX
NCBI GI	g4325338
BLAST score	409
E value	3.0e-40
Match length	110
% identity	67
NCBI Description	(AF128392) No definition line found [Arabidopsis thaliana]

Seq. No.	52591
Seq. ID	uaw700660928.h1
Method	BLASTX
NCBI GI	g2160173
BLAST score	139
E value	1.0e-08
Match length	106
% identity	6
NCBI Description	(AC000132) Similar to N. tabacum salt-inducible protein (gb_U08285). [Arabidopsis thaliana]

Seq. No.	52592
Seq. ID	uaw700660947.h1
Method	BLASTN
NCBI GI	g169980
BLAST score	104
E value	2.0e-51
Match length	196
% identity	88
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	52593
Seq. ID	uaw700660963.h1
Method	BLASTX
NCBI GI	g1351271
BLAST score	118
E value	5.0e-11
Match length	74
% identity	53
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312

(L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	52594
Seq. ID	uaw700661004.h1
Method	BLASTN
NCBI GI	g1495767
BLAST score	126
E value	2.0e-64
Match length	266
% identity	87
NCBI Description	P.sativum mRNA for 110 kD chloroplast inner envelope protein IEP110

Seq. No.	52595
Seq. ID	uaw700661033.h1
Method	BLASTX
NCBI GI	g3036840
BLAST score	189
E value	2.0e-14
Match length	88
% identity	39
NCBI Description	(AJ222967) cystinosin [Homo sapiens] >gi_3036851_emb_CAA75882_ (Y15924) cystinosin [Homo sapiens]

Seq. No.	52596
Seq. ID	uaw700661163.h1
Method	BLASTX
NCBI GI	g136057
BLAST score	312
E value	8.0e-29
Match length	92
% identity	66
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]

Seq. No.	52597
Seq. ID	uaw700661172.h1
Method	BLASTX
NCBI GI	g3287695
BLAST score	192
E value	9.0e-15
Match length	97
% identity	45
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	52598
Seq. ID	uaw700661263.h1
Method	BLASTX
NCBI GI	g2623311
BLAST score	171
E value	1.0e-12

Match length	38
% identity	89
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3402720 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	52599
Seq. ID	uaw700661285.h1
Method	BLASTN
NCBI GI	g1724101
BLAST score	56
E value	6.0e-23
Match length	128
% identity	86
NCBI Description	Mesembryanthemum crystallinum S-adenosyl-L-homocystein hydrolase mRNA, complete cds

Seq. No.	52600
Seq. ID	uaw700661286.h1
Method	BLASTN
NCBI GI	g169040
BLAST score	35
E value	2.0e-10
Match length	102
% identity	84
NCBI Description	Pea 1-aminocyclopropane-1-carboxylate oxidase mRNA, complete cds

Seq. No.	52601
Seq. ID	uaw700661307.h1
Method	BLASTN
NCBI GI	g3021337
BLAST score	136
E value	2.0e-70
Match length	276
% identity	87
NCBI Description	Cicer arietinum mRNA for cytosolic fructose-1,6-bisphosphate aldolase

Seq. No.	52602
Seq. ID	uaw700661328.h1
Method	BLASTX
NCBI GI	g2119719
BLAST score	138
E value	1.0e-18
Match length	52
% identity	94
NCBI Description	heat-shock cognate protein 70-3 - tomato >gi_762844 (L41253) Hsc70 [Lycopersicon esculentum]

Seq. No.	52603
Seq. ID	uaw700661382.h1
Method	BLASTN
NCBI GI	g2970554
BLAST score	260
E value	1.0e-144
Match length	331

% identity	98
NCBI Description	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds

Seq. No.	52604
Seq. ID	uaw700661387.h1
Method	BLASTN
NCBI GI	g2920665
BLAST score	258
E value	1.0e-143
Match length	266
% identity	99
NCBI Description	Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No.	52605
Seq. ID	uaw700661450.h1
Method	BLASTN
NCBI GI	g3046853
BLAST score	33
E value	2.0e-09
Match length	79
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	52606
Seq. ID	uaw700661482.h1
Method	BLASTX
NCBI GI	g2443886
BLAST score	398
E value	6.0e-39
Match length	97
% identity	81
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	52607
Seq. ID	uaw700661586.h1
Method	BLASTN
NCBI GI	g304108
BLAST score	34
E value	8.0e-10
Match length	106
% identity	83
NCBI Description	Arabidopsis thaliana poly(A)-binding protein mRNA, complete cds

Seq. No.	52608
Seq. ID	uaw700661752.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	93
E value	4.0e-45
Match length	177
% identity	92
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	52609
Seq. ID	uaw700661812.h1
Method	BLASTX
NCBI GI	g2492506
BLAST score	200
E value	5.0e-18
Match length	69
% identity	68
NCBI Description	PEROXISOME ASSEMBLY FACTOR-2 (PAF-2) (PEROXISOMAL-TYPE ATPASE 1) (PEROXIN-6) >gi_2135899_pir__S71090 peroxisome biogenesis disorder group 4 protein PXAAA1 - human >gi_1354753 (U56602) Pxaaa1p [Homo sapiens]

Seq. No.	52610
Seq. ID	uaw700661887.h1
Method	BLASTX
NCBI GI	g2146746
BLAST score	137
E value	1.0e-08
Match length	51
% identity	53
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	52611
Seq. ID	uaw700661923.h1
Method	BLASTX
NCBI GI	g2213588
BLAST score	188
E value	2.0e-16
Match length	67
% identity	20
NCBI Description	(AC000348) T7N9.8 [Arabidopsis thaliana]

Seq. No.	52612
Seq. ID	uaw700661980.h1
Method	BLASTX
NCBI GI	g728906
BLAST score	255
E value	4.0e-22
Match length	63
% identity	76
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 5 >gi_1077722_pir__S50669 hypothetical protein YER166w - yeast (Saccharomyces cerevisiae) >gi_603407 (U18922) Yer166wp [Saccharomyces cerevisiae]

Seq. No.	52613
Seq. ID	uaw700662025.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	118
E value	6.0e-60
Match length	242
% identity	88
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	52614
Seq. ID	uaw700662059.h1
Method	BLASTX
NCBI GI	g1071913
BLAST score	184
E value	8.0e-14
Match length	76
% identity	55
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	52615
Seq. ID	uaw700662064.h1
Method	BLASTX
NCBI GI	g2961386
BLAST score	169
E value	4.0e-12
Match length	100
% identity	41
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	52616
Seq. ID	uaw700662075.h1
Method	BLASTX
NCBI GI	g3402758
BLAST score	168
E value	2.0e-22
Match length	111
% identity	58
NCBI Description	(AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	52617
Seq. ID	uaw700662091.h1
Method	BLASTX
NCBI GI	g3831469
BLAST score	333
E value	3.0e-31
Match length	108
% identity	55
NCBI Description	(AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52618
Seq. ID	uaw700662226.h1
Method	BLASTX
NCBI GI	g4263526
BLAST score	147
E value	2.0e-09
Match length	68
% identity	41
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52619
Seq. ID	uaw700662302.h1
Method	BLASTX
NCBI GI	g3047117

BLAST score	231
E value	9.0e-20
Match length	49
% identity	86
NCBI Description	(AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No.	52620
Seq. ID	uaw700662372.h1
Method	BLASTX
NCBI GI	g3540206
BLAST score	242
E value	5.0e-21
Match length	49
% identity	86
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	52621
Seq. ID	uaw700662401.h1
Method	BLASTX
NCBI GI	g2190259
BLAST score	214
E value	1.0e-17
Match length	60
% identity	67
NCBI Description	(D86385) A-type cyclin [Catharanthus roseus]

Seq. No.	52622
Seq. ID	uaw700662410.h1
Method	BLASTX
NCBI GI	g2827656
BLAST score	225
E value	6.0e-19
Match length	67
% identity	64
NCBI Description	(AL021637) DAG-like protein [Arabidopsis thaliana]

Seq. No.	52623
Seq. ID	uaw700662434.h1
Method	BLASTN
NCBI GI	g4115336
BLAST score	92
E value	2.0e-44
Match length	245
% identity	23
NCBI Description	Pisum sativum (Alaska) ubiquitin (PUB3) gene, complete cds

Seq. No.	52624
Seq. ID	uaw700662721.h1
Method	BLASTX
NCBI GI	g3482926
BLAST score	257
E value	2.0e-22
Match length	98
% identity	54
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	52625
Seq. ID	uaw700662768.h1
Method	BLASTX
NCBI GI	g3152566
BLAST score	353
E value	1.0e-33
Match length	107
% identity	62
NCBI Description	(AC002986) Similar to hypothetical protein YLR002c, gb_Z7314 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No.	52626
Seq. ID	uaw700662917.h1
Method	BLASTX
NCBI GI	g3461813
BLAST score	340
E value	2.0e-32
Match length	76
% identity	83
NCBI Description	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]

Seq. No.	52627
Seq. ID	uaw700663189.h1
Method	BLASTX
NCBI GI	g4102839
BLAST score	316
E value	1.0e-29
Match length	76
% identity	75
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	52628
Seq. ID	uaw700663311.h1
Method	BLASTX
NCBI GI	g4539327
BLAST score	279
E value	3.0e-25
Match length	85
% identity	66
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	52629
Seq. ID	uaw700663335.h1
Method	BLASTX
NCBI GI	g1449179
BLAST score	285
E value	7.0e-26
Match length	73
% identity	77
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	52630
Seq. ID	uaw700663379.h1
Method	BLASTX

NCBI GI	g3548808
BLAST score	334
E value	1.0e-31
Match length	82
% identity	72
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	52631
Seq. ID	uaw700663563.h1
Method	BLASTN
NCBI GI	g22635
BLAST score	103
E value	2.0e-51
Match length	115
% identity	97
NCBI Description	P.vulgaris mRNA for 70 kD heat shock protein

Seq. No.	52632
Seq. ID	uaw700663577.h1
Method	BLASTN
NCBI GI	g414831
BLAST score	82
E value	2.0e-38
Match length	207
% identity	92
NCBI Description	Glycine max (Rab1p) mRNA, complete cds

Seq. No.	52633
Seq. ID	uaw700663615.h1
Method	BLASTX
NCBI GI	g2245038
BLAST score	154
E value	4.0e-13
Match length	84
% identity	45
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52634
Seq. ID	uaw700663619.h1
Method	BLASTX
NCBI GI	g1943751
BLAST score	320
E value	6.0e-30
Match length	87
% identity	69
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	52635
Seq. ID	uaw700663652.h1
Method	BLASTN
NCBI GI	g3986749
BLAST score	96
E value	9.0e-47
Match length	215
% identity	92

NCBI Description	Hevea brasiliensis serine/threonine protein phosphatase type 2A (PP2A) mRNA, complete cds

Seq. No.	52636
Seq. ID	uaw700663774.h1
Method	BLASTX
NCBI GI	g2160161
BLAST score	161
E value	2.0e-11
Match length	81
% identity	5
NCBI Description	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]

Seq. No.	52637
Seq. ID	uaw700663842.h1
Method	BLASTN
NCBI GI	g1370149
BLAST score	90
E value	3.0e-43
Match length	126
% identity	93
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAB11E

Seq. No.	52638
Seq. ID	uaw700663868.h1
Method	BLASTX
NCBI GI	g4512613
BLAST score	191
E value	6.0e-15
Match length	80
% identity	53
NCBI Description	(AC004793) F28K20.12 [Arabidopsis thaliana]

Seq. No.	52639
Seq. ID	uaw700663888.h1
Method	BLASTX
NCBI GI	g2739371
BLAST score	303
E value	4.0e-28
Match length	80
% identity	72
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	52640
Seq. ID	uaw700663896.h1
Method	BLASTX
NCBI GI	g4417306
BLAST score	157
E value	6.0e-11
Match length	67
% identity	34
NCBI Description	(AC006446) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]

Seq. No.	52641
Seq. ID	uaw700664253.h1
Method	BLASTX

NCBI GI	g4220519
BLAST score	329
E value	4.0e-31
Match length	71
% identity	87
NCBI Description	(AL035356) putative protein binding protein [Arabidopsis thaliana]

Seq. No.	52642
Seq. ID	uaw700664284.h1
Method	BLASTX
NCBI GI	g4432846
BLAST score	146
E value	1.0e-09
Match length	74
% identity	53
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	52643
Seq. ID	uaw700664285.h1
Method	BLASTX
NCBI GI	g3327394
BLAST score	301
E value	7.0e-28
Match length	79
% identity	68
NCBI Description	(AC004483) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	52644
Seq. ID	uaw700664332.h1
Method	BLASTN
NCBI GI	g3832511
BLAST score	112
E value	3.0e-56
Match length	248
% identity	86
NCBI Description	Astragalus membranaceus granule-bound glycogen (starch) synthase mRNA, complete cds

Seq. No.	52645
Seq. ID	uaw700664453.h1
Method	BLASTX
NCBI GI	g3258571
BLAST score	236
E value	4.0e-20
Match length	70
% identity	69
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	52646
Seq. ID	uaw700664461.h1
Method	BLASTX
NCBI GI	g3036795
BLAST score	151
E value	1.0e-13
Match length	65
% identity	72

NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805857_emb_CAA21477_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	52647
Seq. ID	uaw700664515.h1
Method	BLASTX
NCBI GI	g2827519
BLAST score	190
E value	9.0e-15
Match length	38
% identity	79
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	52648
Seq. ID	uaw700664523.h1
Method	BLASTX
NCBI GI	g3283026
BLAST score	201
E value	5.0e-16
Match length	83
% identity	43
NCBI Description	(AF051562) putative transposase [Arabidopsis thaliana]

Seq. No.	52649
Seq. ID	uaw700664555.h1
Method	BLASTN
NCBI GI	g3599418
BLAST score	101
E value	9.0e-50
Match length	178
% identity	89
NCBI Description	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	52650
Seq. ID	uaw700664559.h1
Method	BLASTX
NCBI GI	g4455323
BLAST score	295
E value	3.0e-27
Match length	67
% identity	84
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	52651
Seq. ID	uaw700664613.h1
Method	BLASTX
NCBI GI	g1352439
BLAST score	167
E value	7.0e-21
Match length	86
% identity	67
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1008881 (L47221) eukaryotic initiation factor 5 [Phaseolus vulgaris]

Seq. No.	52652
Seq. ID	uaw700664723.h1
Method	BLASTX
NCBI GI	g1946355
BLAST score	321
E value	4.0e-30
Match length	85
% identity	73
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	52653
Seq. ID	uaw700664746.h1
Method	BLASTX
NCBI GI	g531389
BLAST score	205
E value	2.0e-16
Match length	73
% identity	49
NCBI Description	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq. No.	52654
Seq. ID	uaw700664790.h1
Method	BLASTX
NCBI GI	g3548806
BLAST score	296
E value	2.0e-27
Match length	80
% identity	75
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	52655
Seq. ID	uaw700664914.h1
Method	BLASTX
NCBI GI	g1532169
BLAST score	155
E value	1.0e-10
Match length	65
% identity	49
NCBI Description	(U63815) similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]

Seq. No.	52656
Seq. ID	uaw700665053.h1
Method	BLASTX
NCBI GI	g2464879
BLAST score	164
E value	8.0e-12
Match length	46
% identity	67
NCBI Description	(Z99707) caltractin-like protein [Arabidopsis thaliana]

Seq. No. 52657

Seq. ID	uaw700665064.h1
Method	BLASTX
NCBI GI	g3273243
BLAST score	212
E value	2.0e-17
Match length	44
% identity	50
NCBI Description	(AB004660) NLS receptor [Oryza sativa] >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]

Seq. No.	52658
Seq. ID	uaw700665078.h1
Method	BLASTX
NCBI GI	g4239845
BLAST score	305
E value	3.0e-28
Match length	79
% identity	66
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	52659
Seq. ID	uaw700665108.h1
Method	BLASTN
NCBI GI	g20355
BLAST score	53
E value	4.0e-21
Match length	65
% identity	95
NCBI Description	Rice rgp1 mRNA for a ras-related GTP-binding protein

Seq. No.	52660
Seq. ID	uaw700665134.h1
Method	BLASTN
NCBI GI	g310560
BLAST score	242
E value	1.0e-134
Match length	256
% identity	99
NCBI Description	Soybean ascorbate peroxidase mRNA, complete cds

Seq. No.	52661
Seq. ID	uaw700665138.h1
Method	BLASTX
NCBI GI	g3047119
BLAST score	234
E value	2.0e-21
Match length	80
% identity	64
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	52662
Seq. ID	uaw700665228.h1
Method	BLASTX
NCBI GI	g3128228
BLAST score	315
E value	2.0e-29

Match length	67
% identity	90
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	52663
Seq. ID	uaw700665239.h1
Method	BLASTX
NCBI GI	g2462828
BLAST score	249
E value	1.0e-21
Match length	85
% identity	53
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52664
Seq. ID	uaw700665255.h1
Method	BLASTX
NCBI GI	g3096920
BLAST score	144
E value	2.0e-09
Match length	82
% identity	34
NCBI Description	(AL023094) putative ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	52665
Seq. ID	uaw700665290.h1
Method	BLASTX
NCBI GI	g2493646
BLAST score	338
E value	2.0e-32
Match length	83
% identity	83
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_309559 (L21008) chaperonin 60 [Zea mays] >gi_309561 (L21006) mitochondrial chaperonin 60 [Zea mays]

Seq. No.	52666
Seq. ID	uaw700665301.h1
Method	BLASTX
NCBI GI	g3426041
BLAST score	163
E value	1.0e-11
Match length	43
% identity	67
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	52667
Seq. ID	uaw700665355.h1
Method	BLASTX
NCBI GI	g2252628
BLAST score	192
E value	6.0e-15
Match length	82
% identity	51

NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52668
Seq. ID	uaw700665359.h1
Method	BLASTX
NCBI GI	g4490736
BLAST score	216
E value	9.0e-18
Match length	85
% identity	44
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	52669
Seq. ID	uaw700665362.h1
Method	BLASTX
NCBI GI	g465602
BLAST score	272
E value	2.0e-24
Match length	86
% identity	64
NCBI Description	HYPOTHETICAL 32.9 KD PROTEIN IN NFO-FRUA INTERGENIC REGION >gi_405885 (U00007) yeiN [Escherichia coli] >gi_1788490 (AE000306) orf, hypothetical protein [Escherichia coli] >gi_744200_prf__2014253BL yeiN gene [Escherichia coli]

Seq. No.	52670
Seq. ID	uaw700665388.h1
Method	BLASTX
NCBI GI	g2388689
BLAST score	298
E value	2.0e-27
Match length	68
% identity	79
NCBI Description	(AF016633) GH1 protein [Glycine max]

Seq. No.	52671
Seq. ID	uaw700665393.h1
Method	BLASTX
NCBI GI	g4559333
BLAST score	205
E value	2.0e-16
Match length	83
% identity	37
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	52672
Seq. ID	uaw700665395.h1
Method	BLASTN
NCBI GI	g2285801
BLAST score	64
E value	1.0e-27
Match length	192
% identity	83
NCBI Description	Spinacia oleracea mRNA for 26S proteasome alpha subunit, complete cds

Seq. No.	52673

Seq. ID	uaw700665445.h1
Method	BLASTN
NCBI GI	g975703
BLAST score	48
E value	4.0e-18
Match length	134
% identity	52
NCBI Description	P.sativum GR gene

Seq. No.	52674
Seq. ID	uaw700665453.h1
Method	BLASTX
NCBI GI	g3367522
BLAST score	225
E value	4.0e-19
Match length	59
% identity	73
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	52675
Seq. ID	uaw700665513.h1
Method	BLASTN
NCBI GI	g644492
BLAST score	142
E value	3.0e-74
Match length	222
% identity	91
NCBI Description	Corn elongation factor 1alpha gene, complete cds

Seq. No.	52676
Seq. ID	uaw700665579.h1
Method	BLASTN
NCBI GI	g497416
BLAST score	128
E value	4.0e-66
Match length	140
% identity	99
NCBI Description	Glycine max Essex dehydrin-like protein mRNA, complete cds

Seq. No.	52677
Seq. ID	uaw700665591.h1
Method	BLASTX
NCBI GI	g729092
BLAST score	87
E value	7.0e-09
Match length	62
% identity	69
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) >gi_477484_pir__A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana >gi_304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	52678
Seq. ID	uaw700665596.h1
Method	BLASTN
NCBI GI	g710431

BLAST score	108
E value	6.0e-54
Match length	155
% identity	93
NCBI Description	Glycine max low molecular weight heat shock protein Hsp23.9 (Gmhsp23.9) mRNA, complete cds

Seq. No.	52679
Seq. ID	uaw700665655.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	248
E value	1.0e-137
Match length	252
% identity	100
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	52680
Seq. ID	uaw700665677.h1
Method	BLASTX
NCBI GI	g3894191
BLAST score	169
E value	2.0e-12
Match length	57
% identity	51
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	52681
Seq. ID	uaw700665705.h1
Method	BLASTX
NCBI GI	g2130080
BLAST score	165
E value	1.0e-13
Match length	63
% identity	70
NCBI Description	Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

Seq. No.	52682
Seq. ID	uaw700665728.h1
Method	BLASTX
NCBI GI	g1806144
BLAST score	160
E value	2.0e-22
Match length	88
% identity	69
NCBI Description	(X97316) cdc2MsE [Medicago sativa]

Seq. No.	52683
Seq. ID	uaw700665805.h1
Method	BLASTN
NCBI GI	g1732555
BLAST score	194
E value	1.0e-105

Match length	217
% identity	98
NCBI Description	Glycine max desiccation protective protein LEA5 (Lea5) mRNA, complete cds

Seq. No.	52684
Seq. ID	uaw700665820.h1
Method	BLASTX
NCBI GI	g3461817
BLAST score	188
E value	1.0e-15
Match length	54
% identity	72
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	52685
Seq. ID	uaw700665828.h1
Method	BLASTX
NCBI GI	g346287
BLAST score	131
E value	2.0e-16
Match length	76
% identity	64
NCBI Description	nucleolar 100K polymyositis-scleroderma protein - human >gi_35555_emb_CAA46904_ (X66113) PM/Scl 100kD nucleolar protein [Homo sapiens]

Seq. No.	52686
Seq. ID	uaw700665830.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	146
E value	1.0e-76
Match length	236
% identity	94
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	52687
Seq. ID	uaw700665833.h1
Method	BLASTX
NCBI GI	g4091008
BLAST score	144
E value	2.0e-09
Match length	33
% identity	82
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	52688
Seq. ID	uaw700665863.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	226
E value	1.0e-124
Match length	233
% identity	27
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	52689
Seq. ID	uaw700665901.h1
Method	BLASTN
NCBI GI	g3831448
BLAST score	50
E value	3.0e-19
Match length	229
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	52690
Seq. ID	uaw700665916.h1
Method	BLASTN
NCBI GI	g170053
BLAST score	156
E value	1.0e-82
Match length	163
% identity	99
NCBI Description	Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.	52691
Seq. ID	uaw700665930.h1
Method	BLASTX
NCBI GI	g585053
BLAST score	281
E value	2.0e-25
Match length	85
% identity	58
NCBI Description	MITOTIC CONTROL PROTEIN DIS3 >gi_283075_pir__A41944 mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) >gi_173381 (M74094) mitotic control protein [Schizosaccharomyces pombe] >gi_3650393_emb_CAA21102_ (AL031743) mitotic control protein dis3. [Schizosaccharomyces pombe]

Seq. No.	52692
Seq. ID	uaw700666017.h1
Method	BLASTX
NCBI GI	g4262222
BLAST score	296
E value	3.0e-27
Match length	80
% identity	65
NCBI Description	(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]

Seq. No.	52693
Seq. ID	uaw700666078.h1
Method	BLASTX
NCBI GI	g3287693
BLAST score	327
E value	5.0e-31
Match length	65
% identity	91
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis

thaliana]

Seq. No.	52694
Seq. ID	uaw700666092.h1
Method	BLASTX
NCBI GI	g4371279
BLAST score	203
E value	2.0e-16
Match length	71
% identity	61
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52695
Seq. ID	uaw700666110.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	141
E value	9.0e-74
Match length	141
% identity	88
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	52696
Seq. ID	uaw700666122.h1
Method	BLASTX
NCBI GI	g3128168
BLAST score	307
E value	2.0e-28
Match length	85
% identity	61
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	52697
Seq. ID	uaw700666157.h1
Method	BLASTX
NCBI GI	g2506277
BLAST score	329
E value	4.0e-31
Match length	81
% identity	79
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808 (U21139) chaperonin precursor [Pisum sativum]

Seq. No.	52698
Seq. ID	uaw700666220.h1
Method	BLASTX
NCBI GI	g3850999
BLAST score	224
E value	1.0e-18
Match length	66
% identity	70
NCBI Description	(AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]

Seq. No. 52699

Seq. ID	uaw700666231.h1
Method	BLASTN
NCBI GI	g2905771
BLAST score	144
E value	2.0e-75
Match length	156
% identity	98
NCBI Description	Glycine max glyceraldehyde-3 phosphate dehydrogenase (GAPDH) mRNA, partial cds

Seq. No.	52700
Seq. ID	uaw700666235.h1
Method	BLASTX
NCBI GI	g1170659
BLAST score	146
E value	7.0e-10
Match length	79
% identity	41
NCBI Description	KINESIN-LIKE PROTEIN KIF4 >gi_1083417_pir__A54803 microtubule-associated motor KIF4 - mouse >gi_563773_dbj_BAA02167_ (D12646) KIF4 [Mus musculus]

Seq. No.	52701
Seq. ID	uaw700666251.h1
Method	BLASTX
NCBI GI	g2894599
BLAST score	140
E value	7.0e-09
Match length	56
% identity	45
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	52702
Seq. ID	uaw700666294.h1
Method	BLASTN
NCBI GI	g2921511
BLAST score	88
E value	5.0e-42
Match length	168
% identity	88
NCBI Description	Fritillaria agrestis GF14 protein (GRF) mRNA, complete cds

Seq. No.	52703
Seq. ID	uaw700666321.h1
Method	BLASTX
NCBI GI	g1469888
BLAST score	218
E value	5.0e-18
Match length	89
% identity	51
NCBI Description	(D63487) The KIAA0153 gene product is related to a putative C.elegans gene encoded in cosmid F42A8. [Homo sapiens]

Seq. No.	52704
Seq. ID	uaw700666332.h1
Method	BLASTX
NCBI GI	g1931647

BLAST score	350
E value	2.0e-33
Match length	90
% identity	71
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	52705
Seq. ID	uaw700666405.h1
Method	BLASTX
NCBI GI	g4508077
BLAST score	384
E value	2.0e-37
Match length	87
% identity	80
NCBI Description	(AC005882) 62114 [Arabidopsis thaliana]

Seq. No.	52706
Seq. ID	uaw700666411.h1
Method	BLASTX
NCBI GI	g4490735
BLAST score	295
E value	6.0e-27
Match length	89
% identity	64
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	52707
Seq. ID	uaw700666427.h1
Method	BLASTN
NCBI GI	g20755
BLAST score	41
E value	6.0e-14
Match length	53
% identity	94
NCBI Description	P.sativum mRNA rab for ras-related GTP-binding protein

Seq. No.	52708
Seq. ID	uaw700666430.h1
Method	BLASTN
NCBI GI	g4519188
BLAST score	42
E value	2.0e-14
Match length	110
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	52709
Seq. ID	uaw700666450.h1
Method	BLASTN
NCBI GI	g257815
BLAST score	99
E value	5.0e-49
Match length	99
% identity	100
NCBI Description	chalcone synthase [soybeans, mRNA, 1119 nt]

Seq. No.	52710
Seq. ID	uaw700666462.h1
Method	BLASTX
NCBI GI	g4309744
BLAST score	350
E value	2.0e-33
Match length	84
% identity	77
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52711
Seq. ID	uaw700666479.h1
Method	BLASTN
NCBI GI	g170023
BLAST score	99
E value	5.0e-49
Match length	99
% identity	100
NCBI Description	Glycine max maturation-associated protein (MAT9) mRNA, complete cds

Seq. No.	52712
Seq. ID	uaw700666501.h1
Method	BLASTX
NCBI GI	g2498706
BLAST score	174
E value	5.0e-13
Match length	43
% identity	79
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	52713
Seq. ID	uaw700666577.h1
Method	BLASTX
NCBI GI	g4263522
BLAST score	172
E value	1.0e-12
Match length	76
% identity	46
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52714
Seq. ID	uaw700666615.h1
Method	BLASTN
NCBI GI	g732814
BLAST score	37
E value	1.0e-11
Match length	73
% identity	88
NCBI Description	L.esculentum LeMA-1 mRNA for putatve Mg-dependent ATPase

Seq. No.	52715
Seq. ID	uaw700666650.h1

Method	BLASTX
NCBI GI	g346287
BLAST score	180
E value	6.0e-16
Match length	68
% identity	59
NCBI Description	nucleolar 100K polymyositis-scleroderma protein - human >gi_35555_emb_CAA46904_ (X66113) PM/Scl 100kD nucleolar protein [Homo sapiens]

Seq. No.	52716
Seq. ID	uaw700666666.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	243
E value	1.0e-134
Match length	254
% identity	99
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	52717
Seq. ID	uaw700666670.h1
Method	BLASTX
NCBI GI	g1698582
BLAST score	172
E value	1.0e-26
Match length	83
% identity	78
NCBI Description	(U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No.	52718
Seq. ID	uaw700666713.h1
Method	BLASTN
NCBI GI	g511937
BLAST score	129
E value	2.0e-66
Match length	199
% identity	91
NCBI Description	Soybean mRNA for cysteine proteinase, complete cds

Seq. No.	52719
Seq. ID	uaw700666731.h1
Method	BLASTX
NCBI GI	g3337356
BLAST score	233
E value	8.0e-20
Match length	47
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	52720
Seq. ID	uaw700666751.h1
Method	BLASTX
NCBI GI	g3548806
BLAST score	151
E value	3.0e-10

Match length	77
% identity	51
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	52721
Seq. ID	uaw700666785.h1
Method	BLASTX
NCBI GI	g4263522
BLAST score	210
E value	4.0e-17
Match length	84
% identity	7
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52722
Seq. ID	uaw700666808.h1
Method	BLASTN
NCBI GI	g1638836
BLAST score	98
E value	6.0e-48
Match length	186
% identity	88
NCBI Description	H.vulgare mRNA for alpha-tubulin

Seq. No.	52723
Seq. ID	uaw700666815.h1
Method	BLASTX
NCBI GI	g2642438
BLAST score	139
E value	9.0e-09
Match length	84
% identity	38
NCBI Description	(AC002391) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	52724
Seq. ID	uaw700666869.h1
Method	BLASTX
NCBI GI	g4454469
BLAST score	295
E value	4.0e-27
Match length	73
% identity	73
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	52725
Seq. ID	uaw700666944.h1
Method	BLASTX
NCBI GI	g3292824
BLAST score	355
E value	4.0e-34
Match length	88
% identity	81
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	52726
Seq. ID	uaw700666951.h1

Method	BLASTX
NCBI GI	g3298551
BLAST score	140
E value	7.0e-09
Match length	82
% identity	7
NCBI Description	(AC004681) putative salt-inducible protein [Arabidopsis thaliana]

Seq. No.	52727
Seq. ID	uaw700666969.h1
Method	BLASTN
NCBI GI	g3128138
BLAST score	34
E value	9.0e-10
Match length	74
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	52728
Seq. ID	uaw700666984.h1
Method	BLASTN
NCBI GI	g3273826
BLAST score	116
E value	1.0e-58
Match length	184
% identity	93
NCBI Description	Glycine max nodule-enhanced malate dehydrogenase (Mdh) gene, complete cds

Seq. No.	52729
Seq. ID	uaw700667042.h1
Method	BLASTX
NCBI GI	g3142302
BLAST score	213
E value	2.0e-17
Match length	78
% identity	58
NCBI Description	(AC002411) Strong similarity to myosin heavy chain gb_Z34293 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	52730
Seq. ID	uaw700667083.h1
Method	BLASTX
NCBI GI	g3763916
BLAST score	360
E value	1.0e-34
Match length	85
% identity	80
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	52731
Seq. ID	uaw700667095.h1
Method	BLASTX

NCBI GI	g3785975
BLAST score	167
E value	5.0e-12
Match length	84
% identity	36
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52732
Seq. ID	ujr700646588.h1
Method	BLASTX
NCBI GI	g485515
BLAST score	250
E value	1.0e-43
Match length	89
% identity	96
NCBI Description	ADR6 protein - soybean >gi_296445_emb_CAA49340_ (X69639) auxin down regulated [Glycine max] >gi_2304955 (U64866) similar to ADR6 encoded by GenBank Accession Number X69639; aluminum induced [Glycine max]

Seq. No.	52733
Seq. ID	ujr700646668.h1
Method	BLASTX
NCBI GI	g2342742
BLAST score	205
E value	5.0e-29
Match length	91
% identity	46
NCBI Description	(AC002045) Unknown protein product CIT987SK-A-589H1_1 splice form 2 [Homo sapiens]

Seq. No.	52734
Seq. ID	ujr700646685.h1
Method	BLASTX
NCBI GI	g4220476
BLAST score	206
E value	1.0e-16
Match length	56
% identity	66
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	52735
Seq. ID	uxk700667104.h1
Method	BLASTN
NCBI GI	g497416
BLAST score	200
E value	1.0e-109
Match length	252
% identity	95
NCBI Description	Glycine max Essex dehydrin-like protein mRNA, complete cds

Seq. No.	52736
Seq. ID	uxk700667189.h1
Method	BLASTX
NCBI GI	g2827699
BLAST score	160
E value	3.0e-11

Match length 72
% identity 50
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 52737
Seq. ID uxk700667240.h1
Method BLASTN
NCBI GI g3869071
BLAST score 45
E value 3.0e-16
Match length 173
% identity 82
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No. 52738
Seq. ID uxk700667248.h1
Method BLASTN
NCBI GI g2970653
BLAST score 89
E value 2.0e-42
Match length 185
% identity 93
NCBI Description Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 52739
Seq. ID uxk700667544.h1
Method BLASTX
NCBI GI g1931655
BLAST score 232
E value 1.0e-19
Match length 84
% identity 58
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No. 52740
Seq. ID uxk700667552.h1
Method BLASTN
NCBI GI g2739005
BLAST score 94
E value 8.0e-46
Match length 114
% identity 96
NCBI Description Glycine max cytochrome P450 monooxygenase CYP93C1p (CYP93C1) mRNA, complete cds

Seq. No. 52741
Seq. ID uxk700667721.h1
Method BLASTX
NCBI GI g3600032
BLAST score 150
E value 4.0e-10
Match length 38
% identity 76
NCBI Description (AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:

ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	52742
Seq. ID	uxk700667729.h1
Method	BLASTN
NCBI GI	g18608
BLAST score	228
E value	1.0e-125
Match length	252
% identity	98
NCBI Description	Glycine max mRNA for glycinin >gi_2170693_dbj_E02462_E02462 cDNA encoding glycinine subunit A2B1a precursor

Seq. No.	52743
Seq. ID	uxk700667734.h1
Method	BLASTN
NCBI GI	g169928
BLAST score	249
E value	1.0e-138
Match length	249
% identity	100
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A

Seq. No.	52744
Seq. ID	uxk700667772.h1
Method	BLASTX
NCBI GI	g4038044
BLAST score	213
E value	2.0e-17
Match length	65
% identity	65
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana] >gi_4406788_gb_AAD20098_ (AC006532) unknown protein [Arabidopsis thaliana]

Seq. No.	52745
Seq. ID	uxk700667785.h1
Method	BLASTN
NCBI GI	g3449327
BLAST score	32
E value	1.0e-08
Match length	80
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	52746
Seq. ID	uxk700667788.h1
Method	BLASTX
NCBI GI	g2494116
BLAST score	274
E value	1.0e-24
Match length	71
% identity	68
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No.	52747
Seq. ID	uxk700667825.h1
Method	BLASTX
NCBI GI	g4335735
BLAST score	229
E value	2.0e-19
Match length	77
% identity	52
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52748
Seq. ID	uxk700667867.h1
Method	BLASTX
NCBI GI	g3927825
BLAST score	176
E value	4.0e-13
Match length	41
% identity	90
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	52749
Seq. ID	uxk700667869.h1
Method	BLASTX
NCBI GI	g3335349
BLAST score	155
E value	1.0e-10
Match length	42
% identity	71
NCBI Description	(AC004512) Similar to gb_U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb_T42908, gb_AA586170 and gb_AA395125 come from this gene. [Arabidopsis thaliana]

Seq. No.	52750
Seq. ID	uxk700667910.h1
Method	BLASTN
NCBI GI	g1794171
BLAST score	204
E value	1.0e-111
Match length	260
% identity	96
NCBI Description	Glycine max lipoxygenase-3 mRNA, complete cds

Seq. No.	52751
Seq. ID	uxk700667992.h1
Method	BLASTX
NCBI GI	g2995405
BLAST score	166
E value	6.0e-12
Match length	77
% identity	42
NCBI Description	(Y12432) polyprotein [Ananas comosus]

Seq. No.	52752
Seq. ID	uxk700668035.h1

Method	BLASTX
NCBI GI	g3355477
BLAST score	385
E value	1.0e-37
Match length	90
% identity	43
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	52753
Seq. ID	uxk700668042.h1
Method	BLASTX
NCBI GI	g4559368
BLAST score	218
E value	5.0e-18
Match length	50
% identity	84
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52754
Seq. ID	uxk700668102.h1
Method	BLASTN
NCBI GI	g432488
BLAST score	57
E value	2.0e-23
Match length	113
% identity	88
NCBI Description	Wheat initiation factor 1A (eIF-1A) mRNA

Seq. No.	52755
Seq. ID	uxk700668132.h1
Method	BLASTX
NCBI GI	g3914062
BLAST score	161
E value	1.0e-11
Match length	56
% identity	64
NCBI Description	DNA MISMATCH REPAIR PROTEIN MSH3 >gi_2980796_emb_CAA18172_ (AL022197) putative DNA mismatch repair protein [Arabidopsis thaliana]

Seq. No.	52756
Seq. ID	uxk700668278.h1
Method	BLASTN
NCBI GI	g1218003
BLAST score	129
E value	2.0e-66
Match length	254
% identity	91
NCBI Description	Glycine max dynamin-like protein SDL5A mRNA, complete cds

Seq. No.	52757
Seq. ID	uxk700668304.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	62
E value	2.0e-26

Match length 194
% identity 84
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No. 52758
Seq. ID uxk700668333.h1
Method BLASTX
NCBI GI g1076647
BLAST score 184
E value 4.0e-14
Match length 54
% identity 61
NCBI Description alcohol dehydrogenase 2 - garden petunia >gi_829592 (U25536) alcohol dehydrogenase-2 [Petunia hybrida]

Seq. No. 52759
Seq. ID uxk700668344.h1
Method BLASTX
NCBI GI g2909420
BLAST score 154
E value 8.0e-11
Match length 70
% identity 25
NCBI Description (AJ224518) LEA protein [Cicer arietinum]

Seq. No. 52760
Seq. ID uxk700668348.h1
Method BLASTN
NCBI GI g2570066
BLAST score 106
E value 1.0e-52
Match length 170
% identity 91
NCBI Description Pisum sativum mRNA for second sucrose synthase

Seq. No. 52761
Seq. ID uxk700668365.h1
Method BLASTN
NCBI GI g497416
BLAST score 96
E value 6.0e-47
Match length 164
% identity 90
NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds

Seq. No. 52762
Seq. ID uxk700668371.h1
Method BLASTX
NCBI GI g2129942
BLAST score 123
E value 4.0e-11
Match length 72
% identity 56
NCBI Description cathepsin B-like cysteine proteinase (EC 3.4.22.-) - Aztec tobacco

Seq. No. 52763

Seq. ID uxk700668404.h1
Method BLASTX
NCBI GI g2262105
BLAST score 199
E value 1.0e-31
Match length 87
% identity 70
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 52764
Seq. ID uxk700668412.h1
Method BLASTN
NCBI GI g2661020
BLAST score 249
E value 1.0e-138
Match length 256
% identity 100
NCBI Description Glycine max catalase (cat4) mRNA, complete cds

Seq. No. 52765
Seq. ID uxk700668413.h1
Method BLASTX
NCBI GI g4325342
BLAST score 114
E value 2.0e-09
Match length 65
% identity 52
NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 52766
Seq. ID uxk700668566.h1
Method BLASTX
NCBI GI g4006881
BLAST score 173
E value 1.0e-12
Match length 46
% identity 70
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 52767
Seq. ID uxk700668568.h1
Method BLASTN
NCBI GI g170007
BLAST score 138
E value 7.0e-72
Match length 222
% identity 91
NCBI Description Soybean 18 kD late embryogenesis abundant (Lea) protein mRNA, complete cds

Seq. No. 52768
Seq. ID uxk700668592.h1
Method BLASTX
NCBI GI g3913425
BLAST score 196
E value 5.0e-33
Match length 85

% identity	89
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	52769
Seq. ID	uxk700668671.h1
Method	BLASTX
NCBI GI	g2244759
BLAST score	328
E value	5.0e-31
Match length	69
% identity	87
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	52770
Seq. ID	uxk700668766.h1
Method	BLASTN
NCBI GI	g1218003
BLAST score	43
E value	4.0e-15
Match length	256
% identity	81
NCBI Description	Glycine max dynamin-like protein SDL5A mRNA, complete cds

Seq. No.	52771
Seq. ID	uxk700668829.h1
Method	BLASTN
NCBI GI	g170023
BLAST score	260
E value	1.0e-144
Match length	267
% identity	100
NCBI Description	Glycine max maturation-associated protein (MAT9) mRNA, complete cds

Seq. No.	52772
Seq. ID	uxk700668877.h1
Method	BLASTX
NCBI GI	g2827635
BLAST score	151
E value	2.0e-13
Match length	59
% identity	59
NCBI Description	(AL021636) predicted protein [Arabidopsis thaliana]

Seq. No.	52773
Seq. ID	uxk700668902.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	81
E value	9.0e-38
Match length	192
% identity	86
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	52774
Seq. ID	uxk700668980.h1
Method	BLASTN
NCBI GI	g18542
BLAST score	99
E value	8.0e-49
Match length	155
% identity	92
NCBI Description	Soybean Bg gene for basic 7S globulin

Seq. No.	52775
Seq. ID	uxk700669092.h1
Method	BLASTX
NCBI GI	g3150406
BLAST score	272
E value	2.0e-24
Match length	78
% identity	63
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	52776
Seq. ID	uxk700669123.h1
Method	BLASTX
NCBI GI	g4510347
BLAST score	194
E value	4.0e-15
Match length	47
% identity	83
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52777
Seq. ID	uxk700669131.h1
Method	BLASTX
NCBI GI	g3152618
BLAST score	252
E value	6.0e-22
Match length	94
% identity	59
NCBI Description	(AC004482) putative pectinesterase [Arabidopsis thaliana] >gi_3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	52778
Seq. ID	uxk700669174.h1
Method	BLASTX
NCBI GI	g2662469
BLAST score	311
E value	7.0e-29
Match length	84
% identity	73
NCBI Description	(AF034217) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	52779
Seq. ID	uxk700669182.h1
Method	BLASTX

NCBI GI	g3850588
BLAST score	203
E value	3.0e-16
Match length	86
% identity	55
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No.	52780
Seq. ID	uxk700669196.h1
Method	BLASTN
NCBI GI	g1326160
BLAST score	59
E value	1.0e-24
Match length	168
% identity	95
NCBI Description	Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No.	52781
Seq. ID	uxk700669220.h1
Method	BLASTN
NCBI GI	g736001
BLAST score	44
E value	6.0e-16
Match length	156
% identity	83
NCBI Description	G.soja (SH1) Gy5 mRNA for glycinin

Seq. No.	52782
Seq. ID	uxk700669244.h1
Method	BLASTN
NCBI GI	g170021
BLAST score	55
E value	2.0e-22
Match length	91
% identity	90
NCBI Description	Glycine max maturation-assocated protein (MAT1) mRNA, complete cds

Seq. No.	52783
Seq. ID	uxk700669274.h1
Method	BLASTX
NCBI GI	g1326161
BLAST score	191
E value	7.0e-15
Match length	65
% identity	75
NCBI Description	(U54703) dehydrin [Phaseolus vulgaris]

Seq. No.	52784
Seq. ID	uxk700669288.h1
Method	BLASTX
NCBI GI	g126078
BLAST score	227
E value	4.0e-19

Match length	61
% identity	42
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34) >gi_81554_pir__S04046 embryonic abundant protein gD-34 - upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea protein [Gossypium hirsutum] >gi_167385 (M19389) storage protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea D-34 gene [Saguinus oedipus]

Seq. No.	52785
Seq. ID	uxk700669373.h1
Method	BLASTX
NCBI GI	g1326161
BLAST score	199
E value	8.0e-16
Match length	62
% identity	76
NCBI Description	(U54703) dehydrin [Phaseolus vulgaris]

Seq. No.	52786
Seq. ID	uxk700669408.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	225
E value	1.0e-123
Match length	261
% identity	97
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	52787
Seq. ID	uxk700669423.h1
Method	BLASTN
NCBI GI	g1401239
BLAST score	104
E value	1.0e-51
Match length	164
% identity	91
NCBI Description	Glycine max 7S seed globulin precursor, mRNA, complete cds

Seq. No.	52788
Seq. ID	uxk700669443.h1
Method	BLASTN
NCBI GI	g515750
BLAST score	95
E value	4.0e-46
Match length	261
% identity	93
NCBI Description	Soybean phytochrome A (phyA) mRNA, complete cds

Seq. No.	52789
Seq. ID	uxk700669583.h1
Method	BLASTX
NCBI GI	g2623307
BLAST score	257
E value	6.0e-26
Match length	78
% identity	74

NCBI Description	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]

Seq. No.	52790
Seq. ID	uxk700669611.h1
Method	BLASTN
NCBI GI	g1498335
BLAST score	57
E value	2.0e-23
Match length	92
% identity	91
NCBI Description	Glycine max actin (Soy120) gene, partial cds

Seq. No.	52791
Seq. ID	uxk700669617.h1
Method	BLASTX
NCBI GI	g1946329
BLAST score	314
E value	3.0e-29
Match length	79
% identity	75
NCBI Description	(U69154) prohibitin [Nicotiana tabacum]

Seq. No.	52792
Seq. ID	uxk700669635.h1
Method	BLASTX
NCBI GI	g3953471
BLAST score	183
E value	6.0e-14
Match length	53
% identity	58
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	52793
Seq. ID	uxk700669649.h1
Method	BLASTX
NCBI GI	g4454471
BLAST score	187
E value	2.0e-14
Match length	47
% identity	70
NCBI Description	(AC006234) putative G protein coupled receptor [Arabidopsis thaliana]

Seq. No.	52794
Seq. ID	uxk700669656.h1
Method	BLASTX
NCBI GI	g2827714
BLAST score	161
E value	2.0e-11
Match length	76
% identity	47
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	52795
Seq. ID	uxk700669677.h1

Method	BLASTN
NCBI GI	g256426
BLAST score	217
E value	1.0e-119
Match length	251
% identity	97
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	52796
Seq. ID	uxk700669711.h1
Method	BLASTN
NCBI GI	g170019
BLAST score	198
E value	1.0e-107
Match length	233
% identity	97
NCBI Description	Soybean maturation protein (MAT1) gene, complete cds

Seq. No.	52797
Seq. ID	uxk700669731.h1
Method	BLASTX
NCBI GI	g2914706
BLAST score	218
E value	5.0e-18
Match length	67
% identity	66
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	52798
Seq. ID	uxk700669735.h1
Method	BLASTX
NCBI GI	g2979551
BLAST score	226
E value	5.0e-19
Match length	83
% identity	55
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	52799
Seq. ID	uxk700669737.h1
Method	BLASTN
NCBI GI	g18614
BLAST score	33
E value	1.0e-09
Match length	109
% identity	83
NCBI Description	Soybean mRNA for glycinin A1aBx precursor >gi_2170694_dbj_E02463_E02463 cDNA encoding glycinine subunit A1aB1b precursor

Seq. No.	52800
Seq. ID	uxk700669902.h1
Method	BLASTX
NCBI GI	g2827551
BLAST score	138

E value	1.0e-08
Match length	37
% identity	57
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	52801
Seq. ID	uxk700669910.h1
Method	BLASTX
NCBI GI	g2979552
BLAST score	150
E value	5.0e-10
Match length	85
% identity	40
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	52802
Seq. ID	uxk700669933.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	175
E value	7.0e-94
Match length	179
% identity	99
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	52803
Seq. ID	uxk700669990.h1
Method	BLASTX
NCBI GI	g2522228
BLAST score	245
E value	3.0e-21
Match length	81
% identity	59
NCBI Description	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq. No.	52804
Seq. ID	uxk700670004.h1
Method	BLASTX
NCBI GI	g2495155
BLAST score	280
E value	2.0e-25
Match length	77
% identity	70
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_1694926_dbj_BAA08910_ (D50407) glutamyl-tRNA reductase [Cucumis sativus]

Seq. No.	52805
Seq. ID	uxk700670010.h1
Method	BLASTN
NCBI GI	g18729
BLAST score	81
E value	8.0e-38
Match length	81
% identity	100
NCBI Description	Soybean (Glycine max) 18S ribosomal RNA

Seq. No.	52806
Seq. ID	uxk700670011.h1
Method	BLASTN
NCBI GI	g18729
BLAST score	77
E value	2.0e-35
Match length	81
% identity	99
NCBI Description	Soybean (Glycine max) 18S ribosomal RNA

Seq. No.	52807
Seq. ID	uxk700670042.h1
Method	BLASTN
NCBI GI	g18850
BLAST score	37
E value	1.0e-11
Match length	81
% identity	86
NCBI Description	H.lupulus (cv.Spalter) RNA (S10o) for 7S (SRP) RNA

Seq. No.	52808
Seq. ID	uxk700670046.h1
Method	BLASTX
NCBI GI	g3643598
BLAST score	165
E value	8.0e-12
Match length	46
% identity	63
NCBI Description	(AC005395) putative poly(A) polymerase [Arabidopsis thaliana]

Seq. No.	52809
Seq. ID	uxk700670156.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	207
E value	1.0e-113
Match length	215
% identity	99
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	52810
Seq. ID	uxk700670166.h1
Method	BLASTX
NCBI GI	g2494120
BLAST score	141
E value	5.0e-09
Match length	44
% identity	55
NCBI Description	(AC002376) Similar to Synechocystis integral membrane protein (gb_D64002). [Arabidopsis thaliana]

Seq. No.	52811
Seq. ID	uxk700670175.h1
Method	BLASTX
NCBI GI	g2959767
BLAST score	183

E value	5.0e-14
Match length	45
% identity	69
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	52812
Seq. ID	uxk700670176.h1
Method	BLASTN
NCBI GI	g862479
BLAST score	124
E value	2.0e-63
Match length	247
% identity	88
NCBI Description	Glycine max valosin-containing protein mRNA, complete cds

Seq. No.	52813
Seq. ID	uxk700670238.h1
Method	BLASTN
NCBI GI	g4206101
BLAST score	192
E value	1.0e-104
Match length	260
% identity	94
NCBI Description	Glycine max retroelement diaspora gag-pol polyprotein (gag-pol) pseudogene, partial sequence

Seq. No.	52814
Seq. ID	uxk700670328.h1
Method	BLASTN
NCBI GI	g2739005
BLAST score	183
E value	1.0e-98
Match length	267
% identity	92
NCBI Description	Glycine max cytochrome P450 monooxygenase CYP93C1p (CYP93C1) mRNA, complete cds

Seq. No.	52815
Seq. ID	uxk700670363.h1
Method	BLASTX
NCBI GI	g2435511
BLAST score	219
E value	4.0e-18
Match length	83
% identity	54
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	52816
Seq. ID	uxk700670367.h1
Method	BLASTX
NCBI GI	g3941322
BLAST score	360
E value	1.0e-34
Match length	86

% identity	77
NCBI Description	(AF041340) gamma-glutamylcysteine synthetase [Medicago truncatula]

Seq. No.	52817
Seq. ID	uxk700670450.h1
Method	BLASTX
NCBI GI	g4468812
BLAST score	150
E value	4.0e-10
Match length	54
% identity	61
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	52818
Seq. ID	uxk700670457.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	108
E value	4.0e-54
Match length	188
% identity	89
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	52819
Seq. ID	uxk700670519.h1
Method	BLASTN
NCBI GI	g18542
BLAST score	37
E value	1.0e-11
Match length	68
% identity	88
NCBI Description	Soybean Bg gene for basic 7S globulin

Seq. No.	52820
Seq. ID	uxk700670579.h1
Method	BLASTN
NCBI GI	g18749
BLAST score	166
E value	2.0e-88
Match length	250
% identity	91
NCBI Description	G.max mRNA for seed maturation polypeptide

Seq. No.	52821
Seq. ID	uxk700670588.h1
Method	BLASTN
NCBI GI	g170019
BLAST score	144
E value	2.0e-75
Match length	152
% identity	99
NCBI Description	Soybean maturation protein (MAT1) gene, complete cds

Seq. No.	52822
Seq. ID	uxk700670688.h1

Method	BLASTN
NCBI GI	g311697
BLAST score	53
E value	3.0e-21
Match length	61
% identity	97
NCBI Description	G.max Lea protein mRNA, complete CDS

Seq. No.	52823
Seq. ID	uxk700670705.h1
Method	BLASTX
NCBI GI	g4160346
BLAST score	111
E value	2.0e-10
Match length	69
% identity	51
NCBI Description	(AL035216) nucleolar protein involved in pre-rRNA processing [Schizosaccharomyces pombe]

Seq. No.	52824
Seq. ID	uxk700670716.h1
Method	BLASTX
NCBI GI	g2213594
BLAST score	155
E value	1.0e-10
Match length	64
% identity	49
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	52825
Seq. ID	uxk700670734.h1
Method	BLASTX
NCBI GI	g543063
BLAST score	149
E value	2.0e-18
Match length	86
% identity	48
NCBI Description	zinc-finger protein, BR140 - human

Seq. No.	52826
Seq. ID	uxk700670754.h1
Method	BLASTX
NCBI GI	g3980412
BLAST score	214
E value	1.0e-21
Match length	88
% identity	92
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	52827
Seq. ID	uxk700670756.h1
Method	BLASTX
NCBI GI	g3641252
BLAST score	204
E value	5.0e-27
Match length	83
% identity	77

NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	52828
Seq. ID	uxk700670872.h1
Method	BLASTX
NCBI GI	g3201626
BLAST score	130
E value	4.0e-15
Match length	73
% identity	51
NCBI Description	(AC004669) putative protein kinase MAP3K [Arabidopsis thaliana]

Seq. No.	52829
Seq. ID	uxk700670873.h1
Method	BLASTX
NCBI GI	g3150406
BLAST score	292
E value	1.0e-26
Match length	89
% identity	64
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	52830
Seq. ID	uxk700670940.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	153
E value	9.0e-81
Match length	251
% identity	95
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	52831
Seq. ID	uxk700670947.h1
Method	BLASTX
NCBI GI	g2245086
BLAST score	151
E value	2.0e-10
Match length	44
% identity	73
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52832
Seq. ID	uxk700670960.h1
Method	BLASTX
NCBI GI	g2980767
BLAST score	140
E value	6.0e-09
Match length	79
% identity	37
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	52833
Seq. ID	uxk700670980.h1

Method	BLASTN
NCBI GI	g3021337
BLAST score	94
E value	1.0e-45
Match length	234
% identity	85
NCBI Description	Cicer arietinum mRNA for cytosolic fructose-1,6-bisphosphate aldolase

Seq. No.	52834
Seq. ID	uxk700671013.h1
Method	BLASTN
NCBI GI	g170023
BLAST score	257
E value	1.0e-143
Match length	265
% identity	99
NCBI Description	Glycine max maturation-associated protein (MAT9) mRNA, complete cds

Seq. No.	52835
Seq. ID	uxk700671059.h1
Method	BLASTX
NCBI GI	g3695408
BLAST score	141
E value	5.0e-09
Match length	48
% identity	56
NCBI Description	(AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable wound-induced protein [Arabidopsis thaliana]

Seq. No.	52836
Seq. ID	uxk700671095.h1
Method	BLASTX
NCBI GI	g2462828
BLAST score	138
E value	8.0e-09
Match length	42
% identity	55
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52837
Seq. ID	uxk700671107.h1
Method	BLASTX
NCBI GI	g2252863
BLAST score	247
E value	2.0e-21
Match length	83
% identity	58
NCBI Description	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]

Seq. No.	52838
Seq. ID	uxk700671177.h1
Method	BLASTX

NCBI GI	g537404
BLAST score	364
E value	3.0e-35
Match length	77
% identity	84
NCBI Description	(D26537) WSI76 protein induced by water stress [Oryza sativa]

Seq. No.	52839
Seq. ID	uxk700671190.h1
Method	BLASTN
NCBI GI	g18542
BLAST score	95
E value	2.0e-46
Match length	151
% identity	92
NCBI Description	Soybean Bg gene for basic 7S globulin

Seq. No.	52840
Seq. ID	uxk700671210.h1
Method	BLASTN
NCBI GI	g18608
BLAST score	239
E value	1.0e-132
Match length	247
% identity	99
NCBI Description	Glycine max mRNA for glycinin >gi_2170693_dbj_E02462_E02462 cDNA encoding glycinine subunit A2B1a precursor

Seq. No.	52841
Seq. ID	uxk700671239.h1
Method	BLASTX
NCBI GI	g2959781
BLAST score	288
E value	5.0e-32
Match length	81
% identity	71
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	52842
Seq. ID	uxk700671305.h1
Method	BLASTN
NCBI GI	g1408321
BLAST score	201
E value	1.0e-109
Match length	213
% identity	99
NCBI Description	Glycine max CYP93A2 mRNA for cytochrome P-450, complete cds

Seq. No.	52843
Seq. ID	uxk700671390.h1
Method	BLASTX
NCBI GI	g1169689
BLAST score	138
E value	1.0e-08
Match length	82
% identity	39

NCBI Description	FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FKPA PRECURSOR (PPIASE) (ROTAMASE) >gi_2121124_pir__I65035 fkpA protein - Escherichia coli >gi_606281 (U18997) ORF_f270 [Escherichia coli] >gi_862300 (L28082) fkpA gene product [Escherichia coli] >gi_1789745 (AE000410) FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli]

Seq. No.	52844
Seq. ID	uxk700671479.h1
Method	BLASTX
NCBI GI	g2909422
BLAST score	143
E value	2.0e-09
Match length	45
% identity	35
NCBI Description	(AJ224519) LEA PROTEIN [Cicer arietinum]

Seq. No.	52845
Seq. ID	uxk700671491.h1
Method	BLASTN
NCBI GI	g2852444
BLAST score	37
E value	2.0e-11
Match length	97
% identity	85
NCBI Description	Salix bakko mRNA for SUI1 homolog, complete cds

Seq. No.	52846
Seq. ID	uxk700671639.h1
Method	BLASTN
NCBI GI	g256428
BLAST score	198
E value	1.0e-107
Match length	264
% identity	95
NCBI Description	KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and Forrest, mRNA, 1259 nt]

Seq. No.	52847
Seq. ID	uxk700671681.h1
Method	BLASTN
NCBI GI	g170007
BLAST score	179
E value	3.0e-96
Match length	215
% identity	96
NCBI Description	Soybean 18 kD late embryogenesis abundant (Lea) protein mRNA, complete cds

Seq. No.	52848
Seq. ID	uxk700671710.h1
Method	BLASTX
NCBI GI	g548900
BLAST score	143
E value	3.0e-11
Match length	71

% identity	51
NCBI Description	SUCROSE-BINDING PROTEIN PRECURSOR (SBP) >gi_322691_pir__JQ1730 62K sucrose-binding protein precursor - soybean >gi_170064 (L06038) glucose binding protein [Glycine max]

Seq. No.	52849
Seq. ID	uxk700671717.h1
Method	BLASTN
NCBI GI	g4455229
BLAST score	37
E value	1.0e-11
Match length	53
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	52850
Seq. ID	uxk700671720.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	183
E value	1.0e-98
Match length	273
% identity	92
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	52851
Seq. ID	uxk700671780.h1
Method	BLASTX
NCBI GI	g1914683
BLAST score	137
E value	3.0e-09
Match length	53
% identity	64
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	52852
Seq. ID	uxk700671789.h1
Method	BLASTN
NCBI GI	g170023
BLAST score	207
E value	1.0e-113
Match length	248
% identity	96
NCBI Description	Glycine max maturation-associated protein (MAT9) mRNA, complete cds

Seq. No.	52853
Seq. ID	uxk700671801.h1
Method	BLASTX
NCBI GI	g166949
BLAST score	138
E value	5.0e-18
Match length	86
% identity	53
NCBI Description	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea

americana]

Seq. No.	52854
Seq. ID	uxk700671829.h1
Method	BLASTX
NCBI GI	g4539335
BLAST score	122
E value	3.0e-13
Match length	77
% identity	52
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	52855
Seq. ID	uxk700671979.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	183
E value	1.0e-98
Match length	218
% identity	96
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	52856
Seq. ID	uxk700671989.h1
Method	BLASTX
NCBI GI	g3913425
BLAST score	302
E value	5.0e-36
Match length	81
% identity	78
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	52857
Seq. ID	uxk700672083.h1
Method	BLASTX
NCBI GI	g3914826
BLAST score	154
E value	5.0e-15
Match length	60
% identity	73
NCBI Description	DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR >gi_2330560_emb_CAA69972_ (Y08722) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_2330564_emb_CAA69717_ (Y08463) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_4115372 (AC005967) chloroplast single subunit DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No.	52858
Seq. ID	uxk700672139.h1
Method	BLASTX
NCBI GI	g4220480
BLAST score	158
E value	4.0e-11
Match length	78

% identity	15
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	52859
Seq. ID	uxk700672158.h1
Method	BLASTN
NCBI GI	g170023
BLAST score	230
E value	1.0e-127
Match length	237
% identity	100
NCBI Description	Glycine max maturation-associated protein (MAT9) mRNA, complete cds

Seq. No.	52860
Seq. ID	uxk700672217.h1
Method	BLASTX
NCBI GI	g2369766
BLAST score	224
E value	1.0e-18
Match length	65
% identity	66
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	52861
Seq. ID	uxk700672236.h1
Method	BLASTX
NCBI GI	g2245136
BLAST score	155
E value	1.0e-10
Match length	63
% identity	57
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]

Seq. No.	52862
Seq. ID	uxk700672273.h1
Method	BLASTN
NCBI GI	g2739005
BLAST score	73
E value	5.0e-33
Match length	219
% identity	97
NCBI Description	Glycine max cytochrome P450 monooxygenase CYP93C1p (CYP93C1) mRNA, complete cds

Seq. No.	52863
Seq. ID	uxk700672285.h1
Method	BLASTX
NCBI GI	g4033735
BLAST score	375
E value	2.0e-36
Match length	87
% identity	82
NCBI Description	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No.	52864

Seq. ID	uxk700672292.h1
Method	BLASTX
NCBI GI	g3402684
BLAST score	245
E value	3.0e-21
Match length	86
% identity	60
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52865
Seq. ID	uxk700672302.h1
Method	BLASTN
NCBI GI	g311697
BLAST score	154
E value	2.0e-81
Match length	228
% identity	96
NCBI Description	G.max Lea protein mRNA, complete CDS

Seq. No.	52866
Seq. ID	uxk700672323.h1
Method	BLASTN
NCBI GI	g4538990
BLAST score	65
E value	3.0e-28
Match length	117
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	52867
Seq. ID	uxk700672324.h1
Method	BLASTX
NCBI GI	g2809249
BLAST score	175
E value	6.0e-13
Match length	84
% identity	10
NCBI Description	(AC002560) F21B7.18 [Arabidopsis thaliana]

Seq. No.	52868
Seq. ID	uxk700672423.h1
Method	BLASTN
NCBI GI	g18542
BLAST score	166
E value	2.0e-88
Match length	237
% identity	100
NCBI Description	Soybean Bg gene for basic 7S globulin

Seq. No.	52869
Seq. ID	uxk700672443.h1
Method	BLASTX
NCBI GI	g2660674
BLAST score	263
E value	2.0e-23
Match length	74

% identity	72
NCBI Description	(AC002342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52870
Seq. ID	uxk700672450.h1
Method	BLASTX
NCBI GI	g996020
BLAST score	292
E value	1.0e-26
Match length	84
% identity	65
NCBI Description	(X91638) BRM protein [Gallus gallus]

Seq. No.	52871
Seq. ID	uxk700672511.h1
Method	BLASTX
NCBI GI	g1549379
BLAST score	218
E value	6.0e-18
Match length	63
% identity	62
NCBI Description	(U62737) putative protein [Synechococcus PCC7942]

Seq. No.	52872
Seq. ID	uxk700672516.h1
Method	BLASTX
NCBI GI	g1389897
BLAST score	245
E value	4.0e-21
Match length	91
% identity	58
NCBI Description	(U59626) LEA protein [Glycine max]

Seq. No.	52873
Seq. ID	uxk700672518.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	241
E value	1.0e-133
Match length	293
% identity	96
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	52874
Seq. ID	uxk700672547.h1
Method	BLASTX
NCBI GI	g4234955
BLAST score	101
E value	1.0e-10
Match length	90
% identity	46
NCBI Description	(AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]

Seq. No.	52875
Seq. ID	uxk700672579.h1
Method	BLASTN
NCBI GI	g169127

BLAST score	53
E value	2.0e-21
Match length	129
% identity	87
NCBI Description	Pisum sativum (clone pCLp) nuclear encoded precursor to chloroplast protein mRNA, complete cds

Seq. No.	52876
Seq. ID	uxk700672608.h1
Method	BLASTX
NCBI GI	g2809253
BLAST score	156
E value	1.0e-10
Match length	92
% identity	42
NCBI Description	(AC002560) F21B7.22 [Arabidopsis thaliana]

Seq. No.	52877
Seq. ID	uxk700672630.h1
Method	BLASTX
NCBI GI	g2244913
BLAST score	313
E value	4.0e-29
Match length	91
% identity	57
NCBI Description	(Z97339) similar to SEN1 protein - yeast [Arabidopsis thaliana]

Seq. No.	52878
Seq. ID	uxk700672649.h1
Method	BLASTX
NCBI GI	g1663537
BLAST score	184
E value	5.0e-14
Match length	71
% identity	51
NCBI Description	(U55803) disease resistance protein homolog [Glycine max]

Seq. No.	52879
Seq. ID	uxk700672743.h1
Method	BLASTN
NCBI GI	g3043427
BLAST score	44
E value	9.0e-16
Match length	60
% identity	93
NCBI Description	Cicer arietinum mRNA for 40S ribosomal protein S5

Seq. No.	52880
Seq. ID	uxk700672789.h1
Method	BLASTX
NCBI GI	g2244771
BLAST score	162
E value	2.0e-11
Match length	59
% identity	61
NCBI Description	(Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No.	52881
Seq. ID	uxk700672815.h1
Method	BLASTN
NCBI GI	g12543
BLAST score	84
E value	1.0e-39
Match length	164
% identity	88
NCBI Description	Cucurbita sp. pMCPN60-1 mRNA for chaperonin

Seq. No.	52882
Seq. ID	uxk700672962.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	104
E value	1.0e-51
Match length	207
% identity	88
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	52883
Seq. ID	uxk700672964.h1
Method	BLASTN
NCBI GI	g4218186
BLAST score	160
E value	5.0e-85
Match length	208
% identity	97
NCBI Description	Glycine max mRNA for leghemoglobin activating factor

Seq. No.	52884
Seq. ID	uxk700673043.h1
Method	BLASTX
NCBI GI	g4263775
BLAST score	181
E value	1.0e-13
Match length	40
% identity	82
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52885
Seq. ID	uxk700673077.h1
Method	BLASTX
NCBI GI	g1914683
BLAST score	145
E value	2.0e-09
Match length	80
% identity	53
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	52886
Seq. ID	uxk700673108.h1
Method	BLASTX
NCBI GI	g99737
BLAST score	163
E value	2.0e-11

Match length	51
% identity	61
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	52887
Seq. ID	uxk700673131.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	159
E value	2.0e-84
Match length	270
% identity	92
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	52888
Seq. ID	uxk700673136.h1
Method	BLASTX
NCBI GI	g3881836
BLAST score	214
E value	1.0e-29
Match length	97
% identity	72
NCBI Description	(Z78019) Similarity to Yeast LPG22P protein (TR:G1151240); cDNA EST EMBL:T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this ge

Seq. No.	52889
Seq. ID	uxk700673144.h1
Method	BLASTX
NCBI GI	g4006878
BLAST score	324
E value	2.0e-30
Match length	90
% identity	66
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	52890
Seq. ID	uxk700673224.h1
Method	BLASTX
NCBI GI	g1906830
BLAST score	183
E value	7.0e-17
Match length	53
% identity	94
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	52891
Seq. ID	uxk700673243.h1
Method	BLASTX
NCBI GI	g1705658
BLAST score	184
E value	4.0e-14
Match length	76

% identity	50
NCBI Description	CCAAT-BINDING FACTOR (CBF) >gi_107937_pir__A36368 transcription factor CBF, CCAAT-binding - human >gi_179969 (M37197) CCAAT-box-binding factor [Homo sapiens]

Seq. No.	52892
Seq. ID	uxk700673266.h1
Method	BLASTX
NCBI GI	g3130034
BLAST score	204
E value	2.0e-16
Match length	64
% identity	61
NCBI Description	(AL023534) dna repair protein rad13 [Schizosaccharomyces pombe]

Seq. No.	52893
Seq. ID	uxk700673310.h1
Method	BLASTN
NCBI GI	g18542
BLAST score	135
E value	5.0e-70
Match length	195
% identity	99
NCBI Description	Soybean Bg gene for basic 7S globulin

Seq. No.	52894
Seq. ID	uxk700673334.h1
Method	BLASTX
NCBI GI	g1708777
BLAST score	235
E value	4.0e-20
Match length	72
% identity	65
NCBI Description	(Z83202) potassium channel [Arabidopsis thaliana] >gi_3063705_emb_CAA18596.1_ (AL022537) potassium channel protein [Arabidopsis thaliana] >gi_4090537 (U73325) K+ inward rectifying channel protein [Arabidopsis thaliana] >gi_4098949 (U81239) K+ inward rectifying channel [Arabidopsis thaliana]

Seq. No.	52895
Seq. ID	uxk700673421.h1
Method	BLASTN
NCBI GI	g1438878
BLAST score	100
E value	1.0e-49
Match length	100
% identity	100
NCBI Description	Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No.	52896
Seq. ID	uxk700673431.h1
Method	BLASTN
NCBI GI	g2920665
BLAST score	119
E value	2.0e-60

Match length	135
% identity	97
NCBI Description	Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No.	52897
Seq. ID	uxk700673478.h1
Method	BLASTN
NCBI GI	g256426
BLAST score	243
E value	1.0e-134
Match length	251
% identity	99
NCBI Description	CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt]

Seq. No.	52898
Seq. ID	vwf700673557.h1
Method	BLASTX
NCBI GI	g2914703
BLAST score	139
E value	8.0e-09
Match length	39
% identity	67
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	52899
Seq. ID	vwf700673606.h1
Method	BLASTN
NCBI GI	g3021337
BLAST score	94
E value	1.0e-45
Match length	194
% identity	87
NCBI Description	Cicer arietinum mRNA for cytosolic fructose-1,6-bisphosphate aldolase

Seq. No.	52900
Seq. ID	vwf700673609.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	87
E value	2.0e-41
Match length	175
% identity	87
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	52901
Seq. ID	vwf700673619.h1
Method	BLASTX
NCBI GI	g2642156
BLAST score	256
E value	2.0e-22
Match length	82
% identity	59
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	52902
Seq. ID	vwf700673625.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	93
E value	5.0e-45
Match length	149
% identity	91
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	52903
Seq. ID	vwf700673639.h1
Method	BLASTN
NCBI GI	g169928
BLAST score	163
E value	9.0e-87
Match length	231
% identity	93
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A

Seq. No.	52904
Seq. ID	vwf700673641.h1
Method	BLASTN
NCBI GI	g3176097
BLAST score	83
E value	5.0e-39
Match length	250
% identity	84
NCBI Description	Medicago truncatula mRNA for annexin

Seq. No.	52905
Seq. ID	vwf700673653.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	73
E value	4.0e-33
Match length	233
% identity	83
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	52906
Seq. ID	vwf700673703.h1
Method	BLASTN
NCBI GI	g312559
BLAST score	69
E value	5.0e-31
Match length	113
% identity	90
NCBI Description	G.max 26S rRNA (partial)

Seq. No.	52907
Seq. ID	vwf700673732.h1
Method	BLASTN

NCBI GI	g18535
BLAST score	153
E value	9.0e-81
Match length	213
% identity	93
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52908
Seq. ID	vwf700673747.h1
Method	BLASTN
NCBI GI	g4191813
BLAST score	62
E value	6.0e-27
Match length	74
% identity	96
NCBI Description	Glycine max mRNA for alpha' subunit of beta-conglycinin, complete cds

Seq. No.	52909
Seq. ID	vwf700673754.h1
Method	BLASTX
NCBI GI	g3176669
BLAST score	238
E value	2.0e-20
Match length	82
% identity	67
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.	52910
Seq. ID	vwf700673785.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	98
E value	2.0e-48
Match length	122
% identity	95
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52911
Seq. ID	vwf700673811.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	59
E value	7.0e-25
Match length	166
% identity	84
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52912
Seq. ID	vwf700673828.h1
Method	BLASTX
NCBI GI	g3193300
BLAST score	201
E value	5.0e-16
Match length	92

% identity	50
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	52913
Seq. ID	vwf700673875.h1
Method	BLASTN
NCBI GI	g18638
BLAST score	266
E value	1.0e-148
Match length	270
% identity	100
NCBI Description	Soybean Gy3 gene for glycinin subunit G3

Seq. No.	52914
Seq. ID	vwf700673883.h1
Method	BLASTX
NCBI GI	g2499612
BLAST score	252
E value	4.0e-22
Match length	57
% identity	86
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (PMEK1) >gi_1076650_pir__S52989 mitogen-activated, extracelluar-regulated protein kinase 1 (EC 2.7.1.-) - garden petunia >gi_603871_emb_CAA58466_ (X83440) MAP/ERK kinase 1 [Petunia x hybrida]

Seq. No.	52915
Seq. ID	vwf700673904.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	214
E value	1.0e-117
Match length	214
% identity	100
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	52916
Seq. ID	vwf700673981.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	102
E value	2.0e-50
Match length	198
% identity	96
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52917
Seq. ID	vwf700673986.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	260
E value	3.0e-23
Match length	57
% identity	88
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	52918
Seq. ID	vwf700674025.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	187
E value	1.0e-101
Match length	187
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52919
Seq. ID	vwf700674030.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	191
E value	1.0e-103
Match length	191
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52920
Seq. ID	vwf700674044.h1
Method	BLASTX
NCBI GI	g1888357
BLAST score	291
E value	1.0e-26
Match length	74
% identity	74
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	52921
Seq. ID	vwf700674054.h1
Method	BLASTN
NCBI GI	g4539309
BLAST score	53
E value	4.0e-21
Match length	145
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	52922
Seq. ID	vwf700674149.h1
Method	BLASTN
NCBI GI	g2760168
BLAST score	58
E value	4.0e-24
Match length	174
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	52923
Seq. ID	vwf700674155.h1

Method	BLASTN
NCBI GI	g210811
BLAST score	111
E value	1.0e-55
Match length	246
% identity	87
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	52924
Seq. ID	vwf700674215.h1
Method	BLASTX
NCBI GI	g2262105
BLAST score	195
E value	3.0e-15
Match length	52
% identity	63
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	52925
Seq. ID	vwf700674240.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	249
E value	1.0e-138
Match length	277
% identity	92
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52926
Seq. ID	vwf700674261.h1
Method	BLASTN
NCBI GI	g4226055
BLAST score	269
E value	1.0e-150
Match length	277
% identity	99
NCBI Description	Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds

Seq. No.	52927
Seq. ID	vwf700674273.h1
Method	BLASTN
NCBI GI	g545762
BLAST score	49
E value	5.0e-19
Match length	53
% identity	98
NCBI Description	Eu4=urease {clone 5E5} [Glycine max=soybeans, cv. Dare, mid-maturation embryos, mRNA Partial, 540 nt]

Seq. No.	52928
Seq. ID	vwf700674329.h1
Method	BLASTN
NCBI GI	g4218188
BLAST score	45
E value	2.0e-16

Match length	85
% identity	88
NCBI Description	Glycine max cytosolic glutamine synthetase (gs15) gene promoter

Seq. No.	52929
Seq. ID	vwf700674332.h1
Method	BLASTX
NCBI GI	g2842490
BLAST score	303
E value	5.0e-28
Match length	72
% identity	79
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	52930
Seq. ID	vwf700674336.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	247
E value	1.0e-137
Match length	251
% identity	100
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No.	52931
Seq. ID	vwf700674385.h1
Method	BLASTN
NCBI GI	g169926
BLAST score	202
E value	1.0e-110
Match length	226
% identity	98
NCBI Description	Soybean beta-conglycinin-alpha subunit mRNA, 3' end

Seq. No.	52932
Seq. ID	vwf700674415.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	227
E value	1.0e-125
Match length	231
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52933
Seq. ID	vwf700674420.h1
Method	BLASTN
NCBI GI	g169928
BLAST score	264
E value	1.0e-147
Match length	268
% identity	100
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A

Seq. No.	52934
Seq. ID	vwf700674437.h1
Method	BLASTN
NCBI GI	g3819098
BLAST score	71
E value	8.0e-32
Match length	135
% identity	88
NCBI Description	Cicer arietinum mRNA for copper containing amine oxidase (DAO)

Seq. No.	52935
Seq. ID	vwf700674438.h1
Method	BLASTX
NCBI GI	g4567304
BLAST score	243
E value	6.0e-21
Match length	64
% identity	72
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	52936
Seq. ID	vwf700674446.h1
Method	BLASTX
NCBI GI	g4538927
BLAST score	167
E value	5.0e-12
Match length	59
% identity	66
NCBI Description	(AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No.	52937
Seq. ID	vwf700674461.h1
Method	BLASTN
NCBI GI	g18638
BLAST score	223
E value	1.0e-122
Match length	255
% identity	97
NCBI Description	Soybean Gy3 gene for glycinin subunit G3

Seq. No.	52938
Seq. ID	vwf700674506.h1
Method	BLASTX
NCBI GI	g465898
BLAST score	166
E value	6.0e-12
Match length	69
% identity	52
NCBI Description	HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III >gi_630692_pir__S44849 K12H4.8 protein - Caenorhabditis elegans >gi_289703 (L14331) homology with eukaryotic initiation factor-4A (eIF-4A) and E. coli Ribonuclease III; coded for by C. elegans cDNA GenBank:T02268; putative [Caenorhabditis elegans]

Seq. No.	52939

Seq. ID	vwf700674549.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	46
E value	3.0e-17
Match length	145
% identity	84
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52940
Seq. ID	vwf700674559.h1
Method	BLASTN
NCBI GI	g545762
BLAST score	79
E value	7.0e-37
Match length	155
% identity	92
NCBI Description	Eu4=urease {clone 5E5} [Glycine max=soybeans, cv. Dare, mid-maturation embryos, mRNA Partial, 540 nt]

Seq. No.	52941
Seq. ID	vwf700674565.h1
Method	BLASTN
NCBI GI	g256634
BLAST score	159
E value	1.0e-84
Match length	163
% identity	50
NCBI Description	KTi1=Kunitz trypsin inhibitor KTi1, KTi2=Kunitz trypsin inhibitor KTi2 [soybeans, Genomic, 3269 nt]

Seq. No.	52942
Seq. ID	vwf700674774.h1
Method	BLASTX
NCBI GI	g3445212
BLAST score	175
E value	6.0e-13
Match length	55
% identity	64
NCBI Description	(AC004786) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	52943
Seq. ID	vwf700674779.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	191
E value	1.0e-103
Match length	215
% identity	97
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	52944
Seq. ID	vwf700674780.h1
Method	BLASTN
NCBI GI	g169972

BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	52945
Seq. ID	vwf700674863.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	221
E value	1.0e-121
Match length	236
% identity	99
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	52946
Seq. ID	vwf700674871.h1
Method	BLASTN
NCBI GI	g166857
BLAST score	39
E value	5.0e-13
Match length	114
% identity	84
NCBI Description	Arabidopsis thaliana cytoplasmic ribosomal protein mRNA, complete cds

Seq. No.	52947
Seq. ID	vwf700674888.h1
Method	BLASTN
NCBI GI	g2605908
BLAST score	54
E value	5.0e-22
Match length	82
% identity	91
NCBI Description	Kosteletzkya virginica clone KVATP2 plasma membrane H+-ATPase mRNA, partial cds

Seq. No.	52948
Seq. ID	vwf700674890.h1
Method	BLASTN
NCBI GI	g170091
BLAST score	196
E value	1.0e-106
Match length	230
% identity	97
NCBI Description	Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No.	52949
Seq. ID	vwf700674895.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	191
E value	1.0e-103
Match length	198
% identity	99

NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin
Seq. No.	52950
Seq. ID	vwf700674919.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	133
E value	7.0e-69
Match length	233
% identity	89
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA
Seq. No.	52951
Seq. ID	vwf700674931.h1
Method	BLASTX
NCBI GI	g4140691
BLAST score	225
E value	8.0e-19
Match length	84
% identity	55
NCBI Description	(AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
Seq. No.	52952
Seq. ID	vwf700675010.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	174
E value	2.0e-93
Match length	216
% identity	33
NCBI Description	Glycine max gene for ubiquitin, complete cds
Seq. No.	52953
Seq. ID	vwf700675105.h1
Method	BLASTX
NCBI GI	g1778015
BLAST score	201
E value	5.0e-16
Match length	88
% identity	47
NCBI Description	(U59508) osmotic stress-induced proline dehydrogenase [Arabidopsis thaliana]
Seq. No.	52954
Seq. ID	vwf700675120.h1
Method	BLASTN
NCBI GI	g736001
BLAST score	166
E value	1.0e-88
Match length	222
% identity	94
NCBI Description	G.soja (SH1) Gy5 mRNA for glycinin
Seq. No.	52955
Seq. ID	vwf700675121.h1
Method	BLASTX

NCBI GI	g1707657
BLAST score	202
E value	3.0e-17
Match length	74
% identity	57
NCBI Description	(Z71640) DnaJ homologue [Pisum sativum]

Seq. No.	52956
Seq. ID	vwf700675178.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	170
E value	1.0e-12
Match length	43
% identity	77
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	52957
Seq. ID	vwf700675231.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	237
E value	1.0e-131
Match length	253
% identity	98
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	52958
Seq. ID	vwf700675281.h1
Method	BLASTN
NCBI GI	g1772305
BLAST score	242
E value	1.0e-134
Match length	246
% identity	100
NCBI Description	Glycine max mRNA for glycinin, complete cds

Seq. No.	52959
Seq. ID	vwf700675327.h1
Method	BLASTN
NCBI GI	g18620
BLAST score	113
E value	5.0e-57
Match length	205
% identity	89
NCBI Description	Soybean mRNA fragment for Gy(4) glycinin

Seq. No.	52960
Seq. ID	vwf700675386.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	178
E value	1.0e-95
Match length	246
% identity	93
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	52961
Seq. ID	vwf700675505.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	61
E value	6.0e-26
Match length	177
% identity	84
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52962
Seq. ID	vwf700675519.h1
Method	BLASTN
NCBI GI	g18556
BLAST score	61
E value	6.0e-26
Match length	123
% identity	91
NCBI Description	G.max DNA for Cab5

Seq. No.	52963
Seq. ID	vwf700675533.h1
Method	BLASTX
NCBI GI	g4580461
BLAST score	178
E value	3.0e-19
Match length	77
% identity	62
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	52964
Seq. ID	vwf700675543.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	246
E value	1.0e-21
Match length	64
% identity	78
NCBI Description	Bean pod mottle virus

Seq. No.	52965
Seq. ID	vwf700675567.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	69
E value	1.0e-30
Match length	213
% identity	84
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52966
Seq. ID	vwf700675592.h1
Method	BLASTX
NCBI GI	g4539324
BLAST score	322

E value	2.0e-30
Match length	78
% identity	81
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	52967
Seq. ID	vwf700675660.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	90
E value	3.0e-43
Match length	166
% identity	89
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52968
Seq. ID	vwf700675665.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	173
E value	9.0e-93
Match length	229
% identity	94
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	52969
Seq. ID	vwf700675671.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	145
E value	1.0e-20
Match length	80
% identity	68
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	52970
Seq. ID	vwf700675685.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	218
E value	1.0e-119
Match length	254
% identity	96
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	52971
Seq. ID	vwf700675732.h1
Method	BLASTN
NCBI GI	g4165487
BLAST score	65
E value	3.0e-28

Match length	101
% identity	91
NCBI Description	Hordeum vulgare mRNA for alpha-tubulin

Seq. No.	52972
Seq. ID	vwf700675740.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	134
E value	2.0e-69
Match length	182
% identity	93
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52973
Seq. ID	vwf700675755.h1
Method	BLASTX
NCBI GI	g2244898
BLAST score	304
E value	4.0e-28
Match length	84
% identity	65
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	52974
Seq. ID	vwf700675765.h1
Method	BLASTX
NCBI GI	g1800307
BLAST score	200
E value	6.0e-16
Match length	82
% identity	26
NCBI Description	(U83883) p105 coactivator [Rattus norvegicus]

Seq. No.	52975
Seq. ID	vwf700675779.h1
Method	BLASTN
NCBI GI	g2160155
BLAST score	39
E value	9.0e-13
Match length	111
% identity	84
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	52976
Seq. ID	vwf700675902.h1
Method	BLASTX
NCBI GI	g2213871
BLAST score	146
E value	1.0e-09
Match length	48
% identity	62
NCBI Description	(AF003126) poly(A)-binding protein [Mesembryanthemum crystallinum]

Seq. No.	52977
Seq. ID	vwf700675903.h1
Method	BLASTN
NCBI GI	g1794171
BLAST score	157
E value	3.0e-83
Match length	220
% identity	93
NCBI Description	Glycine max lipoxygenase-3 mRNA, complete cds

Seq. No.	52978
Seq. ID	vwf700675914.h1
Method	BLASTN
NCBI GI	g3832511
BLAST score	109
E value	2.0e-54
Match length	273
% identity	85
NCBI Description	Astragalus membranaceus granule-bound glycogen (starch) synthase mRNA, complete cds

Seq. No.	52979
Seq. ID	vwf700675939.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	216
E value	1.0e-118
Match length	224
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52980
Seq. ID	vwf700675945.h1
Method	BLASTN
NCBI GI	g1853967
BLAST score	53
E value	3.0e-21
Match length	132
% identity	89
NCBI Description	Vigna unguiculata mRNA for CPRD12 protein, complete cds

Seq. No.	52981
Seq. ID	vwf700675947.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	257
E value	1.0e-143
Match length	257
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52982
Seq. ID	vwf700675950.h1
Method	BLASTX
NCBI GI	g1352681
BLAST score	170
E value	2.0e-12

Match length	38
% identity	87
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	52983
Seq. ID	vwf700675959.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	121
E value	1.0e-61
Match length	257
% identity	87
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52984
Seq. ID	vwf700675966.h1
Method	BLASTN
NCBI GI	g18634
BLAST score	220
E value	1.0e-121
Match length	264
% identity	96
NCBI Description	Soybean Gy1 gene for glycinin subunit G1

Seq. No.	52985
Seq. ID	vwf700675991.h1
Method	BLASTX
NCBI GI	g3367528
BLAST score	176
E value	4.0e-13
Match length	88
% identity	43
NCBI Description	(AC004392) Strong similarity to gi_2160138 F19K23.6 gene product from A. thaliana BAC gb_AC000375. [Arabidopsis thaliana]

Seq. No.	52986
Seq. ID	vwf700676002.h1
Method	BLASTX
NCBI GI	g2444271
BLAST score	242
E value	8.0e-21
Match length	75
% identity	64
NCBI Description	(AF019637) putative amino acid or GABA permease [Arabidopsis thaliana]

Seq. No.	52987
Seq. ID	vwf700676005.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	109
E value	2.0e-54

Match length	193
% identity	90
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52988
Seq. ID	vwf700676013.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	198
E value	1.0e-107
Match length	266
% identity	94
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52989
Seq. ID	vwf700676025.h1
Method	BLASTN
NCBI GI	g169159
BLAST score	128
E value	7.0e-66
Match length	250
% identity	91
NCBI Description	Pea chloroplastic copper/zinc-superoxide dismutase mRNA, complete cds

Seq. No.	52990
Seq. ID	vwf700676028.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	136
E value	5.0e-11
Match length	81
% identity	46
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	52991
Seq. ID	vwf700676031.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	189
E value	1.0e-102
Match length	218
% identity	97
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	52992
Seq. ID	vwf700676116.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	205
E value	1.0e-112
Match length	205
% identity	100
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	52993
Seq. ID	vwf700676146.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	79
E value	1.0e-36
Match length	234
% identity	93
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	52994
Seq. ID	vwf700676174.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	74
E value	1.0e-33
Match length	234
% identity	85
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	52995
Seq. ID	vwf700676279.h1
Method	BLASTX
NCBI GI	g3269287
BLAST score	190
E value	1.0e-14
Match length	42
% identity	88
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	52996
Seq. ID	vwf700676283.h1
Method	BLASTN
NCBI GI	g169968
BLAST score	242
E value	1.0e-134
Match length	246
% identity	100
NCBI Description	Soybean (G.max) glycinin seed storage protein, subunit A3-B4, mRNA. >gi_2170691_dbj_E02460_E02460 cDNA encoding glycinine subunit A3B4 precursor

Seq. No.	52997
Seq. ID	vwf700676288.h1
Method	BLASTX
NCBI GI	g1805654
BLAST score	173
E value	1.0e-12
Match length	76
% identity	50
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No.	52998

Seq. ID	vwf700676325.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	267
E value	1.0e-149
Match length	271
% identity	100
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	52999
Seq. ID	vwf700676331.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	152
E value	3.0e-80
Match length	188
% identity	95
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	53000
Seq. ID	vwf700676340.h1
Method	BLASTX
NCBI GI	g2196878
BLAST score	280
E value	3.0e-25
Match length	59
% identity	92
NCBI Description	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]

Seq. No.	53001
Seq. ID	vwf700676342.h1
Method	BLASTX
NCBI GI	g1711615
BLAST score	355
E value	4.0e-34
Match length	80
% identity	85
NCBI Description	HIGH AFFINITY SULPHATE TRANSPORTER 1 >gi_1085847_pir__S51763 high affinity sulphate transporter - Stylosanthes hamata >gi_607184_emb_CAA57710_ (X82255) high affinity sulphate transporter [Stylosanthes hamata]

Seq. No.	53002
Seq. ID	vwf700676476.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	148
E value	8.0e-78
Match length	244
% identity	90
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53003
Seq. ID	vwf700676503.h1
Method	BLASTX

NCBI GI	g2655889
BLAST score	145
E value	1.0e-09
Match length	51
% identity	49
NCBI Description	(AL009171) 62D9.b [Drosophila melanogaster]

Seq. No.	53004
Seq. ID	vwf700676535.h1
Method	BLASTX
NCBI GI	g4160441
BLAST score	157
E value	6.0e-11
Match length	79
% identity	46
NCBI Description	(AF098674) lateral suppressor protein [Lycopersicon esculentum]

Seq. No.	53005
Seq. ID	vwf700676594.h1
Method	BLASTN
NCBI GI	g1199562
BLAST score	159
E value	2.0e-84
Match length	163
% identity	99
NCBI Description	Glycine max 34 kDa maturing seed vacuolar thiol protease mRNA, complete cds

Seq. No.	53006
Seq. ID	vwf700676603.h1
Method	BLASTN
NCBI GI	g169928
BLAST score	75
E value	3.0e-34
Match length	79
% identity	99
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A

Seq. No.	53007
Seq. ID	vwf700676723.h1
Method	BLASTX
NCBI GI	g4567304
BLAST score	239
E value	2.0e-20
Match length	86
% identity	52
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	53008
Seq. ID	vwf700676729.h1
Method	BLASTX
NCBI GI	g3355474
BLAST score	270
E value	4.0e-24
Match length	74

% identity	66
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	53009
Seq. ID	vwf700676794.h1
Method	BLASTX
NCBI GI	g171569
BLAST score	154
E value	2.0e-10
Match length	52
% identity	52
NCBI Description	(M76739) 1,4-glucan-6-(1,4-glucano)-transferase [Saccharomyces cerevisiae]

Seq. No.	53010
Seq. ID	vwf700676858.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	202
E value	1.0e-110
Match length	217
% identity	99
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	53011
Seq. ID	vwf700676921.h1
Method	BLASTN
NCBI GI	g18769
BLAST score	158
E value	8.0e-84
Match length	238
% identity	93
NCBI Description	G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No.	53012
Seq. ID	vwf700676922.h1
Method	BLASTN
NCBI GI	g2598656
BLAST score	84
E value	1.0e-39
Match length	120
% identity	93
NCBI Description	Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.	53013
Seq. ID	vwf700676932.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	125
E value	4.0e-64
Match length	249
% identity	89
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	53014

Seq. ID	vwf700676958.h1
Method	BLASTX
NCBI GI	g1345132
BLAST score	194
E value	3.0e-15
Match length	77
% identity	9
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	53015
Seq. ID	vwf700676992.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	257
E value	1.0e-143
Match length	257
% identity	100
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	53016
Seq. ID	vwf700677015.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	189
E value	1.0e-18
Match length	73
% identity	65
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53017
Seq. ID	vwf700677066.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	124
E value	2.0e-63
Match length	226
% identity	36
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	53018
Seq. ID	vwf700677082.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	64
E value	9.0e-28
Match length	136
% identity	87
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53019
Seq. ID	vwf700677092.h1

Method	BLASTN
NCBI GI	g218264
BLAST score	254
E value	1.0e-141
Match length	254
% identity	100
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	53020
Seq. ID	vwf700677096.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	164
E value	2.0e-87
Match length	258
% identity	98
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	53021
Seq. ID	vwf700677103.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	84
E value	1.0e-39
Match length	236
% identity	84
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	53022
Seq. ID	vwf700677106.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	69
E value	9.0e-31
Match length	185
% identity	84
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	53023
Seq. ID	vwf700677112.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	51
E value	2.0e-20
Match length	109
% identity	94
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53024
Seq. ID	vwf700677114.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	185
E value	1.0e-100
Match length	249

% identity	94
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53025
Seq. ID	vwf700677115.h1
Method	BLASTX
NCBI GI	g1737222
BLAST score	382
E value	3.0e-37
Match length	86
% identity	77
NCBI Description	(U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No.	53026
Seq. ID	vwf700677126.h1
Method	BLASTN
NCBI GI	g4097895
BLAST score	226
E value	1.0e-124
Match length	248
% identity	98
NCBI Description	Glycine max napin-type 2S albumin 3 mRNA, complete cds

Seq. No.	53027
Seq. ID	vwf700677158.h1
Method	BLASTX
NCBI GI	g2688822
BLAST score	142
E value	3.0e-09
Match length	52
% identity	62
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]

Seq. No.	53028
Seq. ID	vwf700677201.h1
Method	BLASTX
NCBI GI	g3142293
BLAST score	140
E value	8.0e-09
Match length	63
% identity	49
NCBI Description	(AC002411) Contains similarity to myosin IB heavy chain gb_X70400 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	53029
Seq. ID	vwf700677218.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	119
E value	2.0e-60
Match length	259
% identity	86
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53030
Seq. ID	vwf700677219.h1
Method	BLASTN
NCBI GI	g806555
BLAST score	223
E value	1.0e-122
Match length	251
% identity	98
NCBI Description	G.soja mRNA for glycinin

Seq. No.	53031
Seq. ID	vwf700677243.h1
Method	BLASTX
NCBI GI	g4454471
BLAST score	304
E value	4.0e-28
Match length	84
% identity	68
NCBI Description	(AC006234) putative G protein coupled receptor [Arabidopsis thaliana]

Seq. No.	53032
Seq. ID	vwf700677249.h1
Method	BLASTN
NCBI GI	g18634
BLAST score	216
E value	1.0e-118
Match length	263
% identity	96
NCBI Description	Soybean Gy1 gene for glycinin subunit G1

Seq. No.	53033
Seq. ID	vwf700677282.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	212
E value	1.0e-116
Match length	228
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53034
Seq. ID	vwf700677387.h1
Method	BLASTN
NCBI GI	g18769
BLAST score	163
E value	9.0e-87
Match length	235
% identity	93
NCBI Description	G.max mRNA Ti-a for Kunitz trypsin inhibitor subtype A

Seq. No.	53035
Seq. ID	vwf700677415.h1
Method	BLASTX
NCBI GI	g2160185
BLAST score	208
E value	7.0e-17

Match length	67
% identity	54
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	53036
Seq. ID	vwf700677424.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	238
E value	1.0e-131
Match length	250
% identity	99
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No.	53037
Seq. ID	vwf700677445.h1
Method	BLASTX
NCBI GI	g3243234
BLAST score	144
E value	2.0e-09
Match length	77
% identity	35
NCBI Description	(AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No.	53038
Seq. ID	vwf700677480.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	214
E value	1.0e-117
Match length	242
% identity	97
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53039
Seq. ID	vwf700677530.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	77
E value	1.0e-35
Match length	172
% identity	87
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	53040
Seq. ID	vwf700677531.h1
Method	BLASTX
NCBI GI	g2190544
BLAST score	142
E value	4.0e-09
Match length	59
% identity	56

NCBI Description	(AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb_U40828). [Arabidopsis thaliana]

Seq. No.	53041
Seq. ID	vwf700677595.h1
Method	BLASTX
NCBI GI	g3063445
BLAST score	169
E value	2.0e-12
Match length	57
% identity	8
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	53042
Seq. ID	vwf700677629.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	97
E value	1.0e-47
Match length	137
% identity	93
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No.	53043
Seq. ID	vwf700677639.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	138
E value	7.0e-72
Match length	229
% identity	94
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53044
Seq. ID	vwf700677659.h1
Method	BLASTX
NCBI GI	g790687
BLAST score	164
E value	1.0e-11
Match length	52
% identity	62
NCBI Description	(L39651) zinc finger protein [Arabidopsis thaliana]

Seq. No.	53045
Seq. ID	vwf700677663.h1
Method	BLASTN
NCBI GI	g3192930
BLAST score	149
E value	2.0e-78
Match length	169
% identity	97
NCBI Description	Glycine max clone a2 malate dehydrogenase (Mdh-1) mRNA, nuclear gene encoding mitochondrial protein, partial cds

Seq. No.	53046

Seq. ID	vwf700677748.h1
Method	BLASTN
NCBI GI	g3063690
BLAST score	36
E value	5.0e-11
Match length	48
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	53047
Seq. ID	vwf700677771.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	207
E value	1.0e-113
Match length	214
% identity	100
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No.	53048
Seq. ID	vwf700677817.h1
Method	BLASTN
NCBI GI	g169097
BLAST score	49
E value	1.0e-18
Match length	173
% identity	82
NCBI Description	Pea histone H2A mRNA

Seq. No.	53049
Seq. ID	vwf700677867.h1
Method	BLASTX
NCBI GI	g3093294
BLAST score	387
E value	6.0e-38
Match length	80
% identity	93
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	53050
Seq. ID	vwf700677884.h1
Method	BLASTN
NCBI GI	g2924257
BLAST score	181
E value	2.0e-97
Match length	249
% identity	47
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	53051
Seq. ID	vwf700677885.h1
Method	BLASTN
NCBI GI	g4206101
BLAST score	129
E value	2.0e-66

Match length	213
% identity	90
NCBI Description	Glycine max retroelement diaspora gag-pol polyprotein (gag-pol) pseudogene, partial sequence

Seq. No.	53052
Seq. ID	vwf700677903.h1
Method	BLASTX
NCBI GI	g3386604
BLAST score	222
E value	6.0e-19
Match length	74
% identity	67
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	53053
Seq. ID	vwf700677909.h1
Method	BLASTX
NCBI GI	g4455359
BLAST score	144
E value	3.0e-09
Match length	29
% identity	90
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	53054
Seq. ID	vwf700677954.h1
Method	BLASTX
NCBI GI	g4566505
BLAST score	192
E value	7.0e-18
Match length	86
% identity	53
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	53055
Seq. ID	vwf700677980.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	88
E value	6.0e-42
Match length	232
% identity	86
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	53056
Seq. ID	vwf700677994.h1
Method	BLASTX
NCBI GI	g4220532
BLAST score	218
E value	5.0e-18
Match length	84
% identity	56
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	53057
Seq. ID	vwf700678168.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	246
E value	1.0e-136
Match length	253
% identity	100
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	53058
Seq. ID	vwf700678176.h1
Method	BLASTN
NCBI GI	g18628
BLAST score	50
E value	1.0e-19
Match length	126
% identity	86
NCBI Description	Soybean mRNA for A5A4B3 subunits of glycinin >gi_2170692_dbj_E02461_E02461 cDNA encoding glycinine subunit A5A4B3 precursor

Seq. No.	53059
Seq. ID	vwf700678205.h1
Method	BLASTN
NCBI GI	g3617740
BLAST score	54
E value	5.0e-22
Match length	86
% identity	91
NCBI Description	Arabidopsis thaliana BAC F1I21 from chromosome 1, near 59 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	53060
Seq. ID	vwf700678284.h1
Method	BLASTN
NCBI GI	g21142
BLAST score	66
E value	6.0e-29
Match length	170
% identity	85
NCBI Description	Mustard mRNA for cytosolic glyceraldehyde-3-phosphate dehydrogenase (GAPDH, NAD-specific; EC 1.2.1.12)

Seq. No.	53061
Seq. ID	vwf700678327.h1
Method	BLASTX
NCBI GI	g4406789
BLAST score	190
E value	9.0e-15
Match length	81
% identity	53
NCBI Description	(AC006532) putative glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	53062
Seq. ID	vwf700678357.h1

Method	BLASTN
NCBI GI	g169928
BLAST score	72
E value	2.0e-32
Match length	128
% identity	89
NCBI Description	Glycine max alpha'-type beta conglycinin storage protein gene, complete cds, clone ch4A

Seq. No.	53063
Seq. ID	vwf700678382.h1
Method	BLASTN
NCBI GI	g18771
BLAST score	117
E value	2.0e-59
Match length	237
% identity	87
NCBI Description	G.max mRNA Ti-b for Kunitz trypsin inhibitor subtype B

Seq. No.	53064
Seq. ID	vwf700678392.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	107
E value	2.0e-53
Match length	144
% identity	95
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53065
Seq. ID	vwf700678425.h1
Method	BLASTN
NCBI GI	g21054
BLAST score	56
E value	7.0e-23
Match length	200
% identity	87
NCBI Description	P.vulgaris mRNA for tonoplast intrinsic protein

Seq. No.	53066
Seq. ID	vwf700678435.h1
Method	BLASTN
NCBI GI	g1666233
BLAST score	77
E value	1.0e-35
Match length	153
% identity	88
NCBI Description	Pisum sativum actin (PEAc14) mRNA, complete cds >gi_1724142_gb_U81049_PSU81049 Pisum sativum actin (PEAc14) mRNA, complete cds

Seq. No.	53067
Seq. ID	vwf700678472.h1
Method	BLASTN
NCBI GI	g1008880
BLAST score	104

E value	2.0e-51
Match length	264
% identity	85
NCBI Description	Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5) gene, complete cds

Seq. No.	53068
Seq. ID	vwf700678516.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	268
E value	1.0e-149
Match length	268
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53069
Seq. ID	vwf700678542.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	262
E value	1.0e-146
Match length	262
% identity	100
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	53070
Seq. ID	vwf700678553.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	232
E value	1.0e-128
Match length	252
% identity	98
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No.	53071
Seq. ID	vwf700678561.h1
Method	BLASTX
NCBI GI	g4567225
BLAST score	180
E value	1.0e-13
Match length	66
% identity	50
NCBI Description	(AC007119) unknown protein [Arabidopsis thaliana]

Seq. No.	53072
Seq. ID	vwf700678605.h1
Method	BLASTX
NCBI GI	g4115948
BLAST score	192
E value	7.0e-15
Match length	96
% identity	46
NCBI Description	(AF118223) contains similarity to CDP-alcohol phosphatidyltransferases (Pfam: PF01066, score=13.7, E=

0.00016, n=1) [Arabidopsis thaliana]

Seq. No.	53073
Seq. ID	vwf700678608.h1
Method	BLASTX
NCBI GI	g3337350
BLAST score	182
E value	1.0e-13
Match length	39
% identity	85
NCBI Description	(AC004481) putative permease [Arabidopsis thaliana]

Seq. No.	53074
Seq. ID	vwf700678621.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	272
E value	1.0e-151
Match length	288
% identity	99
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	53075
Seq. ID	vwf700678677.h1
Method	BLASTX
NCBI GI	g3522947
BLAST score	225
E value	8.0e-19
Match length	81
% identity	60
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53076
Seq. ID	vwf700678707.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	108
E value	7.0e-54
Match length	232
% identity	88
NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	53077
Seq. ID	vwf700678725.h1
Method	BLASTN
NCBI GI	g476213
BLAST score	125
E value	4.0e-64
Match length	233
% identity	89
NCBI Description	Glycine max Century 84 p24 oleosin isoform A gene, complete cds

Seq. No.	53078
Seq. ID	vwf700678730.h1
Method	BLASTN
NCBI GI	g4097879

BLAST score	100
E value	4.0e-49
Match length	235
% identity	87
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53079
Seq. ID	vwf700678738.h1
Method	BLASTN
NCBI GI	g18634
BLAST score	139
E value	2.0e-72
Match length	255
% identity	89
NCBI Description	Soybean Gy1 gene for glycinin subunit G1

Seq. No.	53080
Seq. ID	vwf700678783.h1
Method	BLASTX
NCBI GI	g3063710
BLAST score	342
E value	2.0e-32
Match length	88
% identity	73
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	53081
Seq. ID	vwf700678806.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	177
E value	4.0e-95
Match length	233
% identity	94
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53082
Seq. ID	vwf700678824.h1
Method	BLASTX
NCBI GI	g4432846
BLAST score	262
E value	3.0e-23
Match length	79
% identity	68
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	53083
Seq. ID	vwf700678863.h1
Method	BLASTN
NCBI GI	g169972
BLAST score	251
E value	1.0e-139
Match length	251
% identity	100
NCBI Description	Soybean glycinin A-1a-B-x subunit mRNA, complete cds

Seq. No.	53084
Seq. ID	vwf700678882.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	82
E value	2.0e-38
Match length	182
% identity	86
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53085
Seq. ID	vwf700678886.h1
Method	BLASTX
NCBI GI	g2244771
BLAST score	256
E value	1.0e-22
Match length	76
% identity	72
NCBI Description	(Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No.	53086
Seq. ID	vwf700678889.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	184
E value	2.0e-99
Match length	192
% identity	99
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53087
Seq. ID	vwf700679115.h1
Method	BLASTN
NCBI GI	g3097265
BLAST score	156
E value	1.0e-82
Match length	260
% identity	93
NCBI Description	Pisum sativum mRNA for translation initiation factor

Seq. No.	53088
Seq. ID	vwf700679151.h1
Method	BLASTX
NCBI GI	g1532171
BLAST score	163
E value	1.0e-11
Match length	39
% identity	77
NCBI Description	(U63815) AT.I.24-9 gene product [Arabidopsis thaliana]

Seq. No.	53089
Seq. ID	vwf700679170.h1
Method	BLASTN
NCBI GI	g18608
BLAST score	270
E value	1.0e-150

Match length	270
% identity	100
NCBI Description	Glycine max mRNA for glycinin >gi_2170693_dbj_E02462_E02462 cDNA encoding glycinine subunit A2B1a precursor

Seq. No.	53090
Seq. ID	vwf700679184.h1
Method	BLASTN
NCBI GI	g218264
BLAST score	175
E value	6.0e-94
Match length	223
% identity	95
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	53091
Seq. ID	vwf700679204.h1
Method	BLASTN
NCBI GI	g169912
BLAST score	89
E value	1.0e-42
Match length	122
% identity	95
NCBI Description	Glycine max beta-amylase mRNA, complete cds

Seq. No.	53092
Seq. ID	vwf700679212.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	259
E value	1.0e-144
Match length	266
% identity	93
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53093
Seq. ID	vwf700679221.h1
Method	BLASTN
NCBI GI	g4063523
BLAST score	151
E value	1.0e-79
Match length	266
% identity	89
NCBI Description	Aesculus pavia ATP synthase beta subunit (atpB) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No.	53094
Seq. ID	vwf700679345.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	230
E value	1.0e-19
Match length	66
% identity	71
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.	53095
Seq. ID	vwf700679469.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	64
E value	8.0e-28
Match length	179
% identity	85
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53096
Seq. ID	vwf700679516.h1
Method	BLASTN
NCBI GI	g210811
BLAST score	154
E value	2.0e-81
Match length	206
% identity	94
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	53097
Seq. ID	vwf700679623.h1
Method	BLASTX
NCBI GI	g4455188
BLAST score	222
E value	2.0e-18
Match length	72
% identity	60
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	53098
Seq. ID	vwf700679649.h1
Method	BLASTX
NCBI GI	g3892052
BLAST score	218
E value	3.0e-18
Match length	65
% identity	71
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	53099
Seq. ID	vwf700679663.h1
Method	BLASTX
NCBI GI	g3273243
BLAST score	253
E value	3.0e-22
Match length	71
% identity	46
NCBI Description	(AB004660) NLS receptor [Oryza sativa] >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]

Seq. No.	53100
Seq. ID	vwf700679667.h1
Method	BLASTN
NCBI GI	g2605509
BLAST score	219
E value	1.0e-120
Match length	231
% identity	99
NCBI Description	Glycine max mRNA for alpha subunit of beta conglycinin, complete cds

Seq. No.	53101
Seq. ID	vwf700679682.h1
Method	BLASTN
NCBI GI	g2662468
BLAST score	42
E value	1.0e-14
Match length	94
% identity	86
NCBI Description	Arabidopsis thaliana ribosomal protein S6 (rps6) mRNA, complete cds

Seq. No.	53102
Seq. ID	vwf700679685.h1
Method	BLASTN
NCBI GI	g18535
BLAST score	240
E value	1.0e-132
Match length	240
% identity	100
NCBI Description	Soybean mRNA for the alpha subunit of beta-conglycinin

Seq. No.	53103
Seq. ID	vwf700679769.h1
Method	BLASTX
NCBI GI	g3033391
BLAST score	174
E value	6.0e-13
Match length	83
% identity	42
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	53104
Seq. ID	vwf700679808.h1
Method	BLASTN
NCBI GI	g3097320
BLAST score	250
E value	1.0e-138
Match length	254
% identity	100
NCBI Description	Glycine max gene for Bd 30K, complete cds

Seq. No.	53105
Seq. ID	vwf700679817.h1
Method	BLASTN
NCBI GI	g218264

BLAST score	233
E value	1.0e-128
Match length	253
% identity	98
NCBI Description	Glycine max mRNA for glycinin A2B1a subunit, complete cds

Seq. No.	53106
Seq. ID	vwf700679824.h1
Method	BLASTX
NCBI GI	g3746070
BLAST score	321
E value	4.0e-30
Match length	65
% identity	89
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]

Seq. No.	53107
Seq. ID	vwf700679828.h1
Method	BLASTX
NCBI GI	g4455359
BLAST score	140
E value	5.0e-09
Match length	36
% identity	78
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	53108
Seq. ID	vwf700679842.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	53109
Seq. ID	vwf700679854.h1
Method	BLASTX
NCBI GI	g3128228
BLAST score	308
E value	1.0e-28
Match length	65
% identity	91
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	53110
Seq. ID	vzy700750518.h1
Method	BLASTX
NCBI GI	g4538913
BLAST score	150
E value	7.0e-15
Match length	80
% identity	59
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	53111
Seq. ID	vzy700750629.h1
Method	BLASTX
NCBI GI	g2764949
BLAST score	315
E value	1.0e-29
Match length	72
% identity	83
NCBI Description	(X98931) heat shock protein 70 [Emericella nidulans]

Seq. No.	53112
Seq. ID	vzy700750747.h1
Method	BLASTX
NCBI GI	g3482933
BLAST score	299
E value	1.0e-27
Match length	82
% identity	65
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	53113
Seq. ID	vzy700750760.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	179
E value	2.0e-13
Match length	39
% identity	85
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	53114
Seq. ID	vzy700750929.h1
Method	BLASTX
NCBI GI	g2160692
BLAST score	281
E value	2.0e-25
Match length	72
% identity	74
NCBI Description	(U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	53115
Seq. ID	vzy700751029.h1
Method	BLASTX
NCBI GI	g2654108
BLAST score	282
E value	1.0e-25
Match length	75
% identity	73
NCBI Description	(AF034419) cytosine-5 DNA methyltransferase [Pisum sativum]

Seq. No.	53116
Seq. ID	vzy700751080.h1
Method	BLASTX
NCBI GI	g1895084

BLAST score 102
E value 7.0e-11
Match length 49
% identity 73
NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No. 53117
Seq. ID vzy700751095.h1
Method BLASTX
NCBI GI g120669
BLAST score 267
E value 6.0e-24
Match length 52
% identity 98
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 53118
Seq. ID vzy700751401.h1
Method BLASTX
NCBI GI g485515
BLAST score 435
E value 2.0e-43
Match length 88
% identity 98
NCBI Description ADR6 protein - soybean >gi_296445_emb_CAA49340_ (X69639) auxin down regulated [Glycine max] >gi_2304955 (U64866) similar to ADR6 encoded by GenBank Accession Number X69639; aluminum induced [Glycine max]

Seq. No. 53119
Seq. ID vzy700751444.h1
Method BLASTX
NCBI GI g2832643
BLAST score 203
E value 3.0e-16
Match length 86
% identity 53
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No. 53120
Seq. ID vzy700751451.h1
Method BLASTX
NCBI GI g4249386
BLAST score 377
E value 1.0e-36
Match length 85
% identity 84
NCBI Description (AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No. 53121
Seq. ID vzy700751510.h1

Method	BLASTX
NCBI GI	g2406565
BLAST score	194
E value	3.0e-15
Match length	76
% identity	32
NCBI Description	(U68140) nuclear VCP-like protein NVLp.2 [Homo sapiens]

Seq. No.	53122
Seq. ID	vzy700751593.h1
Method	BLASTX
NCBI GI	g3805962
BLAST score	267
E value	8.0e-24
Match length	71
% identity	72
NCBI Description	(Y13772) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	53123
Seq. ID	vzy700751645.h1
Method	BLASTX
NCBI GI	g1076485
BLAST score	270
E value	3.0e-24
Match length	51
% identity	98
NCBI Description	SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No.	53124
Seq. ID	vzy700751662.h1
Method	BLASTX
NCBI GI	g4056421
BLAST score	161
E value	2.0e-11
Match length	73
% identity	46
NCBI Description	(AC005322) Similar to gb_Z30094 basic transcripion factor 2, 44 kD subunit from Homo sapiens. EST gb_W43325 comes from this gene. [Arabidopsis thaliana]

Seq. No.	53125
Seq. ID	vzy700751677.h1
Method	BLASTX
NCBI GI	g3913008
BLAST score	249
E value	9.0e-22
Match length	63
% identity	81
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	53126
Seq. ID	vzy700751701.h1
Method	BLASTX

NCBI GI	g3152567
BLAST score	186
E value	3.0e-14
Match length	61
% identity	64
NCBI Description	(AC002986) Contains similarity to membrane associated salt-inducible protein gb_AF007269 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	53127
Seq. ID	vzy700751809.h1
Method	BLASTX
NCBI GI	g121336
BLAST score	262
E value	3.0e-23
Match length	49
% identity	100
NCBI Description	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME (GLUTAMATE--AMMONIA LIGASE) >gi_81774_pir__JQ0937 glutamate--ammonia ligase (EC 6.3.1.2), cytosolic - soybean >gi_256143_bbs_113802 (S46513) cytosolic glutamine synthetase, GS {EC 6.3.1.2} [Glycine max=soybeans, var Prize, Peptide, 355 aa] [Glycine max]

Seq. No.	53128
Seq. ID	vzy700751876.h1
Method	BLASTX
NCBI GI	g1175011
BLAST score	277
E value	6.0e-25
Match length	83
% identity	71
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	53129
Seq. ID	vzy700752032.h1
Method	BLASTX
NCBI GI	g4263522
BLAST score	191
E value	8.0e-15
Match length	85
% identity	7
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53130
Seq. ID	vzy700752040.h1
Method	BLASTX
NCBI GI	g3850579
BLAST score	157
E value	6.0e-11
Match length	58
% identity	55
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota.

	ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an
Seq. No.	53131
Seq. ID	vzy700752274.h1
Method	BLASTX
NCBI GI	g3158474
BLAST score	365
E value	2.0e-35
Match length	78
% identity	87
NCBI Description	(AF067184) aquaporin 1 [Samanea saman]
Seq. No.	53132
Seq. ID	vzy700752376.h1
Method	BLASTX
NCBI GI	g4544412
BLAST score	189
E value	1.0e-14
Match length	78
% identity	44
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.	53133
Seq. ID	vzy700752432.h1
Method	BLASTX
NCBI GI	g2655008
BLAST score	148
E value	8.0e-10
Match length	61
% identity	44
NCBI Description	(AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon esculentum]
Seq. No.	53134
Seq. ID	vzy700752462.h1
Method	BLASTX
NCBI GI	g115581
BLAST score	281
E value	2.0e-25
Match length	78
% identity	74
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) >gi_68031_pir__QYIX2 phosphoenolpyruvate carboxylase (EC 4.1.1.31) 2 - common ice plant >gi_4469271_emb_CAA32728_ (X14588) phosphoenolpyruvate carboxylase [Mesembryanthemum crystallinum]
Seq. No.	53135
Seq. ID	vzy700752506.h1
Method	BLASTX
NCBI GI	g549063
BLAST score	215
E value	6.0e-26
Match length	75
% identity	70

NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]
Seq. No.	53136
Seq. ID	vzy700752513.h1
Method	BLASTX
NCBI GI	g2829910
BLAST score	357
E value	3.0e-34
Match length	89
% identity	16
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.	53137
Seq. ID	vzy700752525.h1
Method	BLASTX
NCBI GI	g3036808
BLAST score	152
E value	2.0e-10
Match length	51
% identity	57
NCBI Description	(AL022373) DnaJ-like protein [Arabidopsis thaliana]
Seq. No.	53138
Seq. ID	vzy700752624.h1
Method	BLASTX
NCBI GI	g3264763
BLAST score	155
E value	7.0e-11
Match length	45
% identity	76
NCBI Description	(AF071891) 40S ribosomal protein S4 [Prunus armeniaca]
Seq. No.	53139
Seq. ID	vzy700752753.h1
Method	BLASTX
NCBI GI	g320585
BLAST score	138
E value	1.0e-08
Match length	67
% identity	40
NCBI Description	polygalacturonase (EC 3.2.1.15) 1 beta chain precursor - tomato >gi_170480 (M98466) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum] >gi_1762586 (U63374) polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum]
Seq. No.	53140
Seq. ID	vzy700752772.h1
Method	BLASTX
NCBI GI	g4467124
BLAST score	138
E value	7.0e-09
Match length	59

% identity	46
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53141
Seq. ID	vzy700752832.h1
Method	BLASTX
NCBI GI	g2500365
BLAST score	153
E value	2.0e-10
Match length	34
% identity	85
NCBI Description	PROBABLE 60 RIBOSOMAL PROTEIN L14 (HYDROXYPROLINE RICH GLYCOPROTEIN HRGP1)

Seq. No.	53142
Seq. ID	vzy700752843.h1
Method	BLASTX
NCBI GI	g485515
BLAST score	446
E value	9.0e-45
Match length	83
% identity	99
NCBI Description	ADR6 protein - soybean >gi_296445_emb_CAA49340_ (X69639) auxin down regulated [Glycine max] >gi_2304955 (U64866) similar to ADR6 encoded by GenBank Accession Number X69639; aluminum induced [Glycine max]

Seq. No.	53143
Seq. ID	vzy700752889.h1
Method	BLASTX
NCBI GI	g3176098
BLAST score	169
E value	3.0e-12
Match length	72
% identity	51
NCBI Description	(Y15036) annexin [Medicago truncatula]

Seq. No.	53144
Seq. ID	vzy700752951.h1
Method	BLASTX
NCBI GI	g3281867
BLAST score	249
E value	6.0e-23
Match length	71
% identity	80
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	53145
Seq. ID	vzy700753133.h1
Method	BLASTX
NCBI GI	g123650
BLAST score	178
E value	5.0e-14
Match length	41
% identity	100
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat shock protein 70 (clone pMON9743) - garden petunia

>gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida]

Seq. No.	53146
Seq. ID	vzy700753188.h1
Method	BLASTX
NCBI GI	g2062175
BLAST score	225
E value	4.0e-19
Match length	55
% identity	82
NCBI Description	(AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53147
Seq. ID	vzy700753262.h1
Method	BLASTX
NCBI GI	g4218120
BLAST score	159
E value	3.0e-11
Match length	76
% identity	47
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	53148
Seq. ID	vzy700753503.h1
Method	BLASTX
NCBI GI	g2252840
BLAST score	190
E value	9.0e-15
Match length	69
% identity	55
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	53149
Seq. ID	vzy700753516.h1
Method	BLASTX
NCBI GI	g1053216
BLAST score	208
E value	5.0e-17
Match length	48
% identity	88
NCBI Description	(U39475) chlorophyll a/b-binding protein [Glycine max]

Seq. No.	53150
Seq. ID	vzy700753519.h1
Method	BLASTX
NCBI GI	g99902
BLAST score	234
E value	2.0e-20
Match length	62
% identity	90
NCBI Description	translation elongation factor eEF-1 alpha chain (gene tefS1) - soybean

Seq. No. 53151

Seq. ID	vzy700753540.h1
Method	BLASTX
NCBI GI	g2507443
BLAST score	235
E value	4.0e-20
Match length	50
% identity	86
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) (23 KD CALLUS PROTEIN) (P23) >gi_1675196 (L47968) callus protein P23 [Pisum sativum]

Seq. No.	53152
Seq. ID	vzy700753557.h1
Method	BLASTX
NCBI GI	g730583
BLAST score	138
E value	8.0e-09
Match length	39
% identity	69
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_ (X78213) 60s acidic ribosomal protein P2 [Parthenium argentatum]

Seq. No.	53153
Seq. ID	vzy700753559.h1
Method	BLASTX
NCBI GI	g2497538
BLAST score	138
E value	8.0e-09
Match length	39
% identity	74
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	53154
Seq. ID	vzy700753588.h1
Method	BLASTX
NCBI GI	g99902
BLAST score	198
E value	8.0e-16
Match length	47
% identity	83
NCBI Description	translation elongation factor eEF-1 alpha chain (gene tefS1) - soybean

Seq. No.	53155
Seq. ID	vzy700753633.h1
Method	BLASTX
NCBI GI	g4234953
BLAST score	166
E value	7.0e-12
Match length	59
% identity	61
NCBI Description	(AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]

Seq. No.	53156
Seq. ID	vzy700753668.h1

Method	BLASTX
NCBI GI	g3913008
BLAST score	299
E value	1.0e-27
Match length	68
% identity	87
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	53157
Seq. ID	vzy700753745.h1
Method	BLASTX
NCBI GI	g4006818
BLAST score	183
E value	5.0e-14
Match length	40
% identity	85
NCBI Description	(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]

Seq. No.	53158
Seq. ID	vzy700753794.h1
Method	BLASTX
NCBI GI	g3668092
BLAST score	271
E value	2.0e-24
Match length	56
% identity	93
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	53159
Seq. ID	vzy700753851.h1
Method	BLASTX
NCBI GI	g729442
BLAST score	149
E value	4.0e-16
Match length	68
% identity	49
NCBI Description	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi_166380 (M80235) glucose-regulated endoplasmic reticular protein precursor [Medicago sativa]

Seq. No.	53160
Seq. ID	vzy700753864.h1
Method	BLASTX
NCBI GI	g2879796
BLAST score	138
E value	1.0e-19
Match length	70
% identity	65
NCBI Description	(AL021813) 60s ribosomal protein [Schizosaccharomyces pombe]

Seq. No.	53161
Seq. ID	vzy700754169.h1
Method	BLASTX

NCBI GI	g4103757
BLAST score	270
E value	4.0e-24
Match length	58
% identity	90
NCBI Description	(AF027376) MADS1 [Corylus avellana]

Seq. No.	53162
Seq. ID	vzy700754180.h1
Method	BLASTX
NCBI GI	g401142
BLAST score	145
E value	1.0e-09
Match length	40
% identity	75
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_322721_pir__S31479 sucrose synthase (EC 2.4.1.13) - fava bean >gi_22038_emb_CAA49428_ (X69773) sucrose synthase [Vicia faba] >gi_295426 (M97551) UDP-glucose:D-fructose-2-glucosyltransferase [Vicia faba]

Seq. No.	53163
Seq. ID	vzy700754246.h1
Method	BLASTX
NCBI GI	g1199806
BLAST score	101
E value	1.0e-08
Match length	53
% identity	68
NCBI Description	(X95663) elongation factor 1 alpha [Brugia pahangi]

Seq. No.	53164
Seq. ID	vzy700754249.h1
Method	BLASTX
NCBI GI	g2662343
BLAST score	123
E value	3.0e-09
Match length	40
% identity	88
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	53165
Seq. ID	vzy700754251.h1
Method	BLASTX
NCBI GI	g3023847
BLAST score	219
E value	4.0e-18
Match length	66
% identity	71
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta subunit-like [Medicago sativa]

Seq. No.	53166
Seq. ID	vzy700754310.h1
Method	BLASTX
NCBI GI	g730536

BLAST score 226
E value 6.0e-26
Match length 79
% identity 80
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal protein subunit L17 [Nicotiana tabacum]

Seq. No. 53167
Seq. ID vzy700754319.h1
Method BLASTX
NCBI GI g2791834
BLAST score 206
E value 2.0e-20
Match length 57
% identity 89
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No. 53168
Seq. ID vzy700754331.h1
Method BLASTX
NCBI GI g4056483
BLAST score 181
E value 9.0e-14
Match length 77
% identity 48
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No. 53169
Seq. ID vzy700754394.h1
Method BLASTX
NCBI GI g417103
BLAST score 184
E value 4.0e-20
Match length 67
% identity 84
NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 53170
Seq. ID vzy700754423.h1

Method	BLASTX
NCBI GI	g2129889
BLAST score	268
E value	6.0e-24
Match length	52
% identity	96
NCBI Description	methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

Seq. No.	53171
Seq. ID	vzy700754507.h1
Method	BLASTX
NCBI GI	g2738248
BLAST score	181
E value	1.0e-13
Match length	62
% identity	63
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	53172
Seq. ID	vzy700754566.h1
Method	BLASTX
NCBI GI	g2960358
BLAST score	184
E value	4.0e-14
Match length	53
% identity	66
NCBI Description	(AJ224895) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi_2960360_emb_CAA12200_ (AJ224896) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi_3550590_emb_CAA11495_ (AJ223620) caffeoyl CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa]

Seq. No.	53173
Seq. ID	vzy700754633.h1
Method	BLASTX
NCBI GI	g2252844
BLAST score	149
E value	4.0e-10
Match length	47
% identity	62
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	53174
Seq. ID	vzy700754759.h1
Method	BLASTX
NCBI GI	g3947735
BLAST score	143
E value	3.0e-09
Match length	64
% identity	50
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	53175
Seq. ID	vzy700754801.h1

Method	BLASTX
NCBI GI	g1277166
BLAST score	194
E value	3.0e-15
Match length	52
% identity	83
NCBI Description	(U51854) cysteine proteinase inhibitor [Glycine max]

Seq. No.	53176
Seq. ID	vzy700754822.h1
Method	BLASTX
NCBI GI	g1711617
BLAST score	286
E value	5.0e-26
Match length	81
% identity	79
NCBI Description	HIGH AFFINITY SULPHATE TRANSPORTER 2 >gi_1085848_pir__S51764 high affinity sulphate transporter - Stylosanthes hamata >gi_607186_emb_CAA57711_ (X82256) high affinity sulphate transporter [Stylosanthes hamata]

Seq. No.	53177
Seq. ID	vzy700754862.h1
Method	BLASTX
NCBI GI	g3549654
BLAST score	209
E value	5.0e-17
Match length	79
% identity	52
NCBI Description	(AL031394) metal-transporting P-type ATPase (fragment) [Arabidopsis thaliana]

Seq. No.	53178
Seq. ID	vzy700754892.h1
Method	BLASTX
NCBI GI	g1582221
BLAST score	230
E value	1.0e-19
Match length	77
% identity	56
NCBI Description	prepro-cathepsin C [Homo sapiens]

Seq. No.	53179
Seq. ID	vzy700754928.h1
Method	BLASTX
NCBI GI	g3193284
BLAST score	172
E value	1.0e-12
Match length	81
% identity	43
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	53180
Seq. ID	vzy700754937.h1
Method	BLASTX
NCBI GI	g66009
BLAST score	327

E value	7.0e-31
Match length	67
% identity	88
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH (AA 1-337) [Zea mays]

Seq. No.	53181
Seq. ID	vzy700755079.h1
Method	BLASTX
NCBI GI	g3914605
BLAST score	265
E value	2.0e-26
Match length	80
% identity	65
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase - apple tree >gi_415852_emb_CAA79857_ (Z21794) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Malus domestica]

Seq. No.	53182
Seq. ID	vzy700755090.h1
Method	BLASTX
NCBI GI	g126151
BLAST score	132
E value	1.0e-08
Match length	56
% identity	54
NCBI Description	LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi_282898_pir__S27365 lectin precursor - soybean >gi_170006 (K00821) lectin prepeptide [Glycine max]

Seq. No.	53183
Seq. ID	vzy700755174.h1
Method	BLASTX
NCBI GI	g2130149
BLAST score	393
E value	1.0e-38
Match length	75
% identity	100
NCBI Description	translation elongation factor eEF-1 alpha chain - maize (fragment)

Seq. No.	53184
Seq. ID	vzy700755182.h1
Method	BLASTX
NCBI GI	g1168189
BLAST score	235
E value	3.0e-20
Match length	57
% identity	82
NCBI Description	14-3-3-LIKE PROTEIN A (VFA-1433A) >gi_1076542_pir__S52899 14-3-3 brain protein homolog - fava bean >gi_695765_emb_CAA88415_ (Z48504) 14-3-3 brain protein homolog [Vicia faba]

Seq. No.	53185
Seq. ID	vzy700755203.h1
Method	BLASTX
NCBI GI	g3212863
BLAST score	245
E value	3.0e-21
Match length	80
% identity	65
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	53186
Seq. ID	vzy700755296.h1
Method	BLASTX
NCBI GI	g1931639
BLAST score	156
E value	8.0e-11
Match length	47
% identity	60
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	53187
Seq. ID	vzy700755386.h1
Method	BLASTX
NCBI GI	g2739366
BLAST score	192
E value	5.0e-15
Match length	54
% identity	57
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	53188
Seq. ID	vzy700755428.h1
Method	BLASTX
NCBI GI	g4544399
BLAST score	141
E value	6.0e-09
Match length	65
% identity	46
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	53189
Seq. ID	vzy700755432.h1
Method	BLASTX
NCBI GI	g3915826
BLAST score	331
E value	3.0e-31
Match length	77
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	53190
Seq. ID	vzy700755653.h1
Method	BLASTX
NCBI GI	g2317900

BLAST score	239
E value	2.0e-29
Match length	70
% identity	96
NCBI Description	(U89693) Sali3-2 [Glycine max]

Seq. No.	53191
Seq. ID	vzy700755701.h1
Method	BLASTX
NCBI GI	g2760345
BLAST score	367
E value	2.0e-35
Match length	74
% identity	25
NCBI Description	(U84967) ubiquitin [Arabidopsis thaliana]

Seq. No.	53192
Seq. ID	vzy700755752.h1
Method	BLASTX
NCBI GI	g2244750
BLAST score	135
E value	9.0e-19
Match length	79
% identity	65
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	53193
Seq. ID	vzy700755788.h1
Method	BLASTX
NCBI GI	g1076414
BLAST score	137
E value	1.0e-08
Match length	31
% identity	77
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	53194
Seq. ID	vzy700755790.h1
Method	BLASTX
NCBI GI	g2317900
BLAST score	316
E value	1.0e-31
Match length	80
% identity	85
NCBI Description	(U89693) Sali3-2 [Glycine max]

Seq. No.	53195
Seq. ID	vzy700755864.h1
Method	BLASTX
NCBI GI	g1352345
BLAST score	268
E value	6.0e-24
Match length	67

% identity	81
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_18765_emb_CAA40182_ (X56856) eEF-1a [Glycine max]

Seq. No.	53196
Seq. ID	vzy700755978.h1
Method	BLASTX
NCBI GI	g2642157
BLAST score	373
E value	3.0e-36
Match length	86
% identity	78
NCBI Description	(AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	53197
Seq. ID	vzy700755983.h1
Method	BLASTX
NCBI GI	g3249103
BLAST score	137
E value	1.0e-08
Match length	72
% identity	23
NCBI Description	(AC003114) Contains similarity to membrane-associated salt-inducible protein homolog TM021B04.10 gb_2191192 from A. thaliana BAC gb_AF007271. [Arabidopsis thaliana]

Seq. No.	53198
Seq. ID	vzy700755986.h1
Method	BLASTX
NCBI GI	g4454968
BLAST score	271
E value	3.0e-24
Match length	83
% identity	61
NCBI Description	(AF106046) unknown [Homo sapiens]

Seq. No.	53199
Seq. ID	vzy700756007.h1
Method	BLASTX
NCBI GI	g4510421
BLAST score	171
E value	2.0e-12
Match length	88
% identity	50
NCBI Description	(AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	53200
Seq. ID	vzy700756037.h1
Method	BLASTX
NCBI GI	g2493771
BLAST score	121
E value	2.0e-09
Match length	51
% identity	63
NCBI Description	COLD SHOCK PROTEIN CAPA (COLD ACCLIMATION PROTEIN A) (C7.0) >gi_1513079 (U62985) cold acclimation protein A [Pseudomonas fragi]

Seq. No.	53201
Seq. ID	vzy700756081.h1
Method	BLASTX
NCBI GI	g3152568
BLAST score	263
E value	3.0e-23
Match length	86
% identity	62
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]

Seq. No.	53202
Seq. ID	vzy700756086.h1
Method	BLASTX
NCBI GI	g4559333
BLAST score	255
E value	2.0e-22
Match length	72
% identity	68
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	53203
Seq. ID	vzy700756087.h1
Method	BLASTX
NCBI GI	g3150410
BLAST score	216
E value	8.0e-18
Match length	81
% identity	53
NCBI Description	(AC004165) unknown protein [Arabidopsis thaliana]

Seq. No.	53204
Seq. ID	vzy700756091.h1
Method	BLASTX
NCBI GI	g3927825
BLAST score	200
E value	6.0e-16
Match length	43
% identity	88
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	53205
Seq. ID	vzy700756148.h1
Method	BLASTX
NCBI GI	g421929
BLAST score	160
E value	2.0e-20
Match length	74
% identity	11
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	53206
Seq. ID	vzy700756158.h1

Method	BLASTX
NCBI GI	g3982596
BLAST score	331
E value	3.0e-31
Match length	81
% identity	85
NCBI Description	(AF039027) cationic peroxidase 2 [Glycine max]

Seq. No.	53207
Seq. ID	vzy700756168.h1
Method	BLASTX
NCBI GI	g2244851
BLAST score	259
E value	7.0e-23
Match length	80
% identity	56
NCBI Description	(Z97337) amine oxidase [Arabidopsis thaliana]

Seq. No.	53208
Seq. ID	vzy700756181.h1
Method	BLASTX
NCBI GI	g4106395
BLAST score	247
E value	2.0e-21
Match length	80
% identity	61
NCBI Description	(AF073744) raffinose synthase [Cucumis sativus]

Seq. No.	53209
Seq. ID	vzy700756242.h1
Method	BLASTX
NCBI GI	g2129825
BLAST score	140
E value	7.0e-09
Match length	41
% identity	71
NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]

Seq. No.	53210
Seq. ID	vzy700756334.h1
Method	BLASTX
NCBI GI	g488571
BLAST score	444
E value	2.0e-44
Match length	88
% identity	100
NCBI Description	(U09462) histone H3.2 [Medicago sativa]

Seq. No.	53211
Seq. ID	vzy700756377.h1
Method	BLASTX
NCBI GI	g4567301
BLAST score	205
E value	2.0e-16
Match length	59
% identity	63

NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]
Seq. No.	53212
Seq. ID	vzy700756393.h1
Method	BLASTX
NCBI GI	g1352345
BLAST score	429
E value	7.0e-43
Match length	84
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_18765_emb_CAA40182_ (X56856) eEF-1a [Glycine max]
Seq. No.	53213
Seq. ID	vzy700756401.h1
Method	BLASTX
NCBI GI	g1707007
BLAST score	234
E value	7.0e-20
Match length	85
% identity	15
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]
Seq. No.	53214
Seq. ID	vzy700756489.h1
Method	BLASTX
NCBI GI	g3763925
BLAST score	173
E value	8.0e-13
Match length	44
% identity	75
NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]
Seq. No.	53215
Seq. ID	vzy700756551.h1
Method	BLASTX
NCBI GI	g3176686
BLAST score	144
E value	1.0e-09
Match length	37
% identity	76
NCBI Description	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb_U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
Seq. No.	53216
Seq. ID	vzy700756556.h1
Method	BLASTX
NCBI GI	g2662343
BLAST score	139
E value	9.0e-09
Match length	59
% identity	58
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]
Seq. No.	53217
Seq. ID	vzy700756577.h1

Method	BLASTX
NCBI GI	g541950
BLAST score	158
E value	6.0e-11
Match length	64
% identity	55
NCBI Description	SPCP1 protein - soybean >gi_310576 (L12257) nodulin-26 [Glycine max]

Seq. No.	53218
Seq. ID	vzy700756612.h1
Method	BLASTX
NCBI GI	g115800
BLAST score	243
E value	6.0e-21
Match length	59
% identity	80
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-3) (LHCP) >gi_81771_pir__S01962 chlorophyll a/b-binding protein 3 precursor - soybean >gi_18552_emb_CAA31419_ (X12981) chlorophyll a/b binding preprotein (AA - 32 to 231) [Glycine max]

Seq. No.	53219
Seq. ID	vzy700756623.h1
Method	BLASTX
NCBI GI	g416581
BLAST score	184
E value	4.0e-14
Match length	48
% identity	69
NCBI Description	ACTIN-LIKE PROTEIN 3 >gi_283066_pir__A41790 actin like protein act2 - fission yeast (Schizosaccharomyces pombe)

Seq. No.	53220
Seq. ID	vzy700756719.h1
Method	BLASTX
NCBI GI	g2996096
BLAST score	279
E value	2.0e-25
Match length	53
% identity	98
NCBI Description	(AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	53221
Seq. ID	vzy700756816.h1
Method	BLASTX
NCBI GI	g2827718
BLAST score	100
E value	4.0e-10
Match length	83
% identity	48
NCBI Description	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]

Seq. No.	53222

Seq. ID	vzy700756889.h1
Method	BLASTX
NCBI GI	g2979559
BLAST score	210
E value	4.0e-29
Match length	81
% identity	75
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	53223
Seq. ID	wrg700785931.h2
Method	BLASTN
NCBI GI	g2373387
BLAST score	174
E value	2.0e-93
Match length	186
% identity	98
NCBI Description	Homo sapiens mRNA, complete cds >gi_4507098_ref_NM_003081.1_SNAP25_ Homo sapiens synaptosomal-associated protein, 25kD (SNAP25) mRNA

Seq. No.	53224
Seq. ID	wrg700785971.h2
Method	BLASTX
NCBI GI	g3831443
BLAST score	148
E value	7.0e-10
Match length	64
% identity	42
NCBI Description	(AC005819) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	53225
Seq. ID	wrg700786029.h2
Method	BLASTX
NCBI GI	g2435517
BLAST score	153
E value	2.0e-10
Match length	54
% identity	50
NCBI Description	(AF024504) contains similarity to peptidase family A1 [Arabidopsis thaliana]

Seq. No.	53226
Seq. ID	wrg700786052.h2
Method	BLASTN
NCBI GI	g1139584
BLAST score	73
E value	3.0e-33
Match length	169
% identity	86
NCBI Description	Lupinus albus tRNA nucleotidyltransferase (CCA1) mRNA, complete cds

Seq. No.	53227
Seq. ID	wrg700786076.h2

Method	BLASTN
NCBI GI	g2905771
BLAST score	136
E value	1.0e-70
Match length	155
% identity	97
NCBI Description	Glycine max glyceraldehyde-3 phosphate dehydrogenase (GAPDH) mRNA, partial cds

Seq. No.	53228
Seq. ID	wrg700786089.h2
Method	BLASTN
NCBI GI	g3560556
BLAST score	236
E value	1.0e-130
Match length	244
% identity	99
NCBI Description	Homo sapiens brain cellular apoptosis susceptibility protein (CSE1) mRNA, complete cds

Seq. No.	53229
Seq. ID	wrg700786094.h2
Method	BLASTN
NCBI GI	g2565418
BLAST score	87
E value	2.0e-41
Match length	139
% identity	91
NCBI Description	Onobrychis viciifolia histone H3 mRNA, complete cds

Seq. No.	53230
Seq. ID	wrg700786224.h2
Method	BLASTN
NCBI GI	g1845164
BLAST score	124
E value	2.0e-63
Match length	232
% identity	95
NCBI Description	Human DNA sequence from phage pTEL from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs

Seq. No.	53231
Seq. ID	wrg700786227.h2
Method	BLASTN
NCBI GI	g1518539
BLAST score	214
E value	1.0e-117
Match length	222
% identity	99
NCBI Description	Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No.	53232
Seq. ID	wrg700786238.h2
Method	BLASTN
NCBI GI	g187292
BLAST score	171

E value	1.0e-91
Match length	222
% identity	95
NCBI Description	Human myelin-associated glycoprotein (MAG) mRNA, complete cds

Seq. No.	53233
Seq. ID	wrg700786329.h1
Method	BLASTX
NCBI GI	g3581916
BLAST score	149
E value	6.0e-10
Match length	80
% identity	40
NCBI Description	(AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]

Seq. No.	53234
Seq. ID	wrg700786347.h1
Method	BLASTN
NCBI GI	g2224560
BLAST score	208
E value	1.0e-113
Match length	223
% identity	98
NCBI Description	Human mRNA for KIAA0310 gene, complete cds

Seq. No.	53235
Seq. ID	wrg700786422.h1
Method	BLASTX
NCBI GI	g1834387
BLAST score	170
E value	1.0e-12
Match length	38
% identity	79
NCBI Description	(Y11022) chalcone synthase [Betula pendula]

Seq. No.	53236
Seq. ID	wrg700786477.h1
Method	BLASTX
NCBI GI	g3036805
BLAST score	143
E value	3.0e-09
Match length	49
% identity	61
NCBI Description	(AL022373) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	53237
Seq. ID	wrg700786487.h1
Method	BLASTX
NCBI GI	g2244834
BLAST score	168
E value	2.0e-12
Match length	40
% identity	85
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53238
Seq. ID	wrg700786522.h1
Method	BLASTN
NCBI GI	g505109
BLAST score	228
E value	1.0e-125
Match length	255
% identity	98
NCBI Description	Human mRNA for KIAA0067 gene, complete cds

Seq. No.	53239
Seq. ID	wrg700786573.h1
Method	BLASTX
NCBI GI	g1856971
BLAST score	186
E value	3.0e-14
Match length	67
% identity	60
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	53240
Seq. ID	wrg700786633.h1
Method	BLASTX
NCBI GI	g3695392
BLAST score	155
E value	1.0e-10
Match length	35
% identity	77
NCBI Description	(AF096371) No definition line found [Arabidopsis thaliana]

Seq. No.	53241
Seq. ID	wrg700786691.h1
Method	BLASTN
NCBI GI	g169920
BLAST score	58
E value	4.0e-24
Match length	223
% identity	88
NCBI Description	Soybean auxin-regulated protein (Aux28) mRNA, complete cds

Seq. No.	53242
Seq. ID	wrg700786706.h2
Method	BLASTX
NCBI GI	g1717850
BLAST score	195
E value	1.0e-15
Match length	69
% identity	57
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_1072386_emb_CAA63352_ (X92664) ubiquitin-conjugating enzyme UbcM2 [Mus musculus]

Seq. No.	53243
Seq. ID	wrg700786710.h2

Method	BLASTX
NCBI GI	g3953475
BLAST score	153
E value	2.0e-10
Match length	55
% identity	51
NCBI Description	(AC002328) F22O2.20 [Arabidopsis thaliana]

Seq. No.	53244
Seq. ID	wrg700786748.h2
Method	BLASTN
NCBI GI	g529145
BLAST score	53
E value	2.0e-21
Match length	105
% identity	88
NCBI Description	Cricetulus griseus PxF mRNA, complete cds

Seq. No.	53245
Seq. ID	wrg700786769.h2
Method	BLASTN
NCBI GI	g2760172
BLAST score	56
E value	7.0e-23
Match length	145
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	53246
Seq. ID	wrg700786794.h2
Method	BLASTX
NCBI GI	g3355476
BLAST score	113
E value	3.0e-10
Match length	47
% identity	72
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	53247
Seq. ID	wrg700786804.h2
Method	BLASTX
NCBI GI	g2160156
BLAST score	169
E value	2.0e-12
Match length	65
% identity	49
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No.	53248
Seq. ID	wrg700786813.h2
Method	BLASTX
NCBI GI	g732194
BLAST score	141
E value	6.0e-09
Match length	91

% identity	40
NCBI Description	HYPOTHETICAL 27.5 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION >gi_2131919_pir__S50731 hypothetical protein YNL200c - yeast (Saccharomyces cerevisiae) >gi_600065_emb_CAA55508_ (X78898) N1370 [Saccharomyces cerevisiae] >gi_1302200_emb_CAA96099_ (Z71476) ORF YNL200c [Saccharomyces cerevisiae]

Seq. No.	53249
Seq. ID	wrg700786828.h2
Method	BLASTN
NCBI GI	g2062153
BLAST score	60
E value	3.0e-25
Match length	185
% identity	88
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	53250
Seq. ID	wrg700786933.h2
Method	BLASTX
NCBI GI	g2789434
BLAST score	180
E value	2.0e-16
Match length	61
% identity	67
NCBI Description	(AB001389) CLB1 [Lycopersicon esculentum]

Seq. No.	53251
Seq. ID	wrg700786945.h2
Method	BLASTN
NCBI GI	g168700
BLAST score	65
E value	1.0e-28
Match length	101
% identity	91
NCBI Description	Z.mays zein mRNA, complete cds

Seq. No.	53252
Seq. ID	wrg700786957.h2
Method	BLASTX
NCBI GI	g2583119
BLAST score	116
E value	1.0e-09
Match length	58
% identity	56
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53253
Seq. ID	wrg700786974.h2
Method	BLASTX
NCBI GI	g3046696
BLAST score	144
E value	1.0e-09
Match length	27
% identity	85

NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	53254
Seq. ID	wrg700787051.h2
Method	BLASTX
NCBI GI	g2624417
BLAST score	150
E value	5.0e-19
Match length	71
% identity	70
NCBI Description	(AJ002959) Ubiquitin carrier protein [Zea mays]

Seq. No.	53255
Seq. ID	wrg700787056.h2
Method	BLASTN
NCBI GI	g1053215
BLAST score	213
E value	1.0e-116
Match length	256
% identity	96
NCBI Description	Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	53256
Seq. ID	wrg700787057.h2
Method	BLASTX
NCBI GI	g3914472
BLAST score	234
E value	6.0e-20
Match length	57
% identity	79
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	53257
Seq. ID	wrg700787071.h2
Method	BLASTX
NCBI GI	g4371280
BLAST score	292
E value	1.0e-26
Match length	76
% identity	82
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53258
Seq. ID	wrg700787113.h2
Method	BLASTN
NCBI GI	g20728
BLAST score	59
E value	1.0e-24
Match length	185
% identity	84
NCBI Description	Pea chloroplast GAPA mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13)

Seq. No.	53259
Seq. ID	wrg700787138.h2
Method	BLASTN
NCBI GI	g2832242
BLAST score	246
E value	1.0e-136
Match length	257
% identity	9
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	53260
Seq. ID	wrg700787152.h2
Method	BLASTN
NCBI GI	g20728
BLAST score	86
E value	8.0e-41
Match length	178
% identity	87
NCBI Description	Pea chloroplast GAPA mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13)

Seq. No.	53261
Seq. ID	wrg700787288.h2
Method	BLASTX
NCBI GI	g3096930
BLAST score	163
E value	1.0e-11
Match length	73
% identity	48
NCBI Description	(AL023094) Homeodomain - like protein [Arabidopsis thaliana]

Seq. No.	53262
Seq. ID	wrg700787309.h2
Method	BLASTX
NCBI GI	g4510426
BLAST score	158
E value	6.0e-11
Match length	87
% identity	53
NCBI Description	(AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53263
Seq. ID	wrg700787344.h2
Method	BLASTN
NCBI GI	g168671
BLAST score	139
E value	1.0e-72
Match length	158
% identity	97
NCBI Description	Maize 19 kd zein protein, mRNA (incomplete)

Seq. No.	53264
Seq. ID	wrg700787362.h2
Method	BLASTN

NCBI GI	g21796
BLAST score	131
E value	1.0e-67
Match length	226
% identity	90
NCBI Description	Wheat histone H3 gene

Seq. No.	53265
Seq. ID	wrg700787368.h2
Method	BLASTX
NCBI GI	g4335745
BLAST score	224
E value	9.0e-19
Match length	74
% identity	54
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	53266
Seq. ID	wrg700787371.h2
Method	BLASTX
NCBI GI	g2498706
BLAST score	150
E value	5.0e-10
Match length	70
% identity	46
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	53267
Seq. ID	wrg700787385.h2
Method	BLASTN
NCBI GI	g2182028
BLAST score	56
E value	4.0e-23
Match length	160
% identity	84
NCBI Description	Oryza sativa mRNA for shaggy-like kinase etha

Seq. No.	53268
Seq. ID	wrg700787411.h2
Method	BLASTN
NCBI GI	g20598
BLAST score	145
E value	6.0e-76
Match length	217
% identity	92
NCBI Description	P.miliaceum mRNA for aspartate aminotransferase (pcAAT2)

Seq. No.	53269
Seq. ID	wrg700787466.h2
Method	BLASTX
NCBI GI	g3063767
BLAST score	424

E value	4.0e-42
Match length	88
% identity	92
NCBI Description	(X79192) pyruvate,orthophosphate dikinase [Flaveria brownii]

Seq. No.	53270
Seq. ID	wrg700787521.h1
Method	BLASTX
NCBI GI	g3757518
BLAST score	165
E value	6.0e-12
Match length	71
% identity	46
NCBI Description	(AC005167) putative immediate-early salicylate-induced glucosyltransferase [Arabidopsis thaliana]

Seq. No.	53271
Seq. ID	wrg700787621.h2
Method	BLASTX
NCBI GI	g4512018
BLAST score	195
E value	2.0e-15
Match length	45
% identity	80
NCBI Description	(AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No.	53272
Seq. ID	wrg700787639.h2
Method	BLASTX
NCBI GI	g3510255
BLAST score	160
E value	3.0e-11
Match length	57
% identity	56
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53273
Seq. ID	wrg700787652.h2
Method	BLASTN
NCBI GI	g1928978
BLAST score	164
E value	2.0e-87
Match length	238
% identity	93
NCBI Description	Vigna unguiculata phospholipase D mRNA, complete cds

Seq. No.	53274
Seq. ID	wrg700787666.h2
Method	BLASTX
NCBI GI	g481812
BLAST score	168
E value	3.0e-12
Match length	46
% identity	36
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana

>gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	53275
Seq. ID	wrg700787743.h2
Method	BLASTX
NCBI GI	g3785994
BLAST score	315
E value	2.0e-29
Match length	81
% identity	73
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53276
Seq. ID	wrg700787745.h2
Method	BLASTX
NCBI GI	g4056457
BLAST score	191
E value	7.0e-15
Match length	49
% identity	76
NCBI Description	(AC005990) ESTs gb_234051 and gb_F13722 come from this gene. [Arabidopsis thaliana]

Seq. No.	53277
Seq. ID	wrg700787765.h2
Method	BLASTX
NCBI GI	g3033384
BLAST score	221
E value	2.0e-18
Match length	61
% identity	66
NCBI Description	(AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No.	53278
Seq. ID	wrg700787784.h2
Method	BLASTX
NCBI GI	g3786011
BLAST score	288
E value	3.0e-26
Match length	66
% identity	82
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	53279
Seq. ID	wrg700787848.h2
Method	BLASTX
NCBI GI	g4220529
BLAST score	145
E value	6.0e-21
Match length	78
% identity	60
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	53280
Seq. ID	wrg700787896.h2

Method	BLASTX
NCBI GI	g4538905
BLAST score	154
E value	1.0e-13
Match length	50
% identity	86
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	53281
Seq. ID	wrg700787908.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	110
E value	2.0e-55
Match length	154
% identity	93
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	53282
Seq. ID	wrg700787955.h1
Method	BLASTX
NCBI GI	g2529707
BLAST score	251
E value	6.0e-22
Match length	81
% identity	56
NCBI Description	(AF001434) Hpast [Homo sapiens]

Seq. No.	53283
Seq. ID	wrg700788011.h1
Method	BLASTX
NCBI GI	g2129473
BLAST score	170
E value	2.0e-12
Match length	63
% identity	49
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	53284
Seq. ID	wrg700788025.h1
Method	BLASTX
NCBI GI	g3075488
BLAST score	251
E value	5.0e-22
Match length	54
% identity	85
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	53285
Seq. ID	wrg700788114.h1
Method	BLASTN
NCBI GI	g927504
BLAST score	98
E value	6.0e-48
Match length	198

% identity	88
NCBI Description	P.sativum mRNA for fructose-1, 6-biphosphate aldolase (clone aldcyt2)

Seq. No.	53286
Seq. ID	wrg700788202.h1
Method	BLASTX
NCBI GI	g3860277
BLAST score	191
E value	6.0e-15
Match length	62
% identity	81
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	53287
Seq. ID	wrg700788349.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	205
E value	1.0e-112
Match length	268
% identity	94
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	53288
Seq. ID	wrg700788593.h1
Method	BLASTX
NCBI GI	g3298548
BLAST score	225
E value	8.0e-19
Match length	78
% identity	59
NCBI Description	(AC004681) putative spliceosomal protein [Arabidopsis thaliana]

Seq. No.	53289
Seq. ID	wrg700788654.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	84
E value	1.0e-39
Match length	186
% identity	87
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	53290
Seq. ID	wrg700788722.h2
Method	BLASTN
NCBI GI	g169036
BLAST score	138
E value	8.0e-72
Match length	234
% identity	90

NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	53291
Seq. ID	wrg700788735.h2
Method	BLASTX
NCBI GI	g309673
BLAST score	154
E value	9.0e-11
Match length	53
% identity	70
NCBI Description	(L19651) light harvesting protein [Pisum sativum]

Seq. No.	53292
Seq. ID	wrg700788752.h2
Method	BLASTN
NCBI GI	g4206305
BLAST score	42
E value	1.0e-14
Match length	82
% identity	44
NCBI Description	Zea mays retrotransposon Cinful-1, complete sequence

Seq. No.	53293
Seq. ID	wrg700788762.h2
Method	BLASTX
NCBI GI	g3420052
BLAST score	230
E value	1.0e-19
Match length	56
% identity	73
NCBI Description	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No.	53294
Seq. ID	wrg700788774.h2
Method	BLASTX
NCBI GI	g432359
BLAST score	209
E value	4.0e-17
Match length	52
% identity	73
NCBI Description	(D23660) ribosomal protein [Homo sapiens]

Seq. No.	53295
Seq. ID	wrg700788807.h2
Method	BLASTX
NCBI GI	g4455340
BLAST score	171
E value	1.0e-12
Match length	80
% identity	50
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

Seq. No.	53296
Seq. ID	wrg700788838.h2
Method	BLASTN
NCBI GI	g168681

BLAST score	161
E value	1.0e-85
Match length	237
% identity	94
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No.	53297
Seq. ID	wrg700788845.h2
Method	BLASTN
NCBI GI	g3694836
BLAST score	56
E value	6.0e-23
Match length	96
% identity	90
NCBI Description	Zea mays centromeric retrotransposon-like repeat CentA, complete sequence

Seq. No.	53298
Seq. ID	wrg700788846.h2
Method	BLASTX
NCBI GI	g4220462
BLAST score	218
E value	4.0e-18
Match length	60
% identity	49
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	53299
Seq. ID	wrg700788869.h2
Method	BLASTN
NCBI GI	g170073
BLAST score	136
E value	1.0e-70
Match length	206
% identity	92
NCBI Description	Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No.	53300
Seq. ID	wrg700788901.h2
Method	BLASTN
NCBI GI	g4140643
BLAST score	184
E value	2.0e-99
Match length	213
% identity	21
NCBI Description	Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No.	53301
Seq. ID	wrg700788909.h2
Method	BLASTX
NCBI GI	g1946331
BLAST score	140
E value	2.0e-12

Match length	51
% identity	71
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	53302
Seq. ID	wrg700788916.h2
Method	BLASTN
NCBI GI	g22509
BLAST score	148
E value	9.0e-78
Match length	257
% identity	97
NCBI Description	Zea mays waxy (wx+) locus for UDP-glucose starch glycosyl transferase

Seq. No.	53303
Seq. ID	wrg700788970.h2
Method	BLASTX
NCBI GI	g2462835
BLAST score	144
E value	1.0e-09
Match length	45
% identity	67
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53304
Seq. ID	wrg700788986.h2
Method	BLASTN
NCBI GI	g168669
BLAST score	174
E value	3.0e-93
Match length	257
% identity	71
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19A2, partial cds

Seq. No.	53305
Seq. ID	wrg700788990.h2
Method	BLASTN
NCBI GI	g632737
BLAST score	105
E value	3.0e-52
Match length	221
% identity	87
NCBI Description	ADP-glucose pyrophosphorylase=grain Bt2 subunit homolog [Zea mays=corn, leaves, mRNA Partial, 615 nt]

Seq. No.	53306
Seq. ID	wrg700789026.h2
Method	BLASTX
NCBI GI	g2702278
BLAST score	145
E value	1.0e-09
Match length	41
% identity	63
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana] >gi_2914690 (AC003974) hypothetical protein [Arabidopsis

thaliana]

Seq. No.	53307
Seq. ID	wrg700789051.h2
Method	BLASTX
NCBI GI	g4490735
BLAST score	191
E value	4.0e-15
Match length	54
% identity	79
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	53308
Seq. ID	wrg700789064.h2
Method	BLASTX
NCBI GI	g4539408
BLAST score	143
E value	3.0e-09
Match length	35
% identity	86
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	53309
Seq. ID	wrg700789077.h2
Method	BLASTN
NCBI GI	g168704
BLAST score	252
E value	1.0e-140
Match length	252
% identity	100
NCBI Description	Zea mays zein protein gene, complete cds

Seq. No.	53310
Seq. ID	wrg700789082.h2
Method	BLASTX
NCBI GI	g4191784
BLAST score	145
E value	2.0e-09
Match length	81
% identity	35
NCBI Description	(AC005917) putative WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	53311
Seq. ID	wrg700789106.h1
Method	BLASTX
NCBI GI	g732189
BLAST score	171
E value	3.0e-15
Match length	84
% identity	48
NCBI Description	HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION >gi_2131922_pir__S50724 hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) >gi_600058_emb_CAA55501_ (X78898) N1342 [Saccharomyces cerevisiae] >gi_1302211_emb_CAA96109_ (Z71483) ORF YNL207w [Saccharomyces cerevisiae]

Seq. No.	53312
Seq. ID	wrg700789129.h1
Method	BLASTX
NCBI GI	g4262142
BLAST score	208
E value	9.0e-17
Match length	70
% identity	53
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	53313
Seq. ID	wrg700789227.h2
Method	BLASTX
NCBI GI	g2804278
BLAST score	215
E value	1.0e-17
Match length	72
% identity	62
NCBI Description	(AB003516) squalene epoxidase [Panax ginseng]

Seq. No.	53314
Seq. ID	wrg700789243.h2
Method	BLASTX
NCBI GI	g3152595
BLAST score	192
E value	2.0e-30
Match length	88
% identity	76
NCBI Description	(AC002986) Similar to D. melanogaster sno gene gb_U95760. EST gb_N97148 and gb_Z26221 come from this gene. [Arabidopsis thaliana]

Seq. No.	53315
Seq. ID	wrg700789259.h2
Method	BLASTX
NCBI GI	g1946300
BLAST score	172
E value	1.0e-12
Match length	82
% identity	22
NCBI Description	(Y12529) hypothetical protein [Silene latifolia]

Seq. No.	53316
Seq. ID	wrg700789273.h2
Method	BLASTN
NCBI GI	g4220637
BLAST score	34
E value	8.0e-10
Match length	70
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	53317
Seq. ID	wrg700789278.h2

Method	BLASTX
NCBI GI	g3204125
BLAST score	142
E value	4.0e-09
Match length	45
% identity	60
NCBI Description	(AJ006766) putative Pi starvation-induced protein [Cicer arietinum]

Seq. No.	53318
Seq. ID	wrg700789290.h2
Method	BLASTN
NCBI GI	g2924257
BLAST score	151
E value	1.0e-79
Match length	250
% identity	90
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	53319
Seq. ID	wrg700789335.h2
Method	BLASTX
NCBI GI	g3395440
BLAST score	147
E value	1.0e-09
Match length	72
% identity	44
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53320
Seq. ID	wrg700789337.h2
Method	BLASTN
NCBI GI	g1617035
BLAST score	158
E value	7.0e-84
Match length	214
% identity	93
NCBI Description	V.unguiculata mRNA for Ted2 protein

Seq. No.	53321
Seq. ID	wrg700789371.h2
Method	BLASTX
NCBI GI	g2244850
BLAST score	148
E value	5.0e-10
Match length	41
% identity	71
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53322
Seq. ID	wrg700789391.h2
Method	BLASTN
NCBI GI	g960290
BLAST score	34
E value	8.0e-10
Match length	58
% identity	90

NCBI Description	Ruta graveolens anthranilate synthase alpha-subunit mRNA, complete cds
Seq. No.	53323
Seq. ID	wrg700789403.h2
Method	BLASTX
NCBI GI	g3236247
BLAST score	202
E value	2.0e-16
Match length	55
% identity	71
NCBI Description	(AC004684) SCARECROW-like protein [Arabidopsis thaliana]
Seq. No.	53324
Seq. ID	wrg700789437.h2
Method	BLASTN
NCBI GI	g2465528
BLAST score	51
E value	4.0e-20
Match length	125
% identity	89
NCBI Description	Medicago truncatula phosphate transporter (MtPT2) mRNA, complete cds
Seq. No.	53325
Seq. ID	wrg700789443.h2
Method	BLASTX
NCBI GI	g2494111
BLAST score	205
E value	2.0e-16
Match length	55
% identity	67
NCBI Description	(AC002376) Contains similarity to Glycine protein kinase 6 (gb_M67449). [Arabidopsis thaliana]
Seq. No.	53326
Seq. ID	wrg700789481.h2
Method	BLASTX
NCBI GI	g4559377
BLAST score	166
E value	4.0e-12
Match length	56
% identity	61
NCBI Description	(AC006526) putative photomorphogenesis repressor protein COP1 [Arabidopsis thaliana]
Seq. No.	53327
Seq. ID	wrg700789570.h2
Method	BLASTX
NCBI GI	g3218550
BLAST score	346
E value	4.0e-33
Match length	78
% identity	85
NCBI Description	(AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
Seq. No.	53328

Seq. ID	wrg700789604.h2
Method	BLASTX
NCBI GI	g2660669
BLAST score	227
E value	4.0e-19
Match length	84
% identity	55
NCBI Description	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]

Seq. No.	53329
Seq. ID	wrg700789615.h2
Method	BLASTN
NCBI GI	g18551
BLAST score	146
E value	1.0e-76
Match length	158
% identity	98
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	53330
Seq. ID	wrg700789722.h1
Method	BLASTX
NCBI GI	g2911056
BLAST score	163
E value	1.0e-11
Match length	62
% identity	48
NCBI Description	(AL021961) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53331
Seq. ID	wrg700789729.h1
Method	BLASTX
NCBI GI	g4115938
BLAST score	206
E value	1.0e-16
Match length	62
% identity	76
NCBI Description	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]

Seq. No.	53332
Seq. ID	wrg700789768.h1
Method	BLASTX
NCBI GI	g4263781
BLAST score	271
E value	2.0e-24
Match length	72
% identity	62
NCBI Description	(AC006068) putative membrane transport protein [Arabidopsis thaliana]

Seq. No.	53333
Seq. ID	wrg700789772.h1
Method	BLASTX

NCBI GI	g4185129
BLAST score	248
E value	1.0e-21
Match length	73
% identity	60
NCBI Description	(AC005724) unknown protein [Arabidopsis thaliana] >gi_4218012 (AC006135) unknown protein [Arabidopsis thaliana]

Seq. No.	53334
Seq. ID	wrg700789849.h2
Method	BLASTX
NCBI GI	g3337350
BLAST score	194
E value	2.0e-20
Match length	75
% identity	69
NCBI Description	(AC004481) putative permease [Arabidopsis thaliana]

Seq. No.	53335
Seq. ID	wrg700789854.h2
Method	BLASTN
NCBI GI	g1150683
BLAST score	85
E value	3.0e-40
Match length	209
% identity	86
NCBI Description	V.radiata atpB, rbcL and trnK genes

Seq. No.	53336
Seq. ID	wrg700789863.h2
Method	BLASTX
NCBI GI	g3785977
BLAST score	254
E value	3.0e-22
Match length	61
% identity	74
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	53337
Seq. ID	wrg700789922.h2
Method	BLASTX
NCBI GI	g2760839
BLAST score	279
E value	4.0e-32
Match length	89
% identity	83
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	53338
Seq. ID	wrg700789955.h2
Method	BLASTX
NCBI GI	g3786017
BLAST score	153
E value	2.0e-10
Match length	74

% identity	49
NCBI Description	(AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No.	53339
Seq. ID	wrg700789972.h2
Method	BLASTX
NCBI GI	g1710530
BLAST score	276
E value	8.0e-25
Match length	50
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	53340
Seq. ID	wrg700789978.h2
Method	BLASTN
NCBI GI	g288058
BLAST score	149
E value	2.0e-78
Match length	197
% identity	94
NCBI Description	Z.mays S13 mRNA for cytoplasmic ribosomal protein S13

Seq. No.	53341
Seq. ID	wrg700790001.h2
Method	BLASTX
NCBI GI	g585110
BLAST score	263
E value	2.0e-23
Match length	71
% identity	72
NCBI Description	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) >gi_479194_pir__S32482 electron transfer flavoprotein beta chain - human >gi_2781203_pdb_1EFV_B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution >gi_297902_emb_CAA50441_ (X71129) electron transfer flavoprotein beta subunit [Homo sapiens] >gi_4503609_ref_NP_001976.1_pETFB_ electron-transfer-flavoprotein, beta polypeptide

Seq. No.	53342
Seq. ID	wrg700790007.h2
Method	BLASTN
NCBI GI	g309672
BLAST score	82
E value	1.0e-38
Match length	134
% identity	90
NCBI Description	Pisum sativum chloroplast photosystem I 24 kDa light harvesting protein (lhca3) mRNA, complete cds

Seq. No.	53343
Seq. ID	wrg700790010.h2

Method	BLASTN
NCBI GI	g4098966
BLAST score	51
E value	7.0e-20
Match length	103
% identity	87
NCBI Description	Glycine max putative reistance gene analog genomic sequence

Seq. No.	53344
Seq. ID	wrg700790029.h2
Method	BLASTX
NCBI GI	g4138912
BLAST score	216
E value	5.0e-18
Match length	47
% identity	85
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]

Seq. No.	53345
Seq. ID	wrg700790038.h2
Method	BLASTN
NCBI GI	g168702
BLAST score	92
E value	1.0e-44
Match length	131
% identity	94
NCBI Description	Corn 22 kDa zein protein gene, complete cds

Seq. No.	53346
Seq. ID	wrg700790063.h2
Method	BLASTN
NCBI GI	g168419
BLAST score	225
E value	1.0e-123
Match length	233
% identity	99
NCBI Description	Maize (Z.mays) aldolase mRNA, complete cds

Seq. No.	53347
Seq. ID	wrg700790064.h2
Method	BLASTN
NCBI GI	g457688
BLAST score	122
E value	3.0e-62
Match length	238
% identity	88
NCBI Description	M.crystallinum mRNA for protein kinase

Seq. No.	53348
Seq. ID	wrg700790074.h2
Method	BLASTX
NCBI GI	g4544451
BLAST score	330
E value	3.0e-31
Match length	84
% identity	77
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]

Seq. No.	53349
Seq. ID	wrg700790079.h2
Method	BLASTN
NCBI GI	g248336
BLAST score	212
E value	1.0e-116
Match length	232
% identity	27
NCBI Description	polyubiquitin [maize, Genomic, 3841 nt]

Seq. No.	53350
Seq. ID	wrg700790090.h2
Method	BLASTX
NCBI GI	g3850101
BLAST score	155
E value	7.0e-11
Match length	40
% identity	70
NCBI Description	(AL033388) putative rna-binding protein [Schizosaccharomyces pombe]

Seq. No.	53351
Seq. ID	wrg700790101.h1
Method	BLASTX
NCBI GI	g2443755
BLAST score	308
E value	1.0e-28
Match length	79
% identity	90
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No.	53352
Seq. ID	wrg700790179.h1
Method	BLASTN
NCBI GI	g2623245
BLAST score	81
E value	7.0e-38
Match length	228
% identity	85
NCBI Description	Pisum sativum poly(A) polymerase mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	53353
Seq. ID	wrg700790212.h2
Method	BLASTN
NCBI GI	g340933
BLAST score	237
E value	1.0e-131
Match length	257
% identity	98
NCBI Description	Zea mays 10-kDa zein gene, complete cds

Seq. No.	53354
Seq. ID	wrg700790247.h2
Method	BLASTN
NCBI GI	g4185305

BLAST score	189
E value	1.0e-102
Match length	253
% identity	94
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No.	53355
Seq. ID	wrg700790260.h2
Method	BLASTX
NCBI GI	g4204284
BLAST score	265
E value	1.0e-23
Match length	69
% identity	65
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	53356
Seq. ID	wrg700790273.h2
Method	BLASTX
NCBI GI	g2190187
BLAST score	323
E value	2.0e-30
Match length	82
% identity	78
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	53357
Seq. ID	wrg700790333.h2
Method	BLASTX
NCBI GI	g586318
BLAST score	150
E value	4.0e-10
Match length	61
% identity	54
NCBI Description	HYPOTHETICAL 30.3 KD PROTEIN IN MBA1-RPS13 INTERGENIC REGION >gi_626233_pir__S46059 probable membrane protein YBR187w - yeast (Saccharomyces cerevisiae) >gi_536548_emb_CAA85148_ (Z36056) ORF YBR187w [Saccharomyces cerevisiae] >gi_575915 (U02073) unknown [Saccharomyces cerevisiae]

Seq. No.	53358
Seq. ID	wrg700790341.h2
Method	BLASTX
NCBI GI	g2244792
BLAST score	217
E value	5.0e-18
Match length	78
% identity	41
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	53359

Seq. ID	wrg700790351.h2
Method	BLASTX
NCBI GI	g4097571
BLAST score	182
E value	7.0e-14
Match length	44
% identity	77
NCBI Description	(U64916) GMFP5 [Glycine max]

Seq. No.	53360
Seq. ID	wrg700790355.h2
Method	BLASTX
NCBI GI	g3738325
BLAST score	339
E value	3.0e-32
Match length	78
% identity	81
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No.	53361
Seq. ID	wrg700790454.h2
Method	BLASTN
NCBI GI	g2529228
BLAST score	116
E value	1.0e-58
Match length	232
% identity	88
NCBI Description	Glycine max mRNA for 6-phosphogluconate dehydrogenase, complete cds

Seq. No.	53362
Seq. ID	wrg700790462.h2
Method	BLASTX
NCBI GI	g4510406
BLAST score	400
E value	2.0e-39
Match length	82
% identity	89
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	53363
Seq. ID	wrg700790465.h2
Method	BLASTX
NCBI GI	g3193292
BLAST score	249
E value	1.0e-21
Match length	65
% identity	74
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	53364
Seq. ID	wrg700790480.h2
Method	BLASTX
NCBI GI	g1931655

BLAST score	146
E value	8.0e-10
Match length	39
% identity	67
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	53365
Seq. ID	wrg700790495.h2
Method	BLASTN
NCBI GI	g169097
BLAST score	51
E value	6.0e-20
Match length	171
% identity	82
NCBI Description	Pea histone H2A mRNA

Seq. No.	53366
Seq. ID	wrg700790587.h2
Method	BLASTX
NCBI GI	g480602
BLAST score	231
E value	1.0e-19
Match length	72
% identity	30
NCBI Description	polyadenylate-binding protein - fern (Anemia phyllitidis) >gi_398327_emb_CAA81127_ (Z26042) poly(A)-mRNA binding protein [Anemia phyllitidis]

Seq. No.	53367
Seq. ID	wrg700790627.h2
Method	BLASTX
NCBI GI	g3461841
BLAST score	126
E value	3.0e-16
Match length	72
% identity	56
NCBI Description	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	53368
Seq. ID	wrg700790685.h2
Method	BLASTN
NCBI GI	g2330650
BLAST score	87
E value	2.0e-41
Match length	226
% identity	85
NCBI Description	Pisum sativum mRNA for topoisomerase II

Seq. No.	53369
Seq. ID	wrg700790848.h1
Method	BLASTX
NCBI GI	g4415917
BLAST score	246
E value	3.0e-21
Match length	88
% identity	53

NCBI Description	(AC006282) putative protein containing zinc finger domain [Arabidopsis thaliana]

Seq. No.	53370
Seq. ID	wrg700790862.h1
Method	BLASTX
NCBI GI	g3021269
BLAST score	168
E value	4.0e-12
Match length	78
% identity	49
NCBI Description	(AL022347) putative protein [Arabidopsis thaliana]

Seq. No.	53371
Seq. ID	wrg700790922.h1
Method	BLASTN
NCBI GI	g20831
BLAST score	43
E value	2.0e-15
Match length	67
% identity	91
NCBI Description	P.sativum petC mRNA for chloroplast Rieske FeS protein

Seq. No.	53372
Seq. ID	wrg700790924.h1
Method	BLASTX
NCBI GI	g1076528
BLAST score	148
E value	5.0e-10
Match length	46
% identity	59
NCBI Description	heat shock protein HSP70b - garden pea >gi_562004 (U08820) HSP70b [Pisum sativum]

Seq. No.	53373
Seq. ID	wrg700790971.h1
Method	BLASTX
NCBI GI	g3044218
BLAST score	142
E value	3.0e-09
Match length	73
% identity	57
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	53374
Seq. ID	wrg700791036.h1
Method	BLASTN
NCBI GI	g1438878
BLAST score	52
E value	2.0e-20
Match length	105
% identity	99
NCBI Description	Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No.	53375
Seq. ID	wrg700791043.h1
Method	BLASTN

NCBI GI	g4406529
BLAST score	96
E value	9.0e-47
Match length	181
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53376
Seq. ID	wrg700791115.h1
Method	BLASTN
NCBI GI	g1208536
BLAST score	186
E value	1.0e-100
Match length	190
% identity	99
NCBI Description	Glycine max guanine nucleotide regulatory protein (rab2) mRNA, complete cds

Seq. No.	53377
Seq. ID	wrg700791194.h1
Method	BLASTN
NCBI GI	g24762
BLAST score	99
E value	6.0e-49
Match length	115
% identity	97
NCBI Description	H.sapiens mRNA fragment for alpha-2 macroglobulin receptor

Seq. No.	53378
Seq. ID	wrg700791212.h1
Method	BLASTX
NCBI GI	g1155090
BLAST score	190
E value	1.0e-14
Match length	53
% identity	64
NCBI Description	(X94986) beta glucosidase [Manihot esculenta]

Seq. No.	53379
Seq. ID	wrg700791276.h1
Method	BLASTX
NCBI GI	g4510389
BLAST score	150
E value	5.0e-10
Match length	46
% identity	54
NCBI Description	(AC007017) putative solute carrier protein [Arabidopsis thaliana]

Seq. No.	53380
Seq. ID	wrg700791292.h1
Method	BLASTX
NCBI GI	g3413716
BLAST score	139
E value	6.0e-09
Match length	42

% identity	36
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643589 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	53381
Seq. ID	wrg700791429.h1
Method	BLASTX
NCBI GI	g1170622
BLAST score	226
E value	3.0e-19
Match length	59
% identity	78
NCBI Description	CASEIN KINASE I, DELTA ISOFORM LIKE (CKI-DELTA) >gi_549973 (U12857) casein kinase I-like protein; similar to the rat delta isoform of casein kinase I, Swiss-Prot Accession Number Q06486 [Arabidopsis thaliana]

Seq. No.	53382
Seq. ID	wrg700791502.h1
Method	BLASTX
NCBI GI	g4376548
BLAST score	268
E value	6.0e-24
Match length	82
% identity	61
NCBI Description	(AE001612) DNA Gyrase Subunit B [Chlamydia pneumoniae]

Seq. No.	53383
Seq. ID	wrg700791511.h1
Method	BLASTX
NCBI GI	g1352736
BLAST score	225
E value	4.0e-19
Match length	61
% identity	64
NCBI Description	PELOTA PROTEIN >gi_973224 (U27197) pelota [Drosophila melanogaster]

Seq. No.	53384
Seq. ID	wrg700791701.h1
Method	BLASTX
NCBI GI	g2245057
BLAST score	193
E value	3.0e-15
Match length	46
% identity	78
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53385
Seq. ID	wrg700791740.h1
Method	BLASTX
NCBI GI	g4544418
BLAST score	208
E value	6.0e-17
Match length	68
% identity	57

NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53386
Seq. ID	wrg700791769.h1
Method	BLASTX
NCBI GI	g1762634
BLAST score	255
E value	1.0e-22
Match length	54
% identity	78
NCBI Description	(U64789) AROGP2 [Lycopersicon esculentum]

Seq. No.	53387
Seq. ID	wrg700791774.h1
Method	BLASTX
NCBI GI	g3242709
BLAST score	148
E value	5.0e-10
Match length	43
% identity	60
NCBI Description	(AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]

Seq. No.	53388
Seq. ID	wrg700791792.h1
Method	BLASTN
NCBI GI	g408791
BLAST score	35
E value	1.0e-10
Match length	111
% identity	86
NCBI Description	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds

Seq. No.	53389
Seq. ID	wrg700791930.h1
Method	BLASTX
NCBI GI	g3925363
BLAST score	307
E value	1.0e-28
Match length	78
% identity	78
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	53390
Seq. ID	wrg700791980.h1
Method	BLASTX
NCBI GI	g1730043
BLAST score	246
E value	2.0e-21
Match length	79
% identity	65
NCBI Description	AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 >gi_2132561_pir__S61137 probable membrane protein YGL180w - yeast (Saccharomyces cerevisiae) >gi_1143567_emb_CAA62794_ (X91489) putative ser/thr protein kinase [Saccharomyces cerevisiae] >gi_1322791_emb_CAA96892_ (Z72702) ORF YGL180w

[Saccharomyces cerevisiae] >gi_2257625_dbj_BAA21481_ (D29991) Apg1p [Saccharomyces cerevisiae]

Seq. No.	53391
Seq. ID	wrg700792010.h1
Method	BLASTX
NCBI GI	g4006869
BLAST score	139
E value	6.0e-09
Match length	45
% identity	64
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	53392
Seq. ID	wrg700792112.h1
Method	BLASTX
NCBI GI	g2827139
BLAST score	315
E value	2.0e-29
Match length	83
% identity	76
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	53393
Seq. ID	wrg700792139.h1
Method	BLASTX
NCBI GI	g3273202
BLAST score	183
E value	5.0e-14
Match length	47
% identity	87
NCBI Description	(AB010918) responce reactor4 [Arabidopsis thaliana]

Seq. No.	53394
Seq. ID	wrg700792165.h1
Method	BLASTX
NCBI GI	g2766452
BLAST score	148
E value	5.0e-10
Match length	50
% identity	58
NCBI Description	(AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]

Seq. No.	53395
Seq. ID	wrg700792173.h1
Method	BLASTX
NCBI GI	g2191144
BLAST score	207
E value	8.0e-17
Match length	75
% identity	51
NCBI Description	(AF007269) A_IG002N01.24 gene product [Arabidopsis thaliana]

Seq. No.	53396
Seq. ID	wrg700792175.h1
Method	BLASTX
NCBI GI	g1770190
BLAST score	150
E value	4.0e-10
Match length	51
% identity	53
NCBI Description	(Y10162) cyclin-D like protein [Chenopodium rubrum]

Seq. No.	53397
Seq. ID	wrg700792189.h1
Method	BLASTX
NCBI GI	g4163997
BLAST score	389
E value	4.0e-38
Match length	80
% identity	79
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	53398
Seq. ID	wrg700792245.h1
Method	BLASTX
NCBI GI	g541949
BLAST score	347
E value	4.0e-33
Match length	83
% identity	77
NCBI Description	rab7 protein - Soybean

Seq. No.	53399
Seq. ID	wvk700679947.h2
Method	BLASTN
NCBI GI	g1619904
BLAST score	76
E value	8.0e-35
Match length	104
% identity	93
NCBI Description	Glycine max thiol protease isoform A mRNA, partial cds

Seq. No.	53400
Seq. ID	wvk700679982.h2
Method	BLASTN
NCBI GI	g210811
BLAST score	46
E value	4.0e-17
Match length	105
% identity	87
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	53401
Seq. ID	wvk700679985.h2
Method	BLASTN
NCBI GI	g169036
BLAST score	50

E value	3.0e-19
Match length	70
% identity	93
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	53402
Seq. ID	wvk700679986.h2
Method	BLASTX
NCBI GI	g3894170
BLAST score	162
E value	2.0e-11
Match length	85
% identity	41
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	53403
Seq. ID	wvk700680002.h2
Method	BLASTN
NCBI GI	g169036
BLAST score	46
E value	7.0e-17
Match length	70
% identity	91
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	53404
Seq. ID	wvk700680017.h2
Method	BLASTX
NCBI GI	g2499087
BLAST score	193
E value	4.0e-15
Match length	66
% identity	58
NCBI Description	UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) >gi_1085170_pir__S54723 UDP-glucose--glycoprotein glucosyltransferase - fruit fly (Drosophila sp.) >gi_790585 (U20554) UDP-glucose:glycoprotein glucosyltransferase precursor [Drosophila melanogaster]

Seq. No.	53405
Seq. ID	wvk700680031.h2
Method	BLASTX
NCBI GI	g1438879
BLAST score	138
E value	1.0e-08
Match length	58
% identity	55
NCBI Description	(U43838) GmCK1p [Glycine max]

Seq. No.	53406
Seq. ID	wvk700680055.h2
Method	BLASTN
NCBI GI	g12139
BLAST score	80
E value	1.0e-37
Match length	100

% identity	95
NCBI Description	Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No.	53407
Seq. ID	wvk700680093.h2
Method	BLASTX
NCBI GI	g4530126
BLAST score	170
E value	2.0e-12
Match length	79
% identity	47
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	53408
Seq. ID	wvk700680146.h2
Method	BLASTX
NCBI GI	g2244847
BLAST score	158
E value	5.0e-11
Match length	64
% identity	50
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	53409
Seq. ID	wvk700680148.h2
Method	BLASTX
NCBI GI	g3482974
BLAST score	250
E value	9.0e-22
Match length	77
% identity	62
NCBI Description	(AL031369) ATP-dependent Clp proteinase-like protein [Arabidopsis thaliana]

Seq. No.	53410
Seq. ID	wvk700680195.h2
Method	BLASTX
NCBI GI	g1001355
BLAST score	169
E value	3.0e-12
Match length	88
% identity	43
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	53411
Seq. ID	wvk700680215.h2
Method	BLASTN
NCBI GI	g3435305
BLAST score	49
E value	9.0e-19
Match length	129
% identity	84
NCBI Description	Medicago sativa glycolate oxidase mRNA, partial cds

Seq. No.	53412
Seq. ID	wvk700680241.h2
Method	BLASTX
NCBI GI	g3928089
BLAST score	174
E value	7.0e-13
Match length	84
% identity	47
NCBI Description	(AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No.	53413
Seq. ID	wvk700680249.h2
Method	BLASTN
NCBI GI	g4406529
BLAST score	180
E value	7.0e-97
Match length	258
% identity	92
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53414
Seq. ID	wvk700680256.h2
Method	BLASTN
NCBI GI	g2661020
BLAST score	63
E value	4.0e-27
Match length	70
% identity	99
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	53415
Seq. ID	wvk700680301.h1
Method	BLASTN
NCBI GI	g2208961
BLAST score	34
E value	4.0e-10
Match length	58
% identity	90
NCBI Description	O.sativa mRNA for signal recognition particle subunit

Seq. No.	53416
Seq. ID	wvk700680316.h1
Method	BLASTN
NCBI GI	g22469
BLAST score	67
E value	1.0e-29
Match length	159
% identity	86
NCBI Description	Maize mRNA for cytoplasmic ribosomal protein S11

Seq. No.	53417
Seq. ID	wvk700680324.h1
Method	BLASTX
NCBI GI	g3582335
BLAST score	146

E value	9.0e-10
Match length	40
% identity	65
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	53418
Seq. ID	wvk700680348.h1
Method	BLASTN
NCBI GI	g602564
BLAST score	56
E value	3.0e-23
Match length	124
% identity	86
NCBI Description	C.paradisi (Macf) INO1 gene

Seq. No.	53419
Seq. ID	wvk700680395.h1
Method	BLASTX
NCBI GI	g2651310
BLAST score	356
E value	5.0e-34
Match length	93
% identity	71
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	53420
Seq. ID	wvk700680413.h1
Method	BLASTN
NCBI GI	g2739216
BLAST score	50
E value	3.0e-19
Match length	86
% identity	90
NCBI Description	Hordeum vulgare L41 ribosomal protein

Seq. No.	53421
Seq. ID	wvk700680456.h1
Method	BLASTX
NCBI GI	g4056506
BLAST score	299
E value	2.0e-27
Match length	101
% identity	60
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	53422
Seq. ID	wvk700680467.h1
Method	BLASTN
NCBI GI	g456567
BLAST score	74
E value	2.0e-33
Match length	145
% identity	88
NCBI Description	Pisum sativum ubiquitin conjugating enzyme (UBC4), complete cds

Seq. No.	53423
Seq. ID	wvk700680511.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	229
E value	1.0e-126
Match length	276
% identity	96
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	53424
Seq. ID	wvk700680580.h1
Method	BLASTX
NCBI GI	g629592
BLAST score	137
E value	1.0e-08
Match length	41
% identity	68
NCBI Description	hypothetical protein - rape

Seq. No.	53425
Seq. ID	wvk700680612.h1
Method	BLASTN
NCBI GI	g3309268
BLAST score	45
E value	9.0e-17
Match length	92
% identity	88
NCBI Description	Glycine max ferric leghemoglobin reductase-2 precursor mRNA, complete cds

Seq. No.	53426
Seq. ID	wvk700680625.h1
Method	BLASTN
NCBI GI	g18551
BLAST score	205
E value	1.0e-112
Match length	285
% identity	94
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	53427
Seq. ID	wvk700680635.h1
Method	BLASTN
NCBI GI	g309670
BLAST score	39
E value	5.0e-13
Match length	131
% identity	89
NCBI Description	Pea chloroplast glyceraldehyde-3-phosphate dehydrogenase (Gpb1) gene, complete cds

Seq. No.	53428
Seq. ID	wvk700680718.h1
Method	BLASTX

NCBI GI	g1346310
BLAST score	276
E value	1.0e-24
Match length	104
% identity	55
NCBI Description	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) >gi_217692_dbj_BAA02660_ (D13390) 4-hydroxyphenylpyruvic acid dioxygenase [Sus scrofa]

Seq. No.	53429
Seq. ID	wvk700680733.h1
Method	BLASTN
NCBI GI	g456567
BLAST score	43
E value	4.0e-15
Match length	103
% identity	85
NCBI Description	Pisum sativum ubiquitin conjugating enzyme (UBC4), complete cds

Seq. No.	53430
Seq. ID	wvk700680780.h1
Method	BLASTX
NCBI GI	g461550
BLAST score	205
E value	2.0e-16
Match length	63
% identity	71
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	53431
Seq. ID	wvk700680815.h1
Method	BLASTX
NCBI GI	g3885342
BLAST score	243
E value	6.0e-21
Match length	82
% identity	55
NCBI Description	(AC005623) putative DNA polymerase [Arabidopsis thaliana]

Seq. No.	53432
Seq. ID	wvk700680881.h1
Method	BLASTX
NCBI GI	g2661608
BLAST score	348
E value	4.0e-33
Match length	94
% identity	65
NCBI Description	(AL009197) hypothetical ctp synthase [Schizosaccharomyces pombe]

Seq. No.	53433
Seq. ID	wvk700680902.h1

Method	BLASTN
NCBI GI	g1055367
BLAST score	126
E value	1.0e-64
Match length	201
% identity	91
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	53434
Seq. ID	wvk700680926.h1
Method	BLASTN
NCBI GI	g497119
BLAST score	150
E value	8.0e-79
Match length	318
% identity	87
NCBI Description	Pisum sativum monodehydroascorbate reductase mRNA, complete cds

Seq. No.	53435
Seq. ID	wvk700680944.h1
Method	BLASTN
NCBI GI	g684941
BLAST score	111
E value	1.0e-55
Match length	227
% identity	87
NCBI Description	Medicago sativa S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase (CCOMT) mRNA, complete cds

Seq. No.	53436
Seq. ID	wvk700680955.h1
Method	BLASTX
NCBI GI	g4115915
BLAST score	298
E value	3.0e-27
Match length	102
% identity	57
NCBI Description	(AF118222) contains similarity to Helix pomatia br-1 protein (GB: X96994) [Arabidopsis thaliana]

Seq. No.	53437
Seq. ID	wvk700680989.h1
Method	BLASTN
NCBI GI	g168498
BLAST score	218
E value	1.0e-119
Match length	330
% identity	92
NCBI Description	Corn histone H4 (H4C13) gene, complete cds

Seq. No.	53438
Seq. ID	wvk700680992.h1
Method	BLASTX
NCBI GI	g1001355
BLAST score	213

E value	3.0e-17
Match length	61
% identity	61
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	53439
Seq. ID	wvk700681004.h1
Method	BLASTX
NCBI GI	g3402673
BLAST score	313
E value	6.0e-29
Match length	113
% identity	63
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	53440
Seq. ID	wvk700681005.h1
Method	BLASTN
NCBI GI	g169056
BLAST score	74
E value	2.0e-33
Match length	181
% identity	86
NCBI Description	P.sativum carbonic anhydrase mRNA, complete cds

Seq. No.	53441
Seq. ID	wvk700681016.h1
Method	BLASTN
NCBI GI	g3982832
BLAST score	53
E value	5.0e-21
Match length	226
% identity	83
NCBI Description	Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds

Seq. No.	53442
Seq. ID	wvk700681039.h1
Method	BLASTX
NCBI GI	g4559385
BLAST score	135
E value	4.0e-16
Match length	89
% identity	49
NCBI Description	(AC006526) putative cyclic nucleotide-regulated ion channel protein [Arabidopsis thaliana]

Seq. No.	53443
Seq. ID	wvk700681043.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	86
E value	1.0e-40
Match length	181
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53444
Seq. ID	wvk700681047.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	86
E value	1.0e-40
Match length	255
% identity	84
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53445
Seq. ID	wvk700681090.h1
Method	BLASTN
NCBI GI	g1561773
BLAST score	33
E value	4.0e-09
Match length	41
% identity	95
NCBI Description	Vitis vinifera malate dehydrogenase (VVME2) mRNA, complete cds

Seq. No.	53446
Seq. ID	wvk700681146.h2
Method	BLASTX
NCBI GI	g461595
BLAST score	212
E value	3.0e-17
Match length	60
% identity	72
NCBI Description	ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II) >gi_479533_pir__S34473 H+-transporting ATP synthase (EC 3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_ (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]

Seq. No.	53447
Seq. ID	wvk700681177.h2
Method	BLASTN
NCBI GI	g349328
BLAST score	65
E value	1.0e-28
Match length	117
% identity	89
NCBI Description	Glycine max glyoxysomal isocitrate lyase isoform 2 (ICL2) mRNA, 3' end

Seq. No.	53448
Seq. ID	wvk700681188.h2
Method	BLASTX
NCBI GI	g133939
BLAST score	146
E value	1.0e-09
Match length	60
% identity	52
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70865_pir__R3NT3 ribosomal protein S3 - common tobacco chloroplast

>gi_11865_emb_CAA77381_ (Z00044) ribosomal protein S3 [Nicotiana tabacum] >gi_225235_prf__1211235BT ribosomal protein S3 [Nicotiana tabacum]

Seq. No.	53449
Seq. ID	wvk700681201.h1
Method	BLASTN
NCBI GI	g38261
BLAST score	191
E value	1.0e-103
Match length	218
% identity	98
NCBI Description	H.sapiens mRNA for mitochondrial phosphate carrier protein >gi_1408428_gb_G28613_G28613 human STS SHGC-35782. >gi_4505774_ref_NM_002635.1_PHC_ Homo sapiens phosphate carrier, mitochondrial (PHC) mRNA

Seq. No.	53450
Seq. ID	wvk700681206.h1
Method	BLASTN
NCBI GI	g3282160
BLAST score	355
E value	0.0e+00
Match length	355
% identity	100
NCBI Description	Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence [Homo sapiens]

Seq. No.	53451
Seq. ID	wvk700681233.h1
Method	BLASTN
NCBI GI	g30308
BLAST score	121
E value	1.0e-61
Match length	187
% identity	91
NCBI Description	Human mRNA for T-cell cyclophilin

Seq. No.	53452
Seq. ID	wvk700681253.h1
Method	BLASTX
NCBI GI	g4415931
BLAST score	218
E value	6.0e-18
Match length	81
% identity	56
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	53453
Seq. ID	wvk700681288.h1
Method	BLASTN
NCBI GI	g219909
BLAST score	293
E value	1.0e-164
Match length	328

% identity	98
NCBI Description	Homo sapiens mRNA for lipocortin II, complete cds

Seq. No.	53454
Seq. ID	wvk700681295.h1
Method	BLASTN
NCBI GI	g1082037
BLAST score	103
E value	5.0e-51
Match length	161
% identity	91
NCBI Description	Human G0S3 mRNA, complete cds

Seq. No.	53455
Seq. ID	wvk700681321.h2
Method	BLASTN
NCBI GI	g170455
BLAST score	76
E value	8.0e-35
Match length	219
% identity	84
NCBI Description	Tomato heat shock cognate protein 80 gene, 3' end

Seq. No.	53456
Seq. ID	wvk700681370.h2
Method	BLASTX
NCBI GI	g1350981
BLAST score	189
E value	1.0e-14
Match length	78
% identity	53
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S PHASE SPECIFIC PROTEIN BIS289) >gi_480282_pir__S36622 hypothetical protein - turnip >gi_387909 (L23553) S-phase-specific protein [Brassica rapa] >gi_397401_emb_CAA81030_ (Z25769) putative product [Brassica rapa]

Seq. No.	53457
Seq. ID	wvk700681408.h2
Method	BLASTN
NCBI GI	g18644
BLAST score	202
E value	1.0e-110
Match length	225
% identity	98
NCBI Description	Soybean mRNA for HMG-1 like protein

Seq. No.	53458
Seq. ID	wvk700681442.h2
Method	BLASTN
NCBI GI	g459961
BLAST score	111
E value	1.0e-55
Match length	249
% identity	89
NCBI Description	Glycine max proplastid omega-6 desaturase mRNA, complete cds

Seq. No.	53459
Seq. ID	wvk700681445.h2
Method	BLASTX
NCBI GI	g2129538
BLAST score	191
E value	2.0e-31
Match length	81
% identity	86
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	53460
Seq. ID	wvk700681469.h2
Method	BLASTN
NCBI GI	g20728
BLAST score	82
E value	2.0e-38
Match length	185
% identity	87
NCBI Description	Pea chloroplast GAPA mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13)

Seq. No.	53461
Seq. ID	wvk700681535.h1
Method	BLASTN
NCBI GI	g4234847
BLAST score	77
E value	2.0e-35
Match length	132
% identity	90
NCBI Description	Zea mays copia-like retrotransposon Sto-3, partial sequence

Seq. No.	53462
Seq. ID	wvk700681538.h1
Method	BLASTX
NCBI GI	g1514643
BLAST score	170
E value	2.0e-12
Match length	41
% identity	68
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	53463
Seq. ID	wvk700681545.h1
Method	BLASTN
NCBI GI	g1162979
BLAST score	77
E value	2.0e-35
Match length	157
% identity	87
NCBI Description	Spinacia oleracea nuclear-encoded chloroplast ribulose-5-phosphate 3-epimerase mRNA, complete cds

Seq. No.	53464
Seq. ID	wvk700681566.h1

Method	BLASTX
NCBI GI	g1174619
BLAST score	123
E value	5.0e-16
Match length	72
% identity	63
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_1078409_pir__S53376 t-complex protein 1 homolog YJL111w - yeast (Saccharomyces cerevisiae) >gi_728699_emb_CAA59383_ (X85021) TCP-1 homologue [Saccharomyces cerevisiae] >gi_1008297_emb_CAA89406_ (Z49386) ORF YJL111w [Saccharomyces cerevisiae]

Seq. No.	53465
Seq. ID	wvk700681579.h1
Method	BLASTN
NCBI GI	g168446
BLAST score	44
E value	7.0e-16
Match length	68
% identity	91
NCBI Description	Zea mays copia-like retrotransposon reverse transcriptase gene, 3' end

Seq. No.	53466
Seq. ID	wvk700681584.h1
Method	BLASTX
NCBI GI	g282921
BLAST score	163
E value	1.0e-11
Match length	70
% identity	51
NCBI Description	carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_169057 (M63627) carbonic anhydrase [Pisum sativum] >gi_227784_prf__1710354A carbonic anhydrase [Pisum sativum]

Seq. No.	53467
Seq. ID	wvk700681587.h1
Method	BLASTN
NCBI GI	g17862
BLAST score	71
E value	5.0e-32
Match length	179
% identity	85
NCBI Description	B.napus mRNA for ribosomal protein S15a (pPCB8)

Seq. No.	53468
Seq. ID	wvk700681635.h1
Method	BLASTN
NCBI GI	g20728
BLAST score	82
E value	2.0e-38
Match length	186
% identity	86
NCBI Description	Pea chloroplast GAPA mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13)

Seq. No.	53469
Seq. ID	wvk700681649.h1
Method	BLASTN
NCBI GI	g1041674
BLAST score	194
E value	1.0e-105
Match length	214
% identity	98
NCBI Description	Z.mays mRNA for V-type H+-ATPase, clone 16-2

Seq. No.	53470
Seq. ID	wvk700681654.h1
Method	BLASTX
NCBI GI	g3298540
BLAST score	186
E value	7.0e-16
Match length	82
% identity	56
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No.	53471
Seq. ID	wvk700681658.h1
Method	BLASTX
NCBI GI	g4263783
BLAST score	274
E value	1.0e-24
Match length	80
% identity	61
NCBI Description	(AC006068) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	53472
Seq. ID	wvk700681719.h1
Method	BLASTX
NCBI GI	g4567235
BLAST score	276
E value	7.0e-25
Match length	77
% identity	68
NCBI Description	(AC007119) putative phosphatidylinositol/phophatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No.	53473
Seq. ID	wvk700681728.h1
Method	BLASTX
NCBI GI	g1169238
BLAST score	398
E value	3.0e-39
Match length	80
% identity	86
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) >gi_1076648_pir__A48767 glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia >gi_294112 (L16797) glutamate decarboxylase [Petunia hybrida] >gi_309680 (L16977) glutamate decarboxylase [Petunia hybrida]

Seq. No. 53474

Seq. ID	wvk700681741.h1
Method	BLASTX
NCBI GI	g584806
BLAST score	267
E value	7.0e-24
Match length	80
% identity	71
NCBI Description	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR >gi_83764_pir__JC1111 H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - Neurospora crassa >gi_168759 (M84191) mitochondrial ATPase alpha-subunit [Neurospora crassa]

Seq. No.	53475
Seq. ID	wvk700681750.h1
Method	BLASTX
NCBI GI	g1707138
BLAST score	147
E value	9.0e-10
Match length	78
% identity	45
NCBI Description	(U80836) similar to E. coli THIJ (GB:U34923) [Caenorhabditis elegans]

Seq. No.	53476
Seq. ID	wvk700681760.h1
Method	BLASTX
NCBI GI	g2342686
BLAST score	249
E value	9.0e-22
Match length	77
% identity	60
NCBI Description	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb_Z49209). ESTs gb_T44436,gb_42252 come from this gene. [Arabidopsis thaliana]

Seq. No.	53477
Seq. ID	wvk700681782.h1
Method	BLASTN
NCBI GI	g1055367
BLAST score	238
E value	1.0e-131
Match length	238
% identity	100
NCBI Description	Glycine max ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	53478
Seq. ID	wvk700681795.h1
Method	BLASTN
NCBI GI	g1658192
BLAST score	126
E value	1.0e-64
Match length	198
% identity	91
NCBI Description	Sorghum bicolor obtusifoliol 14-alpha demethylase CYP51 (CYP51) mRNA, complete cds

Seq. No.	53479
Seq. ID	wvk700681804.h1
Method	BLASTN
NCBI GI	g602564
BLAST score	88
E value	6.0e-42
Match length	168
% identity	88
NCBI Description	C.paradisi (Macf) INO1 gene

Seq. No.	53480
Seq. ID	wvk700681811.h1
Method	BLASTX
NCBI GI	g3885513
BLAST score	150
E value	5.0e-10
Match length	38
% identity	66
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	53481
Seq. ID	wvk700681836.h1
Method	BLASTX
NCBI GI	g1168263
BLAST score	264
E value	2.0e-23
Match length	85
% identity	31
NCBI Description	ATP-BINDING CASSETTE TRANSPORTER 2 >gi_1082239_pir__B54774 ATP binding cassette transporter ABC2 - human (fragment) >gi_495259_emb_CAA53531_ (X75927) abc2 [Mus musculus]

Seq. No.	53482
Seq. ID	wvk700681839.h1
Method	BLASTN
NCBI GI	g1483214
BLAST score	71
E value	8.0e-32
Match length	206
% identity	87
NCBI Description	A.thaliana mRNA for chloroplast FtsH protease

Seq. No.	53483
Seq. ID	wvk700681845.h1
Method	BLASTN
NCBI GI	g218130
BLAST score	91
E value	9.0e-44
Match length	172
% identity	89
NCBI Description	Rice mRNA for Ribosomal protein S15

Seq. No.	53484
Seq. ID	wvk700681851.h1
Method	BLASTX

NCBI GI	g4539422
BLAST score	166
E value	6.0e-12
Match length	38
% identity	76
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	53485
Seq. ID	wvk700681853.h1
Method	BLASTN
NCBI GI	g602564
BLAST score	80
E value	3.0e-37
Match length	168
% identity	87
NCBI Description	C.paradisi (Macf) INO1 gene

Seq. No.	53486
Seq. ID	wvk700681860.h1
Method	BLASTN
NCBI GI	g564023
BLAST score	121
E value	1.0e-61
Match length	224
% identity	92
NCBI Description	Zea mays dihydrolipoamide acetyl transferase (ZM/DHLAAT) mRNA, complete cds

Seq. No.	53487
Seq. ID	wvk700681937.h1
Method	BLASTN
NCBI GI	g303856
BLAST score	103
E value	6.0e-51
Match length	119
% identity	97
NCBI Description	Rice mRNA for ubiquitin protein fused to a ribosomal protein, complete cds

Seq. No.	53488
Seq. ID	wvk700681959.h1
Method	BLASTX
NCBI GI	g4079800
BLAST score	208
E value	4.0e-35
Match length	82
% identity	98
NCBI Description	(AF052503) S-phase-specific ribosomal protein [Oryza sativa]

Seq. No.	53489
Seq. ID	wvk700681965.h1
Method	BLASTX
NCBI GI	g3123843
BLAST score	144
E value	3.0e-09
Match length	63

% identity	38
NCBI Description	(U66035) X-linked deafness dystonia protein [Homo sapiens]

Seq. No.	53490
Seq. ID	wvk700681984.h1
Method	BLASTN
NCBI GI	g168547
BLAST score	116
E value	1.0e-58
Match length	183
% identity	91
NCBI Description	Zea mays putative brain specific 14-3-3 protein, tau protein homolog mRNA, partial cds

Seq. No.	53491
Seq. ID	wvk700681988.h1
Method	BLASTX
NCBI GI	g2827888
BLAST score	334
E value	1.0e-31
Match length	87
% identity	72
NCBI Description	(AF016621) ATP-dependent Clp protease proteolytic subunit [Arabidopsis thaliana]

Seq. No.	53492
Seq. ID	wvk700681991.h1
Method	BLASTX
NCBI GI	g1168195
BLAST score	264
E value	2.0e-23
Match length	73
% identity	73
NCBI Description	14-3-3-LIKE PROTEIN >gi_478595_pir__S20580 protein kinase C inhibitor homolog - Hooker's evening primrose >gi_20062_emb_CAA44642_ (X62838) protein kinase C inhibitor homologue [Oenothera elata subsp. hookeri]

Seq. No.	53493
Seq. ID	wvk700682013.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	78
E value	4.0e-36
Match length	210
% identity	84
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53494
Seq. ID	wvk700682017.h1
Method	BLASTX
NCBI GI	g2462741
BLAST score	297
E value	3.0e-27
Match length	73
% identity	79

NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	53495
Seq. ID	wvk700682023.h1
Method	BLASTN
NCBI GI	g1184775
BLAST score	230
E value	1.0e-126
Match length	262
% identity	97
NCBI Description	Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4) mRNA, complete cds

Seq. No.	53496
Seq. ID	wvk700682027.h1
Method	BLASTX
NCBI GI	g3953471
BLAST score	289
E value	2.0e-26
Match length	84
% identity	63
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	53497
Seq. ID	wvk700682028.h1
Method	BLASTX
NCBI GI	g461812
BLAST score	205
E value	2.0e-16
Match length	73
% identity	51
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	53498
Seq. ID	wvk700682032.h1
Method	BLASTX
NCBI GI	g1402876
BLAST score	303
E value	6.0e-28
Match length	67
% identity	46
NCBI Description	(X98130) putative phosphate permease [Arabidopsis thaliana] >gi_1495255_emb_CAA66116_ (X97484) orf01 [Arabidopsis thaliana]

Seq. No.	53499
Seq. ID	wvk700682046.h1
Method	BLASTN
NCBI GI	g3108052
BLAST score	228
E value	1.0e-125
Match length	260

% identity	97
NCBI Description	Zea mays myo-inositol 1-phosphate synthase mRNA, complete cds

Seq. No.	53500
Seq. ID	wvk700682052.h1
Method	BLASTX
NCBI GI	g1619321
BLAST score	191
E value	7.0e-15
Match length	82
% identity	44
NCBI Description	(Y07563) hin1 [Nicotiana tabacum]

Seq. No.	53501
Seq. ID	wvk700682055.h1
Method	BLASTX
NCBI GI	g3451068
BLAST score	142
E value	5.0e-11
Match length	72
% identity	50
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	53502
Seq. ID	wvk700682056.h1
Method	BLASTN
NCBI GI	g1785614
BLAST score	142
E value	3.0e-74
Match length	222
% identity	91
NCBI Description	Pisum sativum protein kinase homolog PsPK4 mRNA, complete cds

Seq. No.	53503
Seq. ID	wvk700682063.h1
Method	BLASTX
NCBI GI	g2088658
BLAST score	250
E value	7.0e-22
Match length	81
% identity	64
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	53504
Seq. ID	wvk700682078.h1
Method	BLASTX
NCBI GI	g2980795
BLAST score	343
E value	1.0e-32
Match length	86
% identity	81
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	53505
Seq. ID	wvk700682089.h1

Method	BLASTX
NCBI GI	g1653033
BLAST score	128
E value	4.0e-14
Match length	83
% identity	58
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	53506
Seq. ID	wvk700682106.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	56
E value	7.0e-23
Match length	136
% identity	85
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53507
Seq. ID	wvk700682143.h1
Method	BLASTX
NCBI GI	g1361979
BLAST score	138
E value	1.0e-08
Match length	31
% identity	90
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - watermelon >gi_1350550_dbj_BAA12843_ (D85624) serine acetyltransferase [Citrullus lanatus] >gi_1841312_dbj_BAA08479_ (D49535) serine acetyltransferase. [Citrullus lanatus] >gi_2337772_dbj_BAA21827_ (AB006530) serine acetyltransferase [Citrullus lanatus]

Seq. No.	53508
Seq. ID	wvk700682144.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	179
E value	3.0e-96
Match length	251
% identity	93
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53509
Seq. ID	wvk700682250.h1
Method	BLASTX
NCBI GI	g4138265
BLAST score	253
E value	4.0e-22
Match length	84
% identity	52
NCBI Description	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]

Seq. No.	53510

Seq. ID	wvk700682259.h1
Method	BLASTN
NCBI GI	g1553128
BLAST score	59
E value	1.0e-24
Match length	143
% identity	85
NCBI Description	Gossypium hirsutum ribosomal protein L44 isoform a (RL44), complete cds

Seq. No.	53511
Seq. ID	wvk700682266.h1
Method	BLASTX
NCBI GI	g2244898
BLAST score	99
E value	5.0e-09
Match length	78
% identity	41
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	53512
Seq. ID	wvk700682271.h1
Method	BLASTX
NCBI GI	g2118425
BLAST score	251
E value	7.0e-22
Match length	70
% identity	74
NCBI Description	subtilisin/chymotrypsin inhibitor - maize >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea mays] >gi_475922_emb_CAA49593_ (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187) substilin /chymotrypsin-like inhibitor [Zea mays]

Seq. No.	53513
Seq. ID	wvk700682278.h1
Method	BLASTX
NCBI GI	g2347088
BLAST score	216
E value	1.0e-17
Match length	61
% identity	66
NCBI Description	(U72765) non-specific lipid transfer protein PvLTP-24 [Phaseolus vulgaris]

Seq. No.	53514
Seq. ID	wvk700682285.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	94
E value	1.0e-45
Match length	182
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53515
Seq. ID	wvk700682319.h2
Method	BLASTX
NCBI GI	g3860264
BLAST score	188
E value	3.0e-18
Match length	60
% identity	78
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	53516
Seq. ID	wvk700682328.h2
Method	BLASTN
NCBI GI	g4406529
BLAST score	93
E value	5.0e-45
Match length	180
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53517
Seq. ID	wvk700682376.h2
Method	BLASTX
NCBI GI	g3152559
BLAST score	289
E value	2.0e-26
Match length	63
% identity	84
NCBI Description	(AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No.	53518
Seq. ID	wvk700682377.h2
Method	BLASTX
NCBI GI	g4538963
BLAST score	203
E value	2.0e-16
Match length	50
% identity	76
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana]

Seq. No.	53519
Seq. ID	wvk700682385.h2
Method	BLASTN
NCBI GI	g4406529
BLAST score	60
E value	3.0e-25
Match length	120
% identity	88
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53520
Seq. ID	wvk700682412.h2

Method	BLASTX
NCBI GI	g1305549
BLAST score	124
E value	4.0e-13
Match length	80
% identity	59
NCBI Description	(U55874) asparagine synthetase [Glycine max]

Seq. No.	53521
Seq. ID	wvk700682428.h2
Method	BLASTX
NCBI GI	g2129739
BLAST score	185
E value	2.0e-14
Match length	53
% identity	72
NCBI Description	shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No.	53522
Seq. ID	wvk700682490.h2
Method	BLASTX
NCBI GI	g399333
BLAST score	132
E value	3.0e-12
Match length	69
% identity	65
NCBI Description	CYSTEINE SYNTHASE CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8) precursor - pepper >gi_17944_emb_CAA46086_ (X64874) O-acetylserine (thiol)-lyase [Capsicum annuum]

Seq. No.	53523
Seq. ID	wvk700682506.h2
Method	BLASTN
NCBI GI	g3550039
BLAST score	218
E value	1.0e-119
Match length	254
% identity	98
NCBI Description	Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B

Seq. No.	53524
Seq. ID	wvk700682534.h2
Method	BLASTN
NCBI GI	g30081
BLAST score	58
E value	4.0e-24
Match length	81
% identity	94
NCBI Description	Human COL8A1 mRNA for alpha 1(VIII) collagen

>gi_4502962_ref_NM_001850.1_COL8A1_ Homo sapiens collagen, type VIII, alpha 1 (COL8A1) mRNA

Seq. No.	53525
Seq. ID	wvk700682577.h2
Method	BLASTN
NCBI GI	g256142
BLAST score	113
E value	7.0e-57
Match length	120
% identity	99
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	53526
Seq. ID	wvk700682587.h2
Method	BLASTX
NCBI GI	g4220462
BLAST score	115
E value	9.0e-15
Match length	74
% identity	66
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	53527
Seq. ID	wvk700682628.h2
Method	BLASTX
NCBI GI	g3549665
BLAST score	158
E value	5.0e-11
Match length	63
% identity	56
NCBI Description	(AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53528
Seq. ID	wvk700682728.h1
Method	BLASTN
NCBI GI	g20852
BLAST score	39
E value	1.0e-12
Match length	127
% identity	83
NCBI Description	P. sativum mRNA for phosphate translocator

Seq. No.	53529
Seq. ID	wvk700682737.h1
Method	BLASTX
NCBI GI	g1922242
BLAST score	145
E value	2.0e-09
Match length	49
% identity	49
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]

Seq. No. 53530

Seq. ID	wvk700682788.h1
Method	BLASTX
NCBI GI	g2506139
BLAST score	140
E value	1.0e-15
Match length	54
% identity	71
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	53531
Seq. ID	wvk700682794.h1
Method	BLASTN
NCBI GI	g1053215
BLAST score	171
E value	2.0e-91
Match length	267
% identity	93
NCBI Description	Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	53532
Seq. ID	wvk700682894.h1
Method	BLASTN
NCBI GI	g18376
BLAST score	241
E value	1.0e-133
Match length	253
% identity	99
NCBI Description	Glycine max PAL1 gene for phenylalanine ammonia lyase (EC 4.3.1.5)

Seq. No.	53533
Seq. ID	wvk700682904.h1
Method	BLASTN
NCBI GI	g1237081
BLAST score	47
E value	8.0e-18
Match length	91
% identity	88
NCBI Description	P.sativum mRNA for ADP-glucose pyrophosphorylase (agpS2)

Seq. No.	53534
Seq. ID	wvk700683019.h1
Method	BLASTX
NCBI GI	g3355662
BLAST score	144
E value	6.0e-16
Match length	77
% identity	56
NCBI Description	(AJ009693) ribosomal protein L9 [Podocoryne carnea]

Seq. No.	53535
Seq. ID	wvk700683042.h1
Method	BLASTN
NCBI GI	g18551

BLAST score	221
E value	1.0e-121
Match length	260
% identity	97
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	53536
Seq. ID	wvk700683048.h1
Method	BLASTN
NCBI GI	g169056
BLAST score	55
E value	3.0e-22
Match length	111
% identity	87
NCBI Description	P.sativum carbonic anhydrase mRNA, complete cds

Seq. No.	53537
Seq. ID	wvk700683152.h1
Method	BLASTX
NCBI GI	g2832625
BLAST score	171
E value	2.0e-12
Match length	77
% identity	47
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	53538
Seq. ID	wvk700683191.h1
Method	BLASTN
NCBI GI	g2351063
BLAST score	34
E value	9.0e-10
Match length	90
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	53539
Seq. ID	wvk700683196.h1
Method	BLASTX
NCBI GI	g2392895
BLAST score	177
E value	3.0e-13
Match length	83
% identity	45
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	53540
Seq. ID	wvk700683248.h1
Method	BLASTX
NCBI GI	g2429343
BLAST score	297
E value	3.0e-27
Match length	86
% identity	67

NCBI Description	(AF019376) calreticulin [Brassica napus]
Seq. No.	53541
Seq. ID	wvk700683302.h1
Method	BLASTX
NCBI GI	g2832661
BLAST score	224
E value	1.0e-18
Match length	67
% identity	69
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]
Seq. No.	53542
Seq. ID	wvk700683395.h1
Method	BLASTX
NCBI GI	g3914052
BLAST score	113
E value	4.0e-10
Match length	70
% identity	57
NCBI Description	DNA MISMATCH REPAIR PROTEIN MSH6 >gi_2104549 (AF001535) AGAA.3 [Arabidopsis thaliana]
Seq. No.	53543
Seq. ID	wvk700683405.h1
Method	BLASTN
NCBI GI	g984307
BLAST score	129
E value	8.0e-67
Match length	129
% identity	100
NCBI Description	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso
Seq. No.	53544
Seq. ID	wvk700683450.h1
Method	BLASTN
NCBI GI	g2502086
BLAST score	32
E value	6.0e-09
Match length	64
% identity	88
NCBI Description	Vigna radiata adenosine triphosphatase mRNA, complete cds
Seq. No.	53545
Seq. ID	wvk700683464.h1
Method	BLASTN
NCBI GI	g18551
BLAST score	185
E value	1.0e-100
Match length	205
% identity	97
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No.	53546
Seq. ID	wvk700683507.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	202
E value	1.0e-110
Match length	230
% identity	97
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	53547
Seq. ID	wvk700683511.h1
Method	BLASTX
NCBI GI	g2353175
BLAST score	186
E value	3.0e-14
Match length	70
% identity	49
NCBI Description	(AF015544) sigma factor 3 [Arabidopsis thaliana] >gi_2463554_dbj_BAA22530_ (D89994) SigC [Arabidopsis thaliana]

Seq. No.	53548
Seq. ID	wvk700683523.h1
Method	BLASTX
NCBI GI	g3860262
BLAST score	144
E value	2.0e-09
Match length	39
% identity	69
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	53549
Seq. ID	wvk700683558.h1
Method	BLASTN
NCBI GI	g1419684
BLAST score	47
E value	2.0e-17
Match length	146
% identity	87
NCBI Description	M.sativa mRNA for TCTP-like protein

Seq. No.	53550
Seq. ID	wvk700683615.h1
Method	BLASTX
NCBI GI	g3150406
BLAST score	258
E value	1.0e-22
Match length	84
% identity	54
NCBI Description	(AC004165) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	53551
Seq. ID	wvk700683621.h1

Method	BLASTN
NCBI GI	g169038
BLAST score	48
E value	3.0e-18
Match length	103
% identity	94
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	53552
Seq. ID	wvk700683674.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	169
E value	3.0e-90
Match length	233
% identity	93
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53553
Seq. ID	wvk700683703.h1
Method	BLASTX
NCBI GI	g2827546
BLAST score	247
E value	2.0e-21
Match length	91
% identity	49
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	53554
Seq. ID	wvk700683721.h1
Method	BLASTN
NCBI GI	g3309268
BLAST score	129
E value	2.0e-66
Match length	281
% identity	91
NCBI Description	Glycine max ferric leghemoglobin reductase-2 precursor mRNA, complete cds

Seq. No.	53555
Seq. ID	wvk700683733.h1
Method	BLASTX
NCBI GI	g3914472
BLAST score	274
E value	1.0e-24
Match length	66
% identity	80
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	53556
Seq. ID	wvk700683750.h1
Method	BLASTX

NCBI GI	g1173638
BLAST score	274
E value	2.0e-24
Match length	92
% identity	54
NCBI Description	(U35779) 1-aminocyclopropane-1-carboxylate synthase [Triticum aestivum]

Seq. No.	53557
Seq. ID	wvk700683783.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	105
E value	4.0e-52
Match length	253
% identity	85
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	53558
Seq. ID	wvk700683791.h1
Method	BLASTX
NCBI GI	g128825
BLAST score	291
E value	1.0e-26
Match length	82
% identity	68
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) >gi_108830_pir__A33552 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) precursor - bovine >gi_163414 (J02877) NADH:ubiquinone reductase precursor [Bos taurus]

Seq. No.	53559
Seq. ID	wvk700683792.h1
Method	BLASTX
NCBI GI	g2129941
BLAST score	264
E value	2.0e-23
Match length	86
% identity	62
NCBI Description	zeaxanthin epoxidase precursor - curled-leaved tobacco >gi_1370274_emb_CAA65048_ (X95732) zeaxanthin epoxidase [Nicotiana plumbaginifolia]

Seq. No.	53560
Seq. ID	wvk700683795.h1
Method	BLASTX
NCBI GI	g4580470
BLAST score	312
E value	5.0e-29
Match length	70
% identity	79
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53561
Seq. ID	wvk700683813.h1

Method	BLASTX
NCBI GI	g3776557
BLAST score	267
E value	6.0e-24
Match length	75
% identity	65
NCBI Description	(AC005388) Contains similarity to gi_2924495 hypothetical protein Rv1920 from Mycobacterium tuberculosis genome gb_AL022020. [Arabidopsis thaliana]

Seq. No.	53562
Seq. ID	wvk700683849.h1
Method	BLASTX
NCBI GI	g2632252
BLAST score	309
E value	8.0e-29
Match length	74
% identity	73
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	53563
Seq. ID	wvk700683905.h1
Method	BLASTX
NCBI GI	g1136434
BLAST score	90
E value	1.0e-08
Match length	62
% identity	50
NCBI Description	(D80009) KIAA0187 [Homo sapiens]

Seq. No.	53564
Seq. ID	wvk700683907.h1
Method	BLASTX
NCBI GI	g2191197
BLAST score	152
E value	1.0e-22
Match length	85
% identity	72
NCBI Description	(AF007271) contains similarity to Synechococcus PCC7942 chromosomal region used as basis of neutral siteII recombinational cloning vector (PID:g1174192) [Arabidopsis thaliana]

Seq. No.	53565
Seq. ID	wvk700683924.h1
Method	BLASTN
NCBI GI	g2801669
BLAST score	41
E value	6.0e-14
Match length	41
% identity	100
NCBI Description	Mycosphaerella graminicola succinate dehydrogenase iron-sulphur protein gene, complete cds

Seq. No.	53566
Seq. ID	wvk700684008.h1
Method	BLASTX

NCBI GI	g4115379
BLAST score	153
E value	2.0e-10
Match length	48
% identity	58
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	53567
Seq. ID	wvk700684038.h1
Method	BLASTN
NCBI GI	g2773269
BLAST score	132
E value	3.0e-68
Match length	273
% identity	96
NCBI Description	Glycine max ferredoxin-dependent glutamate synthase (glu) mRNA, partial cds

Seq. No.	53568
Seq. ID	wvk700684068.h1
Method	BLASTN
NCBI GI	g535764
BLAST score	45
E value	3.0e-16
Match length	89
% identity	88
NCBI Description	Stylosanthes humilis peroxidase mRNA

Seq. No.	53569
Seq. ID	wvk700684094.h1
Method	BLASTX
NCBI GI	g1514643
BLAST score	215
E value	1.0e-17
Match length	55
% identity	60
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	53570
Seq. ID	wvk700684111.h1
Method	BLASTX
NCBI GI	g3914472
BLAST score	274
E value	1.0e-24
Match length	66
% identity	80
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	53571
Seq. ID	wvk700684128.h1
Method	BLASTX
NCBI GI	g2905643
BLAST score	139

E value	9.0e-09
Match length	80
% identity	34
NCBI Description	(AF045244) ribitol kinase [Klebsiella pneumoniae]

Seq. No.	53572
Seq. ID	wvk700684150.h1
Method	BLASTX
NCBI GI	g4455331
BLAST score	205
E value	2.0e-16
Match length	84
% identity	48
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	53573
Seq. ID	wvk700684188.h1
Method	BLASTN
NCBI GI	g169056
BLAST score	58
E value	4.0e-24
Match length	86
% identity	92
NCBI Description	P.sativum carbonic anhydrase mRNA, complete cds

Seq. No.	53574
Seq. ID	wvk700684206.h1
Method	BLASTX
NCBI GI	g4406809
BLAST score	149
E value	7.0e-19
Match length	67
% identity	55
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	53575
Seq. ID	wvk700684221.h1
Method	BLASTX
NCBI GI	g4530126
BLAST score	212
E value	3.0e-17
Match length	89
% identity	51
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	53576
Seq. ID	wvk700684238.h1
Method	BLASTX
NCBI GI	g3927830
BLAST score	142
E value	4.0e-09
Match length	87
% identity	43
NCBI Description	(AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53577

Seq. ID	wvk700684286.h1
Method	BLASTX
NCBI GI	g4510375
BLAST score	258
E value	1.0e-22
Match length	66
% identity	77
NCBI Description	(AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No.	53578
Seq. ID	wvk700684333.h1
Method	BLASTN
NCBI GI	g2632108
BLAST score	76
E value	8.0e-35
Match length	104
% identity	93
NCBI Description	Pisum sativum mRNA for phospholipid glutathione peroxidase

Seq. No.	53579
Seq. ID	wvk700684345.h1
Method	BLASTX
NCBI GI	g3377812
BLAST score	265
E value	2.0e-23
Match length	78
% identity	65
NCBI Description	(AF076275) contains similarity to heavy-metal-associated domain containing proteins (Pfam: HMA.hm, score: 12.02) [Arabidopsis thaliana]

Seq. No.	53580
Seq. ID	wvk700684396.h1
Method	BLASTX
NCBI GI	g4559351
BLAST score	217
E value	6.0e-18
Match length	86
% identity	52
NCBI Description	(AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53581
Seq. ID	wvk700684441.h1
Method	BLASTX
NCBI GI	g3785974
BLAST score	123
E value	2.0e-09
Match length	48
% identity	71
NCBI Description	(AC005560) putative DNA recombinase [Arabidopsis thaliana]

Seq. No.	53582
Seq. ID	wvk700684479.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	335

E value	8.0e-32
Match length	81
% identity	85
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	53583
Seq. ID	wvk700684617.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	89
E value	1.0e-42
Match length	181
% identity	87
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	53584
Seq. ID	wvk700684670.h1
Method	BLASTN
NCBI GI	g12139
BLAST score	89
E value	1.0e-42
Match length	189
% identity	87
NCBI Description	Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No.	53585
Seq. ID	wvk700684679.h1
Method	BLASTX
NCBI GI	g266893
BLAST score	149
E value	4.0e-10
Match length	43
% identity	60
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase activase - cucumber >gi_18284_emb_CAA47906_ (X67674) rubisco activase [Cucumis sativus]

Seq. No.	53586
Seq. ID	wvk700684683.h1
Method	BLASTN
NCBI GI	g1053215
BLAST score	83
E value	3.0e-39
Match length	127
% identity	91
NCBI Description	Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	53587
Seq. ID	wvk700684727.h1
Method	BLASTX
NCBI GI	g4220524

BLAST score	223
E value	9.0e-19
Match length	65
% identity	62
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	53588
Seq. ID	wvk700684737.h1
Method	BLASTX
NCBI GI	g3608154
BLAST score	212
E value	2.0e-17
Match length	76
% identity	55
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	53589
Seq. ID	wvk700684844.h1
Method	BLASTX
NCBI GI	g3108161
BLAST score	201
E value	5.0e-16
Match length	83
% identity	46
NCBI Description	(AF061106) putative monosaccharide transporter 1 [Petunia x hybrida]

Seq. No.	53590
Seq. ID	wvk700684881.h1
Method	BLASTN
NCBI GI	g20732
BLAST score	113
E value	5.0e-57
Match length	161
% identity	93
NCBI Description	Pea chloroplast GAPB mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B (EC 1.2.1.13)

Seq. No.	53591
Seq. ID	wvk700684885.h1
Method	BLASTN
NCBI GI	g2924257
BLAST score	67
E value	2.0e-29
Match length	126
% identity	89
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	53592
Seq. ID	wvk700684896.h1
Method	BLASTN
NCBI GI	g20740
BLAST score	48
E value	4.0e-18
Match length	88
% identity	89

NCBI Description	Pisum sativum mRNA for P protein, a part of glycine cleavage complex
Seq. No.	53593
Seq. ID	wvk700684930.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	121
E value	1.0e-61
Match length	249
% identity	87
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds
Seq. No.	53594
Seq. ID	wvk700684931.h1
Method	BLASTN
NCBI GI	g516853
BLAST score	160
E value	7.0e-85
Match length	227
% identity	34
NCBI Description	Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.	53595
Seq. ID	wvk700684932.h1
Method	BLASTN
NCBI GI	g872115
BLAST score	41
E value	7.0e-14
Match length	61
% identity	92
NCBI Description	G.max gmsti mRNA
Seq. No.	53596
Seq. ID	wvk700684958.h1
Method	BLASTX
NCBI GI	g2181184
BLAST score	167
E value	3.0e-17
Match length	87
% identity	66
NCBI Description	(Y13577) JR3 protein [Arabidopsis thaliana]
Seq. No.	53597
Seq. ID	wvk700684992.h1
Method	BLASTN
NCBI GI	g18741
BLAST score	185
E value	1.0e-100
Match length	269
% identity	96
NCBI Description	Glycine max gene encoding ribulose-1,5-bisphosphate carboxylase small subunit
Seq. No.	53598
Seq. ID	wvk700685085.h1

Method	BLASTX
NCBI GI	g2833389
BLAST score	405
E value	6.0e-40
Match length	85
% identity	85
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III) >gi_1200154_emb_CAA65065_ (X95759) glycogen (starch) synthase [Solanum tuberosum]

Seq. No.	53599
Seq. ID	wvk700685107.h1
Method	BLASTX
NCBI GI	g1653059
BLAST score	210
E value	5.0e-17
Match length	79
% identity	47
NCBI Description	(D90910) hypothetical protein [Synechocystis sp.]

Seq. No.	53600
Seq. ID	wvk700685124.h1
Method	BLASTX
NCBI GI	g3132479
BLAST score	370
E value	6.0e-36
Match length	81
% identity	84
NCBI Description	(AC003096) multidrug resistance-associated protein, AtMRP2 [Arabidopsis thaliana]

Seq. No.	53601
Seq. ID	wvk700685166.h1
Method	BLASTN
NCBI GI	g12147
BLAST score	89
E value	1.0e-42
Match length	266
% identity	88
NCBI Description	Pea chloroplast genes for ATP synthetase subunits beta and epsilon (atpB and atpE)

Seq. No.	53602
Seq. ID	wvk700685167.h1
Method	BLASTX
NCBI GI	g99733
BLAST score	186
E value	2.0e-14
Match length	43
% identity	84
NCBI Description	hypothetical protein H1flk - Arabidopsis thaliana (fragment) >gi_16482_emb_CAA44318_ (X62461) H1flk [Arabidopsis thaliana]

Seq. No.	53603
Seq. ID	wvk700685226.h1
Method	BLASTX

NCBI GI	g3913996
BLAST score	257
E value	2.0e-22
Match length	73
% identity	64
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2208927_dbj_BAA20482_ (D85610) ATP-dependent protease Lon [Spinacia oleracea]

Seq. No.	53604
Seq. ID	wvk700685242.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	253
E value	1.0e-140
Match length	273
% identity	98
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	53605
Seq. ID	wvk700685326.h1
Method	BLASTX
NCBI GI	g3171001
BLAST score	157
E value	6.0e-11
Match length	77
% identity	45
NCBI Description	(AF061946) dihydroxyacetone kinase [Pichia angusta]

Seq. No.	53606
Seq. ID	wvk700685327.h1
Method	BLASTX
NCBI GI	g4454470
BLAST score	315
E value	2.0e-29
Match length	87
% identity	71
NCBI Description	(AC006234) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	53607
Seq. ID	wvk700685338.h1
Method	BLASTX
NCBI GI	g1669341
BLAST score	428
E value	1.0e-42
Match length	82
% identity	90
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	53608
Seq. ID	wvk700685372.h1
Method	BLASTX
NCBI GI	g228403
BLAST score	151
E value	3.0e-10

Match length	53
% identity	62
NCBI Description	glycolate oxidase [Lens culinaris]

Seq. No.	53609
Seq. ID	wvk700685410.h1
Method	BLASTX
NCBI GI	g1708060
BLAST score	144
E value	1.0e-15
Match length	61
% identity	77
NCBI Description	GLUTATHIONE REDUCTASE (GR) (GRASE) >gi_2117552_pir__S61975 glutathione reductase (NADPH) (EC 1.6.4.2) - yeast (Saccharomyces cerevisiae) >gi_1151235 (U43281) Glr1p,Lpg17p [Saccharomyces cerevisiae]

Seq. No.	53610
Seq. ID	wvk700685452.h1
Method	BLASTX
NCBI GI	g2494895
BLAST score	135
E value	1.0e-18
Match length	84
% identity	56
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi_2136321_pir__S60335 TRIP-1 protein - human >gi_1036805 (U36764) TGF-beta receptor interacting protein 1 [Homo sapiens] >gi_1718195 (U39067) translation initiation factor eIF3 p36 subunit [Homo sapiens] >gi_4503513_ref_NP_003748.1_pEIF3S2_ UNKNOWN

Seq. No.	53611
Seq. ID	wvk700685507.h1
Method	BLASTX
NCBI GI	g2911067
BLAST score	335
E value	7.0e-32
Match length	74
% identity	85
NCBI Description	(AL021960) UV-damaged DNA-binding protein- like [Arabidopsis thaliana]

Seq. No.	53612
Seq. ID	wvk700685520.h1
Method	BLASTX
NCBI GI	g2914709
BLAST score	223
E value	7.0e-19
Match length	71
% identity	62
NCBI Description	(AC003974) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53613
Seq. ID	wvk700685541.h1
Method	BLASTX

NCBI GI	g3608263
BLAST score	344
E value	6.0e-33
Match length	72
% identity	86
NCBI Description	(AB017565) Dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	53614
Seq. ID	wvk700685607.h1
Method	BLASTN
NCBI GI	g408791
BLAST score	47
E value	2.0e-17
Match length	59
% identity	95
NCBI Description	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds

Seq. No.	53615
Seq. ID	wvk700685644.h1
Method	BLASTN
NCBI GI	g1066858
BLAST score	203
E value	1.0e-110
Match length	259
% identity	95
NCBI Description	Glycine max (clone 91) acetyl-CoA-carboxylase (ACCase-A) mRNA, 3' end of cds

Seq. No.	53616
Seq. ID	wvk700685651.h1
Method	BLASTN
NCBI GI	g1150683
BLAST score	76
E value	8.0e-35
Match length	225
% identity	83
NCBI Description	V.radiata atpB, rbcL and trnK genes

Seq. No.	53617
Seq. ID	wvk700685655.h1
Method	BLASTX
NCBI GI	g90313
BLAST score	162
E value	2.0e-11
Match length	48
% identity	60
NCBI Description	aspartate transaminase (EC 2.6.1.1), cytosolic - mouse >gi_871422_emb_CAA30275_ (X07302) aspartate aminotransferase [Mus musculus]

Seq. No.	53618
Seq. ID	wvk700685661.h1
Method	BLASTX
NCBI GI	g2245120
BLAST score	175
E value	6.0e-13

Match length	79
% identity	44
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53619
Seq. ID	wvk700685733.h1
Method	BLASTX
NCBI GI	g1402879
BLAST score	140
E value	6.0e-09
Match length	77
% identity	43
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495247_emb_CAA66220_ (X97616) orf 05 [Arabidopsis thaliana]

Seq. No.	53620
Seq. ID	wvk700685744.h1
Method	BLASTX
NCBI GI	g4063751
BLAST score	421
E value	8.0e-42
Match length	87
% identity	93
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	53621
Seq. ID	wvk700685755.h1
Method	BLASTX
NCBI GI	g4115946
BLAST score	180
E value	1.0e-13
Match length	75
% identity	49
NCBI Description	(AF118223) contains similarity to Ipomoea nil leaf protein (GB: D85101) [Arabidopsis thaliana]

Seq. No.	53622
Seq. ID	wvk700685790.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	47
E value	2.0e-17
Match length	59
% identity	95
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	53623
Seq. ID	wvk700685813.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	50
E value	3.0e-19
Match length	70
% identity	93

NCBI Description	Pisum sativum L. aldolase gene, 3' end cds
Seq. No.	53624
Seq. ID	wvk700685842.h1
Method	BLASTX
NCBI GI	g564018
BLAST score	171
E value	1.0e-12
Match length	70
% identity	51
NCBI Description	(U16156) dihydrofolate synthetase [Streptococcus pneumoniae]
Seq. No.	53625
Seq. ID	wvk700685873.h1
Method	BLASTX
NCBI GI	g421948
BLAST score	177
E value	3.0e-13
Match length	80
% identity	40
NCBI Description	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - garden petunia
Seq. No.	53626
Seq. ID	wvk700685908.h1
Method	BLASTN
NCBI GI	g532706
BLAST score	38
E value	3.0e-12
Match length	80
% identity	94
NCBI Description	Glycine max clone GMFP6 isoprenylated protein mRNA, partial cds
Seq. No.	53627
Seq. ID	wvk700685909.h1
Method	BLASTN
NCBI GI	g2980787
BLAST score	33
E value	4.0e-09
Match length	49
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)
Seq. No.	53628
Seq. ID	wvk700685946.h1
Method	BLASTN
NCBI GI	g169157
BLAST score	44
E value	1.0e-15
Match length	56
% identity	95
NCBI Description	Pisum sativum serine hydroxymethyltransferase mRNA, complete cds

Seq. No.	53629
Seq. ID	wvk700685957.h1
Method	BLASTN
NCBI GI	g3033512
BLAST score	157
E value	4.0e-83
Match length	240
% identity	91
NCBI Description	Phaseolus vulgaris rubisco activase (Rca1) mRNA, complete cds

Seq. No.	53630
Seq. ID	wvk700685976.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	50
E value	3.0e-19
Match length	70
% identity	93
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	53631
Seq. ID	wvk700685983.h1
Method	BLASTN
NCBI GI	g3175989
BLAST score	70
E value	3.0e-31
Match length	146
% identity	95
NCBI Description	Cicer arietinum mRNA for GDP dissociation inhibitor (gdi)

Seq. No.	53632
Seq. ID	wvk700685985.h1
Method	BLASTX
NCBI GI	g4309734
BLAST score	156
E value	9.0e-11
Match length	45
% identity	62
NCBI Description	(AC006439) putative 26S proteosome regulatory subunit 8 [Arabidopsis thaliana]

Seq. No.	53633
Seq. ID	wvk700686016.h1
Method	BLASTX
NCBI GI	g4324714
BLAST score	245
E value	3.0e-21
Match length	79
% identity	67
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	53634
Seq. ID	wvk700686027.h1
Method	BLASTX
NCBI GI	g2352492
BLAST score	250

E value	7.0e-22
Match length	80
% identity	61
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	53635
Seq. ID	wvk700686070.h1
Method	BLASTX
NCBI GI	g3913031
BLAST score	323
E value	2.0e-30
Match length	79
% identity	76
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_2559006 (AF026217) beta-amylase [Medicago sativa]

Seq. No.	53636
Seq. ID	wvk700686108.h1
Method	BLASTX
NCBI GI	g3135274
BLAST score	231
E value	2.0e-36
Match length	89
% identity	74
NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	53637
Seq. ID	wvk700686133.h1
Method	BLASTN
NCBI GI	g3033512
BLAST score	220
E value	1.0e-120
Match length	271
% identity	96
NCBI Description	Phaseolus vulgaris rubisco activase (Rca1) mRNA, complete cds

Seq. No.	53638
Seq. ID	wvk700686144.h1
Method	BLASTN
NCBI GI	g20728
BLAST score	81
E value	8.0e-38
Match length	161
% identity	88
NCBI Description	Pea chloroplast GAPA mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13)

Seq. No.	53639
Seq. ID	wvk700686149.h1
Method	BLASTX
NCBI GI	g4494003
BLAST score	117

E value	4.0e-12
Match length	68
% identity	52
NCBI Description	(AL034559) predicted using hexExon; MAL3P7.35 (PFC1020c), 40S Ribosomal protein S3A, len: 263 aa; Similarity to 40S ribosomal protein S3A. H.annuus 40S ribosomal protien S3A (SW:RS3A_HELAN) BLAST Score: 795, sum P(1) = 2.5e-7

Seq. No.	53640
Seq. ID	wvk700686151.h1
Method	BLASTX
NCBI GI	g731936
BLAST score	96
E value	7.0e-09
Match length	64
% identity	46
NCBI Description	HYPOTHETICAL 33.9 KD ESTERASE IN SMC3-MRPL8 INTERGENIC REGION >gi_1077819_pir__S50803 hypothetical protein YJL068c - yeast (Saccharomyces cerevisiae) >gi_498998_emb_CAA84054_ (Z34288) 39.8% identity in 289 aa overlap with human esterase D [Saccharomyces cerevisiae] >gi_1008219_emb_CAA89359_ (Z49343) ORF YJL068c [Saccharomyces cerevisiae]

Seq. No.	53641
Seq. ID	wvk700686161.h1
Method	BLASTX
NCBI GI	g2618691
BLAST score	287
E value	4.0e-26
Match length	85
% identity	66
NCBI Description	(AC002510) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	53642
Seq. ID	wvk700686231.h1
Method	BLASTX
NCBI GI	g2252847
BLAST score	281
E value	2.0e-25
Match length	56
% identity	88
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	53643
Seq. ID	wvk700686256.h1
Method	BLASTX
NCBI GI	g2342682
BLAST score	214
E value	1.0e-17
Match length	72
% identity	61
NCBI Description	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No.	53644

Seq. ID	wvk700686371.h1
Method	BLASTN
NCBI GI	g288187
BLAST score	188
E value	1.0e-101
Match length	232
% identity	95
NCBI Description	V.unguiculata cysteine proteinase inhibitor mRNA

Seq. No.	53645
Seq. ID	wvk700686383.h1
Method	BLASTX
NCBI GI	g4314371
BLAST score	139
E value	1.0e-08
Match length	91
% identity	35
NCBI Description	(AC006340) putative G9a protein [Arabidopsis thaliana]

Seq. No.	53646
Seq. ID	wvk700686385.h1
Method	BLASTX
NCBI GI	g3056588
BLAST score	205
E value	2.0e-16
Match length	77
% identity	48
NCBI Description	(AC004255) T1F9.9 [Arabidopsis thaliana]

Seq. No.	53647
Seq. ID	wvk700686433.h1
Method	BLASTX
NCBI GI	g3080441
BLAST score	181
E value	9.0e-14
Match length	78
% identity	55
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	53648
Seq. ID	wvk700686436.h1
Method	BLASTX
NCBI GI	g2346978
BLAST score	212
E value	2.0e-17
Match length	72
% identity	58
NCBI Description	(AB006601) ZPT2-14 [Petunia x hybrida]

Seq. No.	53649
Seq. ID	wvk700686447.h1
Method	BLASTX
NCBI GI	g3860264
BLAST score	298
E value	2.0e-27
Match length	61
% identity	85

NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.	53650
Seq. ID	wvk700686450.h1
Method	BLASTX
NCBI GI	g3724087
BLAST score	394
E value	1.0e-38
Match length	85
% identity	88
NCBI Description	(AJ011840) 1-deoxyxylulose 5-phosphate synthase [Catharanthus roseus]
Seq. No.	53651
Seq. ID	wvk700686452.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	70
E value	3.0e-31
Match length	194
% identity	89
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds
Seq. No.	53652
Seq. ID	wvk700686463.h1
Method	BLASTN
NCBI GI	g4510360
BLAST score	35
E value	2.0e-10
Match length	47
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence
Seq. No.	53653
Seq. ID	wvk700686487.h1
Method	BLASTX
NCBI GI	g2462733
BLAST score	203
E value	3.0e-16
Match length	48
% identity	79
NCBI Description	(AC002292) Putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana]
Seq. No.	53654
Seq. ID	wvk700686491.h1
Method	BLASTX
NCBI GI	g4510424
BLAST score	214
E value	4.0e-23
Match length	82
% identity	62
NCBI Description	(AC006929) putative carboxypeptidase [Arabidopsis thaliana]
Seq. No.	53655
Seq. ID	wvk700686546.h1

Method	BLASTX
NCBI GI	g4455350
BLAST score	196
E value	2.0e-15
Match length	66
% identity	50
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	53656
Seq. ID	wvk700686571.h1
Method	BLASTN
NCBI GI	g3869075
BLAST score	36
E value	6.0e-11
Match length	80
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	53657
Seq. ID	wvk700686576.h1
Method	BLASTX
NCBI GI	g2388586
BLAST score	156
E value	1.0e-10
Match length	40
% identity	70
NCBI Description	(AC000098) Similar to Saccharomyces RAD16 (gb_X78993). [Arabidopsis thaliana]

Seq. No.	53658
Seq. ID	wvk700686602.h1
Method	BLASTX
NCBI GI	g2760830
BLAST score	431
E value	6.0e-43
Match length	95
% identity	85
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	53659
Seq. ID	wvk700686619.h1
Method	BLASTX
NCBI GI	g418507
BLAST score	167
E value	6.0e-12
Match length	56
% identity	57
NCBI Description	S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical protein f161 - Escherichia coli >gi_305032 (L19201) ORF_f161 [Escherichia coli] >gi_1336002 (U56082) S-adenosylmethionine:2-demethylmenaquinone methyltransferase [Escherichia coli] >gi_1790364 (AE000467) menaquinone biosynthesis, unknown [Escherichia coli]

Seq. No.	53660
Seq. ID	wvk700686631.h1
Method	BLASTN
NCBI GI	g3900979
BLAST score	42
E value	1.0e-14
Match length	62
% identity	92
NCBI Description	Eichhornia crassipes mRNA for metallothionein-like protein, clone A

Seq. No.	53661
Seq. ID	wvk700686654.h1
Method	BLASTX
NCBI GI	g2529686
BLAST score	205
E value	2.0e-16
Match length	63
% identity	67
NCBI Description	(AC002535) putative G-beta-repeat containing protein, 5' partial [Arabidopsis thaliana]

Seq. No.	53662
Seq. ID	xpa700792324.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	235
E value	2.0e-40
Match length	93
% identity	85
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53663
Seq. ID	xpa700792325.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	401
E value	1.0e-39
Match length	80
% identity	99
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53664
Seq. ID	xpa700792401.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	241
E value	1.0e-20
Match length	89
% identity	60
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53665
Seq. ID	xpa700792410.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	188
E value	1.0e-14
Match length	43
% identity	84
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53666
Seq. ID	xpa700792435.h1
Method	BLASTX
NCBI GI	g4455276
BLAST score	145
E value	3.0e-13
Match length	81
% identity	53
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	53667
Seq. ID	xpa700792468.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	213
E value	4.0e-26
Match length	66
% identity	94
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53668
Seq. ID	xpa700792494.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	209
E value	3.0e-17
Match length	42
% identity	98
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53669
Seq. ID	xpa700792541.h1
Method	BLASTX
NCBI GI	g229707
BLAST score	327
E value	9.0e-31
Match length	89
% identity	75
NCBI Description	Bean pod mottle virus

Seq. No.	53670
Seq. ID	xpa700792542.h1

Method	BLASTX
NCBI GI	g541948
BLAST score	118
E value	3.0e-14
Match length	79
% identity	62
NCBI Description	rab1 protein - Soybean >gi_414832 (L14929) Rab7p [Glycine max]

Seq. No.	53671
Seq. ID	xpa700792562.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	449
E value	5.0e-45
Match length	91
% identity	93
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53672
Seq. ID	xpa700792642.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	482
E value	6.0e-49
Match length	85
% identity	100
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53673
Seq. ID	xpa700792664.h1
Method	BLASTX
NCBI GI	g4006884
BLAST score	144
E value	3.0e-09
Match length	61
% identity	51
NCBI Description	(Z99707) BEL1-like homeodomain protein [Arabidopsis thaliana]

Seq. No.	53674
Seq. ID	xpa700792670.h1
Method	BLASTX
NCBI GI	g1871577
BLAST score	146
E value	1.0e-09
Match length	50
% identity	60
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	53675
Seq. ID	xpa700792709.h1
Method	BLASTX
NCBI GI	g3850588

BLAST score	373
E value	4.0e-36
Match length	89
% identity	76
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No.	53676
Seq. ID	xpa700792730.h1
Method	BLASTX
NCBI GI	g2317900
BLAST score	418
E value	2.0e-41
Match length	80
% identity	96
NCBI Description	(U89693) Sali3-2 [Glycine max]

Seq. No.	53677
Seq. ID	xpa700792735.h1
Method	BLASTX
NCBI GI	g1172495
BLAST score	128
E value	5.0e-12
Match length	58
% identity	67
NCBI Description	PHYTOCHROME A >gi_515749 (L34842) phytochrome A [Glycine max] >gi_515751 (L34844) phytochrome A [Glycine max]

Seq. No.	53678
Seq. ID	xpa700792780.h1
Method	BLASTX
NCBI GI	g114950
BLAST score	192
E value	6.0e-15
Match length	61
% identity	64
NCBI Description	GLU S.GRISEUS PROTEASE INHIBITOR (BGIA) >gi_81581_pir__A41174 endopeptidase inhibitor - balsam pear >gi_234607_bbs_53154 BGIA=acidic amino acid-specific endopeptidase inhibitor [Momordica charantia L.=bitter gourd, Peptide, 68 aa]

Seq. No.	53679
Seq. ID	xpa700792796.h1
Method	BLASTX
NCBI GI	g2264373
BLAST score	171
E value	1.0e-12
Match length	45
% identity	71
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]

Seq. No.	53680
Seq. ID	xpa700792833.h1

Method	BLASTX
NCBI GI	g138364
BLAST score	342
E value	2.0e-32
Match length	95
% identity	73
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53681
Seq. ID	xpa700792854.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	300
E value	3.0e-37
Match length	89
% identity	92
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53682
Seq. ID	xpa700792883.h1
Method	BLASTX
NCBI GI	g4490341
BLAST score	389
E value	5.0e-38
Match length	89
% identity	74
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	53683
Seq. ID	xpa700792937.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	505
E value	1.0e-51
Match length	89
% identity	99
NCBI Description	Bean pod mottle virus

Seq. No.	53684
Seq. ID	xpa700792996.h1
Method	BLASTX
NCBI GI	g548751
BLAST score	359
E value	1.0e-34
Match length	80
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L19 >gi_1079135_pir__A61627 ribosomal protein L19 - fruit fly (Drosophila melanogaster) >gi_400448_emb_CAA52784_ (X74776) ribosomal protein L19 [Drosophila melanogaster]

Seq. No.	53685
Seq. ID	xpa700793069.h1
Method	BLASTX

NCBI GI	g4097880
BLAST score	348
E value	3.0e-33
Match length	73
% identity	89
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53686
Seq. ID	xpa700793081.h1
Method	BLASTX
NCBI GI	g4530126
BLAST score	227
E value	5.0e-19
Match length	70
% identity	63
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	53687
Seq. ID	xpa700793138.h1
Method	BLASTX
NCBI GI	g1076678
BLAST score	139
E value	1.0e-11
Match length	58
% identity	62
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	53688
Seq. ID	xpa700793160.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	459
E value	2.0e-46
Match length	81
% identity	100
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53689
Seq. ID	xpa700793233.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	208
E value	4.0e-17
Match length	57
% identity	74
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53690
Seq. ID	xpa700793306.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	191
E value	1.0e-17

Match length	64
% identity	74
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53691
Seq. ID	xpa700793331.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	301
E value	5.0e-28
Match length	64
% identity	89
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53692
Seq. ID	xpa700793426.h1
Method	BLASTX
NCBI GI	g2829923
BLAST score	208
E value	5.0e-17
Match length	50
% identity	76
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	53693
Seq. ID	xpa700793487.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	338
E value	3.0e-32
Match length	74
% identity	85
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53694
Seq. ID	xpa700793536.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	365
E value	3.0e-35
Match length	82
% identity	84
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53695
Seq. ID	xpa700793540.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	333
E value	2.0e-31

Match length	88
% identity	74
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53696
Seq. ID	xpa700793581.h1
Method	BLASTX
NCBI GI	g1749546
BLAST score	264
E value	2.0e-23
Match length	69
% identity	74
NCBI Description	(D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

Seq. No.	53697
Seq. ID	xpa700793658.h1
Method	BLASTX
NCBI GI	g3334405
BLAST score	151
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E [Gossypium hirsutum]

Seq. No.	53698
Seq. ID	xpa700793706.h1
Method	BLASTX
NCBI GI	g3947985
BLAST score	309
E value	8.0e-29
Match length	91
% identity	68
NCBI Description	(U78948) MADS-box protein 2 [Malus domestica]

Seq. No.	53699
Seq. ID	xpa700793710.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	418
E value	2.0e-41
Match length	90
% identity	91
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53700
Seq. ID	xpa700793735.h1
Method	BLASTX
NCBI GI	g4262222
BLAST score	336
E value	8.0e-32

Match length	75
% identity	85
NCBI Description	(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]

Seq. No.	53701
Seq. ID	xpa700793743.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	404
E value	8.0e-40
Match length	87
% identity	92
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53702
Seq. ID	xpa700793792.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	295
E value	3.0e-27
Match length	70
% identity	86
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53703
Seq. ID	xpa700793803.h1
Method	BLASTX
NCBI GI	g1236781
BLAST score	218
E value	6.0e-18
Match length	59
% identity	73
NCBI Description	(X96732) cuticular collagen [Ostertagia circumcincta]

Seq. No.	53704
Seq. ID	xpa700793806.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	290
E value	6.0e-32
Match length	79
% identity	91
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53705
Seq. ID	xpa700793895.h1
Method	BLASTX
NCBI GI	g1703375
BLAST score	259
E value	6.0e-23
Match length	53
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)

DcARF1 [Daucus carota]

Seq. No.	53706
Seq. ID	xpa700793917.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	145
E value	1.0e-09
Match length	38
% identity	74
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53707
Seq. ID	xpa700793940.h1
Method	BLASTX
NCBI GI	g3337356
BLAST score	204
E value	2.0e-16
Match length	56
% identity	73
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	53708
Seq. ID	xpa700793944.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	195
E value	2.0e-25
Match length	75
% identity	85
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53709
Seq. ID	xpa700793974.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	238
E value	2.0e-20
Match length	58
% identity	81
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53710
Seq. ID	xpa700793992.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	165
E value	8.0e-12
Match length	64
% identity	58
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53711

Seq. ID	xpa700794083.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	279
E value	2.0e-25
Match length	63
% identity	89
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53712
Seq. ID	xpa700794090.h1
Method	BLASTX
NCBI GI	g3021409
BLAST score	278
E value	4.0e-25
Match length	86
% identity	17
NCBI Description	(Y12781) transducin (beta) like 1 protein [Homo sapiens]

Seq. No.	53713
Seq. ID	xpa700794115.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	317
E value	1.0e-29
Match length	82
% identity	78
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53714
Seq. ID	xpa700794179.h1
Method	BLASTX
NCBI GI	g2842494
BLAST score	256
E value	1.0e-30
Match length	83
% identity	80
NCBI Description	(AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No.	53715
Seq. ID	xpa700794186.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	346
E value	4.0e-33
Match length	84
% identity	86
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53716
Seq. ID	xpa700794232.h1
Method	BLASTX
NCBI GI	g3451463
BLAST score	174
E value	8.0e-13
Match length	72
% identity	46
NCBI Description	(AL031349) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	53717
Seq. ID	xpa700794235.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	224
E value	8.0e-19
Match length	80
% identity	64
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53718
Seq. ID	xpa700794266.h1
Method	BLASTX
NCBI GI	g1730622
BLAST score	194
E value	3.0e-15
Match length	82
% identity	39
NCBI Description	HYPOTHETICAL 56.1 KD PROTEIN F59A2.4 IN CHROMOSOME III

Seq. No.	53719
Seq. ID	xpa700794384.h1
Method	BLASTX
NCBI GI	g134194
BLAST score	264
E value	1.0e-23
Match length	51
% identity	100
NCBI Description	STRESS-INDUCED PROTEIN SAM22 >gi_99918_pir__S20518 hypothetical protein - soybean >gi_18744_emb_CAA42646_ (X60043) ORF [Glycine max]

Seq. No.	53720
Seq. ID	xpa700794395.h1
Method	BLASTX
NCBI GI	g3202042
BLAST score	152
E value	2.0e-10
Match length	45
% identity	78
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	53721
Seq. ID	xpa700794454.h1
Method	BLASTX
NCBI GI	g3202042

BLAST score	197
E value	8.0e-16
Match length	60
% identity	73
NCBI Description	(AF069324) 26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]

Seq. No.	53722
Seq. ID	xpa700794484.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	407
E value	3.0e-40
Match length	81
% identity	100
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53723
Seq. ID	xpa700794542.h1
Method	BLASTX
NCBI GI	g3201682
BLAST score	272
E value	2.0e-24
Match length	75
% identity	69
NCBI Description	(AF060942) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	53724
Seq. ID	xpa700794646.h1
Method	BLASTX
NCBI GI	g2394306
BLAST score	271
E value	2.0e-24
Match length	68
% identity	69
NCBI Description	(AF017269) 73 kDA subunit of cleavage and polyadenylation specificity factor [Homo sapiens]

Seq. No.	53725
Seq. ID	xpa700794770.h1
Method	BLASTX
NCBI GI	g1881585
BLAST score	212
E value	1.0e-17
Match length	58
% identity	69
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	53726
Seq. ID	xpa700794805.h1
Method	BLASTX
NCBI GI	g3641845
BLAST score	114
E value	4.0e-09
Match length	71
% identity	48
NCBI Description	(AJ223358) stelar K+ outward rectifying channel

[Arabidopsis thaliana]

Seq. No.	53727
Seq. ID	xpa700794846.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	423
E value	4.0e-42
Match length	82
% identity	100
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53728
Seq. ID	xpa700794959.h1
Method	BLASTX
NCBI GI	g4210948
BLAST score	206
E value	9.0e-17
Match length	41
% identity	95
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	53729
Seq. ID	xpa700794991.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	356
E value	3.0e-34
Match length	83
% identity	86
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53730
Seq. ID	xpa700795103.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	259
E value	8.0e-23
Match length	78
% identity	73
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53731
Seq. ID	xpa700795125.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	280
E value	3.0e-25
Match length	84
% identity	69
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53732
Seq. ID	xpa700795138.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	340

E value	2.0e-32
Match length	69
% identity	96
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53733
Seq. ID	xpa700795158.h1
Method	BLASTX
NCBI GI	g4510345
BLAST score	222
E value	1.0e-18
Match length	57
% identity	65
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	53734
Seq. ID	xpa700795207.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	435
E value	1.0e-43
Match length	79
% identity	99
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53735
Seq. ID	xpa700795232.h1
Method	BLASTX
NCBI GI	g4580513
BLAST score	223
E value	1.0e-18
Match length	65
% identity	69
NCBI Description	(AF036300) scarecrow-like 1 [Arabidopsis thaliana]

Seq. No.	53736
Seq. ID	xpa700795249.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	385
E value	9.0e-38
Match length	80
% identity	95
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53737
Seq. ID	xpa700795263.h1
Method	BLASTX
NCBI GI	g4455276
BLAST score	113
E value	2.0e-10

Match length	66
% identity	59
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	53738
Seq. ID	xpa700795270.h1
Method	BLASTX
NCBI GI	g3242715
BLAST score	322
E value	3.0e-30
Match length	78
% identity	74
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53739
Seq. ID	xpa700795271.h1
Method	BLASTX
NCBI GI	g3549639
BLAST score	214
E value	1.0e-17
Match length	74
% identity	66
NCBI Description	(AJ005194) receiver-like protein 3 [Arabidopsis thaliana]

Seq. No.	53740
Seq. ID	xpa700795291.h1
Method	BLASTX
NCBI GI	g4490756
BLAST score	172
E value	1.0e-12
Match length	70
% identity	54
NCBI Description	(AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53741
Seq. ID	xpa700795336.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	180
E value	9.0e-14
Match length	43
% identity	84
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53742
Seq. ID	xpa700795342.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	399
E value	3.0e-39
Match length	84
% identity	92
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53743
Seq. ID	xpa700795377.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	349
E value	2.0e-33
Match length	82
% identity	83
NCBI Description	Bean pod mottle virus

Seq. No.	53744
Seq. ID	xpa700795380.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	383
E value	2.0e-37
Match length	81
% identity	93
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53745
Seq. ID	xpa700795422.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	230
E value	8.0e-30
Match length	65
% identity	91
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53746
Seq. ID	xpa700795442.h1
Method	BLASTX
NCBI GI	g541944
BLAST score	269
E value	3.0e-24
Match length	55
% identity	98
NCBI Description	nodulin-26 - soybean

Seq. No.	53747
Seq. ID	xpa700795539.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	341
E value	1.0e-32
Match length	74
% identity	91
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53748
Seq. ID	xpa700795591.h1
Method	BLASTX
NCBI GI	g4539295
BLAST score	151
E value	6.0e-13
Match length	50
% identity	80
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	53749
Seq. ID	xpa700795614.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	107
E value	4.0e-10
Match length	63
% identity	57
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53750
Seq. ID	xpa700795728.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	330
E value	3.0e-31
Match length	81
% identity	84
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53751
Seq. ID	xpa700795741.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	444
E value	1.0e-44
Match length	80
% identity	99
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53752
Seq. ID	xpa700795830.h1
Method	BLASTX
NCBI GI	g4580393
BLAST score	173
E value	1.0e-12
Match length	63
% identity	52
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No. 53753

Seq. ID xpa700795842.h1
Method BLASTX
NCBI GI g4097880
BLAST score 262
E value 1.0e-26
Match length 87
% identity 80
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 53754
Seq. ID xpa700795961.h1
Method BLASTX
NCBI GI g4097880
BLAST score 418
E value 2.0e-41
Match length 85
% identity 94
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 53755
Seq. ID xpa700796020.h1
Method BLASTX
NCBI GI g138364
BLAST score 430
E value 6.0e-43
Match length 83
% identity 94
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 53756
Seq. ID xpa700796041.h1
Method BLASTX
NCBI GI g138364
BLAST score 314
E value 2.0e-29
Match length 79
% identity 81
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 53757
Seq. ID xpa700796111.h1
Method BLASTX
NCBI GI g1628473
BLAST score 405
E value 3.0e-40
Match length 80
% identity 100
NCBI Description (X96665) NIb protein [Soybean mosaic virus]

Seq. No. 53758
Seq. ID xpa700796205.h1

Method	BLASTX
NCBI GI	g2052029
BLAST score	239
E value	2.0e-20
Match length	47
% identity	100
NCBI Description	(Y10820) glutathione transferase [Glycine max]

Seq. No.	53759
Seq. ID	xpa700796230.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	434
E value	2.0e-43
Match length	82
% identity	95
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53760
Seq. ID	xpa700796269.h1
Method	BLASTX
NCBI GI	g2444180
BLAST score	311
E value	5.0e-29
Match length	80
% identity	69
NCBI Description	(U94785) unconventional myosin [Helianthus annuus]

Seq. No.	53761
Seq. ID	xpa700796280.h1
Method	BLASTX
NCBI GI	g3482933
BLAST score	341
E value	2.0e-32
Match length	83
% identity	76
NCBI Description	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]

Seq. No.	53762
Seq. ID	xpa700796284.h1
Method	BLASTX
NCBI GI	g2541876
BLAST score	210
E value	4.0e-17
Match length	79
% identity	56
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	53763
Seq. ID	xpa700796327.h1
Method	BLASTX
NCBI GI	g464986

BLAST score	233
E value	2.0e-25
Match length	63
% identity	91
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	53764
Seq. ID	xpa700796352.h1
Method	BLASTX
NCBI GI	g1076678
BLAST score	295
E value	4.0e-27
Match length	69
% identity	87
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	53765
Seq. ID	xpa700796357.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	382
E value	3.0e-37
Match length	80
% identity	90
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53766
Seq. ID	xpa700796373.h1
Method	BLASTX
NCBI GI	g3643085
BLAST score	264
E value	2.0e-23
Match length	70
% identity	70
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	53767
Seq. ID	xpa700796406.h1
Method	BLASTX
NCBI GI	g4558672
BLAST score	226
E value	5.0e-19
Match length	80
% identity	53
NCBI Description	(AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis thaliana]

Seq. No.	53768
Seq. ID	xpa700796507.h1
Method	BLASTX
NCBI GI	g3450889
BLAST score	316
E value	1.0e-29
Match length	79
% identity	82
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	53769
Seq. ID	xpa700796557.h1
Method	BLASTX
NCBI GI	g281428
BLAST score	289
E value	2.0e-37
Match length	78
% identity	100
NCBI Description	genome polyprotein - soybean mosaic virus (strain G7)

Seq. No.	53770
Seq. ID	xpa700796586.h1
Method	BLASTX
NCBI GI	g3450889
BLAST score	214
E value	1.0e-17
Match length	78
% identity	62
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	53771
Seq. ID	xpa700796652.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	155
E value	7.0e-11
Match length	51
% identity	69
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53772
Seq. ID	xpa700796672.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	170
E value	2.0e-12
Match length	35
% identity	91
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53773
Seq. ID	xpa700796677.h1
Method	BLASTX

NCBI GI g1666234
BLAST score 224
E value 7.0e-19
Match length 47
% identity 91
NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No. 53774
Seq. ID xpa700796685.h1
Method BLASTX
NCBI GI g4206196
BLAST score 194
E value 2.0e-15
Match length 36
% identity 97
NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 53775
Seq. ID xpa700796688.h1
Method BLASTX
NCBI GI g2052029
BLAST score 155
E value 3.0e-12
Match length 65
% identity 54
NCBI Description (Y10820) glutathione transferase [Glycine max]

Seq. No. 53776
Seq. ID xpa700796742.h1
Method BLASTX
NCBI GI g4193388
BLAST score 198
E value 8.0e-16
Match length 75
% identity 59
NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No. 53777
Seq. ID xpa700796757.h1
Method BLASTX
NCBI GI g4204695
BLAST score 245
E value 3.0e-21
Match length 67
% identity 69
NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No. 53778
Seq. ID xpa700796859.h1
Method BLASTX
NCBI GI g4097880
BLAST score 246
E value 2.0e-21
Match length 76

% identity	75
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53779
Seq. ID	xpa700796904.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	251
E value	6.0e-22
Match length	50
% identity	94
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53780
Seq. ID	xpa700796917.h1
Method	BLASTX
NCBI GI	g3258575
BLAST score	154
E value	3.0e-16
Match length	83
% identity	55
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	53781
Seq. ID	xpa700796923.h1
Method	BLASTX
NCBI GI	g2598575
BLAST score	157
E value	6.0e-11
Match length	69
% identity	45
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	53782
Seq. ID	xpa700796937.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	355
E value	4.0e-34
Match length	76
% identity	87
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53783
Seq. ID	xpa700797055.h1
Method	BLASTX
NCBI GI	g2642153
BLAST score	315
E value	2.0e-29
Match length	85
% identity	68
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	53784
Seq. ID	xpa700797149.h1
Method	BLASTX
NCBI GI	g2605887
BLAST score	145
E value	1.0e-09
Match length	75
% identity	47
NCBI Description	(AF029242) dormancy-associated protein [Pisum sativum]

Seq. No.	53785
Seq. ID	xpa700797320.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	235
E value	5.0e-20
Match length	82
% identity	66
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53786
Seq. ID	xpa700797348.h1
Method	BLASTX
NCBI GI	g3702339
BLAST score	195
E value	3.0e-15
Match length	56
% identity	68
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	53787
Seq. ID	xpa700797358.h1
Method	BLASTX
NCBI GI	g3892709
BLAST score	253
E value	3.0e-22
Match length	80
% identity	65
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	53788
Seq. ID	xpa700797417.h1
Method	BLASTX
NCBI GI	g1173198
BLAST score	126
E value	1.0e-10
Match length	53
% identity	75
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	53789
Seq. ID	xpa700797436.h1
Method	BLASTX
NCBI GI	g2245015

BLAST score	276
E value	7.0e-25
Match length	80
% identity	62
NCBI Description	(Z97341) unnamed protein product [Arabidopsis thaliana]

Seq. No.	53790
Seq. ID	xpa700797437.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	406
E value	4.0e-40
Match length	79
% identity	90
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53791
Seq. ID	xpa700797462.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	341
E value	2.0e-32
Match length	80
% identity	84
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53792
Seq. ID	xpa700797473.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	309
E value	8.0e-29
Match length	73
% identity	82
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53793
Seq. ID	xpa700797560.h1
Method	BLASTX
NCBI GI	g123379
BLAST score	223
E value	7.0e-19
Match length	53
% identity	83
NCBI Description	HMG1/2-LIKE PROTEIN (SB11 PROTEIN) >gi_99914_pir__S22309 HMG-1-like protein - soybean >gi_18645_emb_CAA41200_ (X58245) HMG-1 like protein gene [Glycine max]

Seq. No.	53794
Seq. ID	xpa700797581.h1
Method	BLASTX

NCBI GI	g138364
BLAST score	326
E value	8.0e-31
Match length	61
% identity	97
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	53795
Seq. ID	xpa700797590.h1
Method	BLASTX
NCBI GI	g1172495
BLAST score	278
E value	3.0e-25
Match length	67
% identity	82
NCBI Description	PHYTOCHROME A >gi_515749 (L34842) phytochrome A [Glycine max] >gi_515751 (L34844) phytochrome A [Glycine max]

Seq. No.	53796
Seq. ID	xpa700797601.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	387
E value	6.0e-38
Match length	78
% identity	96
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53797
Seq. ID	xpa700797636.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	249
E value	8.0e-22
Match length	69
% identity	75
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53798
Seq. ID	xpa700797658.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	232
E value	7.0e-20
Match length	54
% identity	78
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53799
Seq. ID	xpa700797672.h1
Method	BLASTN
NCBI GI	g1165321
BLAST score	34
E value	7.0e-10

Match length 92
% identity 75
NCBI Description Glycine max extensin (SbHRGP3) gene, complete cds

Seq. No. 53800
Seq. ID xpa700797681.h1
Method BLASTN
NCBI GI g470126
BLAST score 36
E value 2.0e-11
Match length 60
% identity 90
NCBI Description N.tabacum (cv.Samsun NN) L19 mRNA for ribosomal protein L19

Seq. No. 53801
Seq. ID xpa700797689.h1
Method BLASTX
NCBI GI g3885342
BLAST score 179
E value 1.0e-13
Match length 64
% identity 59
NCBI Description (AC005623) putative DNA polymerase [Arabidopsis thaliana]

Seq. No. 53802
Seq. ID xpa700797707.h1
Method BLASTX
NCBI GI g4097880
BLAST score 152
E value 2.0e-10
Match length 65
% identity 52
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 53803
Seq. ID xpa700797726.h1
Method BLASTX
NCBI GI g730456
BLAST score 131
E value 2.0e-13
Match length 49
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 53804
Seq. ID xpa700797735.h1
Method BLASTN
NCBI GI g2058281
BLAST score 59
E value 9.0e-25
Match length 146
% identity 86
NCBI Description A.thaliana mRNA for AtRanBP1a protein

Seq. No. 53805
Seq. ID xpa700797748.h1
Method BLASTN

NCBI GI	g210811
BLAST score	93
E value	5.0e-45
Match length	149
% identity	91
NCBI Description	Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.	53806
Seq. ID	xpa700797755.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	364
E value	2.0e-35
Match length	71
% identity	94
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	53807
Seq. ID	xpa700797825.h1
Method	BLASTX
NCBI GI	g1769895
BLAST score	328
E value	5.0e-31
Match length	78
% identity	79
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	53808
Seq. ID	xpa700797864.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	90
E value	3.0e-43
Match length	234
% identity	85
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53809
Seq. ID	xpa700797873.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	122
E value	2.0e-62
Match length	226
% identity	88
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53810
Seq. ID	xpa700797962.h1
Method	BLASTX
NCBI GI	g1173624
BLAST score	192
E value	5.0e-15
Match length	52

% identity	67
NCBI Description	(U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid SM9108']

Seq. No.	53811
Seq. ID	xpa700798016.h1
Method	BLASTX
NCBI GI	g130829
BLAST score	137
E value	1.0e-08
Match length	53
% identity	49
NCBI Description	PATHOGENESIS-RELATED PROTEIN 1 (PVPR1) (PR2) >gi_72369_pir__SNFB1 pathogenesis-related protein 1 - kidney bean >gi_21044_emb_CAA43637_ (X61365) pathogenesis-related protein 1 (PvPR1) [Phaseolus vulgaris] >gi_227586_prf__1707270A pathogenesis related protein 1 [Phaseolus vulgaris]

Seq. No.	53812
Seq. ID	xpa700798048.h1
Method	BLASTX
NCBI GI	g4033446
BLAST score	142
E value	3.0e-09
Match length	74
% identity	45
NCBI Description	AGGLUTININ II PRECURSOR (CLAII) (LECCLAII) >gi_2147661_pir__S72502 mannose/glucose-binding lectin CLAII precursor - Cladrastis lutea >gi_1141759 (U21959) lectin precursor [Cladrastis lutea]

Seq. No.	53813
Seq. ID	xpa700798117.h1
Method	BLASTN
NCBI GI	g4325340
BLAST score	71
E value	7.0e-32
Match length	239
% identity	82
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	53814
Seq. ID	xpa700798131.h1
Method	BLASTX
NCBI GI	g3953601
BLAST score	217
E value	6.0e-18
Match length	66
% identity	68
NCBI Description	(AB008489) response regulator 6 [Arabidopsis thaliana]

Seq. No.	53815
Seq. ID	xpa700798204.h1
Method	BLASTX
NCBI GI	g3834310
BLAST score	168

E value	2.0e-21
Match length	82
% identity	77
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	53816
Seq. ID	xpa700798212.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	103
E value	6.0e-51
Match length	243
% identity	87
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53817
Seq. ID	xpa700798249.h1
Method	BLASTX
NCBI GI	g4467126
BLAST score	156
E value	8.0e-11
Match length	81
% identity	33
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	53818
Seq. ID	xpa700798266.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	102
E value	2.0e-50
Match length	218
% identity	87
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	53819
Seq. ID	xpa700798279.h1
Method	BLASTX
NCBI GI	g3402694
BLAST score	250
E value	7.0e-22
Match length	67
% identity	72
NCBI Description	(AC004697) putative Mlo-hi protein [Arabidopsis thaliana]

Seq. No.	53820
Seq. ID	xzm700763721.h1
Method	BLASTX
NCBI GI	g4336610
BLAST score	222
E value	3.0e-18

Match length	106
% identity	46
NCBI Description	(AF099112) sigma factor; Sig3 [Zea mays]

Seq. No.	53821
Seq. ID	xzm700763757.h1
Method	BLASTX
NCBI GI	g3600033
BLAST score	429
E value	1.0e-42
Match length	102
% identity	82
NCBI Description	(AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]

Seq. No.	53822
Seq. ID	xzm700763760.h1
Method	BLASTN
NCBI GI	g12158
BLAST score	83
E value	6.0e-39
Match length	300
% identity	84
NCBI Description	Pea gpa1 gene for subunit A of chloroplast glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)

Seq. No.	53823
Seq. ID	xzm700763801.h1
Method	BLASTX
NCBI GI	g2344889
BLAST score	245
E value	2.0e-24
Match length	112
% identity	59
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	53824
Seq. ID	xzm700763854.h1
Method	BLASTN
NCBI GI	g11763
BLAST score	191
E value	1.0e-103
Match length	293
% identity	93
NCBI Description	N.rustica chloroplast atpB gene for ATPase subunit beta

Seq. No.	53825
Seq. ID	xzm700763862.h1
Method	BLASTX
NCBI GI	g4102598
BLAST score	442
E value	5.0e-44
Match length	109
% identity	70
NCBI Description	(AF013466) auxin response factor 4 [Arabidopsis thaliana]

Seq. No.	53826
Seq. ID	xzy700966711.h1
Method	BLASTX
NCBI GI	g2062169
BLAST score	298
E value	2.0e-27
Match length	82
% identity	68
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	53827
Seq. ID	xzy700966721.h1
Method	BLASTX
NCBI GI	g4115373
BLAST score	283
E value	1.0e-25
Match length	87
% identity	66
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	53828
Seq. ID	xzy700966746.h1
Method	BLASTX
NCBI GI	g3287693
BLAST score	406
E value	5.0e-40
Match length	87
% identity	84
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	53829
Seq. ID	xzy700966749.h1
Method	BLASTX
NCBI GI	g3193308
BLAST score	156
E value	1.0e-10
Match length	58
% identity	50
NCBI Description	(AF069300) similar to Medicago truncatula MtN2 (GB:Y15293) [Arabidopsis thaliana]

Seq. No.	53830
Seq. ID	xzy700966765.h1
Method	BLASTX
NCBI GI	g4335742
BLAST score	216
E value	9.0e-18
Match length	77
% identity	68
NCBI Description	(AC006248) putative AR781 [Arabidopsis thaliana]

Seq. No.	53831
Seq. ID	xzy700966775.h1

Method	BLASTX
NCBI GI	g3600048
BLAST score	336
E value	7.0e-32
Match length	74
% identity	76
NCBI Description	(AF080120) similar to hypothetical proteins in Schizosaccharomyces pombe (GB:Z98533) and C. elegans (GB:Z48334 and Z78419) [Arabidopsis thaliana]

Seq. No.	53832
Seq. ID	xzy700966784.h1
Method	BLASTX
NCBI GI	g4469014
BLAST score	188
E value	2.0e-14
Match length	66
% identity	58
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	53833
Seq. ID	xzy700966815.h1
Method	BLASTX
NCBI GI	g2429288
BLAST score	168
E value	2.0e-12
Match length	45
% identity	67
NCBI Description	(AF014468) peroxidase [Oryza sativa]

Seq. No.	53834
Seq. ID	xzy700966838.h1
Method	BLASTX
NCBI GI	g2749943
BLAST score	147
E value	4.0e-13
Match length	55
% identity	64
NCBI Description	(U71244) pathogenesis-related group 5 protein [Brassica rapa]

Seq. No.	53835
Seq. ID	xzy700966843.h1
Method	BLASTN
NCBI GI	g18674
BLAST score	89
E value	1.0e-42
Match length	179
% identity	89
NCBI Description	G.max mRNA for lipoxygenase

Seq. No.	53836
Seq. ID	yuv700862713.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	279
E value	1.0e-156

Match length	279
% identity	100
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	53837
Seq. ID	yuv700862746.h1
Method	BLASTN
NCBI GI	g479059
BLAST score	171
E value	2.0e-91
Match length	178
% identity	99
NCBI Description	G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No.	53838
Seq. ID	yuv700862802.h1
Method	BLASTX
NCBI GI	g3834324
BLAST score	297
E value	3.0e-27
Match length	87
% identity	70
NCBI Description	(AC005679) Similar to gb_X92762 tafazzins protein from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	53839
Seq. ID	yuv700862817.h1
Method	BLASTX
NCBI GI	g99783
BLAST score	234
E value	4.0e-20
Match length	48
% identity	88
NCBI Description	acetolactate synthase (EC 4.1.3.18) 2 precursor - rape >gi_167119 (M60068) acetolactate synthase [Brassica napus]

Seq. No.	53840
Seq. ID	yuv700862819.h1
Method	BLASTX
NCBI GI	g3914083
BLAST score	279
E value	4.0e-25
Match length	95
% identity	60
NCBI Description	MUTS2 PROTEIN >gi_1652751_dbj_BAA17670_ (D90908) DNA mismatch repair protein MutS [Synechocystis sp.]

Seq. No.	53841
Seq. ID	yuv700862838.h1
Method	BLASTX
NCBI GI	g3004564
BLAST score	211
E value	4.0e-17
Match length	95
% identity	48
NCBI Description	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	53842
Seq. ID	yuv700862871.h1
Method	BLASTN
NCBI GI	g170019
BLAST score	204
E value	1.0e-111
Match length	236
% identity	97
NCBI Description	Soybean maturation protein (MAT1) gene, complete cds

Seq. No.	53843
Seq. ID	yuv700862877.h1
Method	BLASTN
NCBI GI	g18749
BLAST score	174
E value	3.0e-93
Match length	193
% identity	98
NCBI Description	G.max mRNA for seed maturation polypeptide

Seq. No.	53844
Seq. ID	yza700763918.h1
Method	BLASTX
NCBI GI	g2244865
BLAST score	150
E value	4.0e-10
Match length	83
% identity	43
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53845
Seq. ID	yza700764063.h1
Method	BLASTN
NCBI GI	g18551
BLAST score	58
E value	2.0e-24
Match length	138
% identity	86
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	53846
Seq. ID	yza700764066.h1
Method	BLASTX
NCBI GI	g4512263
BLAST score	220
E value	2.0e-18
Match length	52
% identity	83
NCBI Description	(AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No.	53847
Seq. ID	yzl700967021.h1
Method	BLASTN
NCBI GI	g1902893
BLAST score	101

E value	9.0e-50
Match length	237
% identity	86
NCBI Description	Solanum melongena mRNA for QM family protein, complete cds

Seq. No.	53848
Seq. ID	yzl700967037.h1
Method	BLASTX
NCBI GI	g2832698
BLAST score	349
E value	2.0e-33
Match length	84
% identity	69
NCBI Description	(AL021713) starch synthase-like protein [Arabidopsis thaliana]

Seq. No.	53849
Seq. ID	zhf700951720.h1
Method	BLASTX
NCBI GI	g3646450
BLAST score	220
E value	3.0e-18
Match length	81
% identity	52
NCBI Description	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]

Seq. No.	53850
Seq. ID	zhf700951736.h1
Method	BLASTX
NCBI GI	g131754
BLAST score	184
E value	4.0e-14
Match length	59
% identity	54
NCBI Description	PPLZ02 PROTEIN >gi_99973_pir__S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_ (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]

Seq. No.	53851
Seq. ID	zhf700951739.h1
Method	BLASTX
NCBI GI	g4206196
BLAST score	140
E value	5.0e-09
Match length	76
% identity	46
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53852
Seq. ID	zhf700951818.h1
Method	BLASTX
NCBI GI	g3582436
BLAST score	421
E value	9.0e-42
Match length	91

% identity	84
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No.	53853
Seq. ID	zhf700951827.h1
Method	BLASTX
NCBI GI	g1657619
BLAST score	231
E value	2.0e-19
Match length	89
% identity	47
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No.	53854
Seq. ID	zhf700951834.h1
Method	BLASTN
NCBI GI	g18569
BLAST score	95
E value	2.0e-46
Match length	95
% identity	100
NCBI Description	G.max coxII gene for cytochrome oxidase subunit

Seq. No.	53855
Seq. ID	zhf700951863.h1
Method	BLASTX
NCBI GI	g1362091
BLAST score	315
E value	4.0e-31
Match length	85
% identity	78
NCBI Description	cellulase (EC 3.2.1.4) precursor - tomato >gi_924622 (U20590) endo-1,4-beta-glucanase precursor [Solanum lycopersicum]

Seq. No.	53856
Seq. ID	zhf700951880.h1
Method	BLASTX
NCBI GI	g3309086
BLAST score	142
E value	2.0e-13
Match length	47
% identity	91
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	53857
Seq. ID	zhf700951904.h1
Method	BLASTX
NCBI GI	g1495273
BLAST score	363
E value	5.0e-35
Match length	87
% identity	79
NCBI Description	(Z50752) sugar transporter [Arabidopsis thaliana]

Seq. No.	53858
Seq. ID	zhf700951905.h1
Method	BLASTX
NCBI GI	g2494165
BLAST score	261
E value	4.0e-23
Match length	78
% identity	65
NCBI Description	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No.	53859
Seq. ID	zhf700951931.h1
Method	BLASTN
NCBI GI	g1155260
BLAST score	52
E value	2.0e-20
Match length	164
% identity	83
NCBI Description	Arabidopsis thaliana eukaryotic release factor 1 homolog (eRF1) mRNA, complete cds

Seq. No.	53860
Seq. ID	zhf700952013.h1
Method	BLASTN
NCBI GI	g18644
BLAST score	203
E value	1.0e-110
Match length	254
% identity	95
NCBI Description	Soybean mRNA for HMG-1 like protein

Seq. No.	53861
Seq. ID	zhf700952051.h1
Method	BLASTX
NCBI GI	g3212848
BLAST score	215
E value	1.0e-17
Match length	78
% identity	58
NCBI Description	(AC004005) putative inositol polyphosphate-5-phosphatase [Arabidopsis thaliana]

Seq. No.	53862
Seq. ID	zhf700952075.h1
Method	BLASTN
NCBI GI	g169127
BLAST score	71
E value	7.0e-32
Match length	118
% identity	91
NCBI Description	Pisum sativum (clone pCLp) nuclear encoded precursor to chloroplast protein mRNA, complete cds

Seq. No. 53863

Seq. ID	zhf700952090.h1
Method	BLASTN
NCBI GI	g603218
BLAST score	117
E value	3.0e-59
Match length	216
% identity	89
NCBI Description	Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete cds

Seq. No.	53864
Seq. ID	zhf700952143.h1
Method	BLASTX
NCBI GI	g3334162
BLAST score	189
E value	1.0e-14
Match length	79
% identity	46
NCBI Description	DOWN SYNDROME CRITICAL REGION PROTEIN A >gi_2588993_dbj_BAA23270_ (AB001990) Dcra [Mus musculus]

Seq. No.	53865
Seq. ID	zhf700952193.h1
Method	BLASTN
NCBI GI	g572605
BLAST score	44
E value	9.0e-16
Match length	164
% identity	87
NCBI Description	B.napus ACCg8 gene

Seq. No.	53866
Seq. ID	zhf700952194.h1
Method	BLASTX
NCBI GI	g3914832
BLAST score	335
E value	7.0e-32
Match length	77
% identity	77
NCBI Description	DNA-DIRECTED RNA POLYMERASE MITOCHONDRIAL PRECURSOR >gi_1742971_emb_CAA70583_ (Y09432) mitochondrial singel subunit DNA-directed RNA polymerase [Arabidopsis thaliana] >gi_2330566_emb_CAA70210_ (Y09006) mitochondrial single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No.	53867
Seq. ID	zhf700952223.h1
Method	BLASTX
NCBI GI	g2244785
BLAST score	293
E value	7.0e-27
Match length	80
% identity	68
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 53868

Seq. ID	zhf700952234.h1
Method	BLASTX
NCBI GI	g1532169
BLAST score	358
E value	2.0e-34
Match length	81
% identity	81
NCBI Description	(U63815) similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]

Seq. No.	53869
Seq. ID	zhf700952283.h1
Method	BLASTN
NCBI GI	g2828184
BLAST score	71
E value	7.0e-32
Match length	183
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	53870
Seq. ID	zhf700952302.h1
Method	BLASTX
NCBI GI	g3757521
BLAST score	198
E value	1.0e-15
Match length	59
% identity	61
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	53871
Seq. ID	zhf700952323.h1
Method	BLASTX
NCBI GI	g3298547
BLAST score	188
E value	2.0e-14
Match length	56
% identity	64
NCBI Description	(AC004681) putative condensin protein [Arabidopsis thaliana]

Seq. No.	53872
Seq. ID	zhf700952482.h1
Method	BLASTX
NCBI GI	g4512685
BLAST score	306
E value	2.0e-28
Match length	79
% identity	70
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53873
Seq. ID	zhf700952492.h1

Method	BLASTX
NCBI GI	g3860247
BLAST score	224
E value	6.0e-19
Match length	41
% identity	100
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	53874
Seq. ID	zhf700952587.h1
Method	BLASTN
NCBI GI	g2511696
BLAST score	79
E value	1.0e-36
Match length	183
% identity	86
NCBI Description	Phaseolus vulgaris Moldavian encoding asparagine-specific endopeptidase precursor (clone cp6b)

Seq. No.	53875
Seq. ID	zhf700952646.h1
Method	BLASTN
NCBI GI	g18764
BLAST score	251
E value	1.0e-139
Match length	251
% identity	100
NCBI Description	G.max tefS1 gene for elongation factor EF-1a

Seq. No.	53876
Seq. ID	zhf700952662.h1
Method	BLASTX
NCBI GI	g3914472
BLAST score	250
E value	7.0e-22
Match length	60
% identity	80
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum]

Seq. No.	53877
Seq. ID	zhf700952682.h1
Method	BLASTX
NCBI GI	g2464855
BLAST score	145
E value	2.0e-09
Match length	33
% identity	79
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No.	53878
Seq. ID	zhf700952717.h1
Method	BLASTX
NCBI GI	g2947069
BLAST score	289

E value	3.0e-26
Match length	90
% identity	58
NCBI Description	(AC002521) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	53879
Seq. ID	zhf700952755.h1
Method	BLASTX
NCBI GI	g2316016
BLAST score	221
E value	2.0e-18
Match length	85
% identity	48
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	53880
Seq. ID	zhf700952770.h1
Method	BLASTX
NCBI GI	g2618689
BLAST score	443
E value	2.0e-44
Match length	88
% identity	94
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	53881
Seq. ID	zhf700952774.h1
Method	BLASTX
NCBI GI	g2829888
BLAST score	247
E value	2.0e-21
Match length	89
% identity	55
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	53882
Seq. ID	zhf700952825.h1
Method	BLASTX
NCBI GI	g3096949
BLAST score	343
E value	1.0e-32
Match length	78
% identity	82
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	53883
Seq. ID	zhf700952834.h1
Method	BLASTX
NCBI GI	g166341
BLAST score	231
E value	1.0e-19
Match length	85
% identity	51
NCBI Description	(M98267) alliinase [Allium cepa] >gi_1044969 (L48614) allinase [Allium cepa]

Seq. No.	53884
Seq. ID	zhf700952836.h1
Method	BLASTX
NCBI GI	g2062167
BLAST score	151
E value	3.0e-10
Match length	30
% identity	87
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	53885
Seq. ID	zhf700952840.h1
Method	BLASTX
NCBI GI	g3688187
BLAST score	186
E value	3.0e-14
Match length	81
% identity	51
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	53886
Seq. ID	zhf700952952.h1
Method	BLASTX
NCBI GI	g3451075
BLAST score	147
E value	1.0e-09
Match length	41
% identity	66
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	53887
Seq. ID	zhf700953068.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	90
E value	3.0e-43
Match length	166
% identity	89
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	53888
Seq. ID	zhf700953075.h1
Method	BLASTX
NCBI GI	g3913425
BLAST score	428
E value	1.0e-42
Match length	79
% identity	99
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	53889
Seq. ID	zhf700953110.h1

Method	BLASTX
NCBI GI	g3746067
BLAST score	261
E value	4.0e-23
Match length	83
% identity	64
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53890
Seq. ID	zhf700953114.h1
Method	BLASTX
NCBI GI	g4467126
BLAST score	284
E value	7.0e-26
Match length	82
% identity	73
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	53891
Seq. ID	zhf700953145.h1
Method	BLASTX
NCBI GI	g4049353
BLAST score	266
E value	1.0e-23
Match length	82
% identity	60
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	53892
Seq. ID	zhf700953175.h1
Method	BLASTX
NCBI GI	g1717870
BLAST score	139
E value	8.0e-09
Match length	79
% identity	38
NCBI Description	PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8A4.01C (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)

Seq. No.	53893
Seq. ID	zhf700953204.h1
Method	BLASTX
NCBI GI	g4522008
BLAST score	248
E value	2.0e-21
Match length	76
% identity	62
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53894
Seq. ID	zhf700953205.h1
Method	BLASTX
NCBI GI	g3249068
BLAST score	152
E value	3.0e-10

Match length	82
% identity	44
NCBI Description	(AC004473) Contains similarity to zinc-binding protein (PWA33) gb_L04190 from Pleurodeles waltlii. [Arabidopsis thaliana]

Seq. No.	53895
Seq. ID	zhf700953242.h1
Method	BLASTX
NCBI GI	g1326161
BLAST score	214
E value	2.0e-17
Match length	64
% identity	77
NCBI Description	(U54703) dehydrin [Phaseolus vulgaris]

Seq. No.	53896
Seq. ID	zhf700953257.h1
Method	BLASTN
NCBI GI	g1853969
BLAST score	54
E value	5.0e-22
Match length	122
% identity	86
NCBI Description	Vigna unguiculata mRNA for CPRD46 protein, complete cds

Seq. No.	53897
Seq. ID	zhf700953304.h1
Method	BLASTX
NCBI GI	g585973
BLAST score	335
E value	2.0e-33
Match length	87
% identity	80
NCBI Description	FRUCTOKINASE >gi_626018_pir__S39997 fructokinase (EC 2.7.1.4) - potato >gi_297015_emb_CAA78283_ (Z12823) fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A fructokinase [Solanum tuberosum]

Seq. No.	53898
Seq. ID	zhf700953315.h1
Method	BLASTX
NCBI GI	g3024387
BLAST score	193
E value	5.0e-15
Match length	73
% identity	55
NCBI Description	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) >gi_668998 (U20431) polygalacturonase [Medicago sativa]

Seq. No.	53899
Seq. ID	zhf700953331.h1
Method	BLASTX
NCBI GI	g3875463
BLAST score	270
E value	4.0e-24
Match length	80

% identity	61
NCBI Description	(Z68341) predicted using Genefinder; Similarity to Human SNF2alpha protein (PIR Acc. No. S45251); cDNA EST EMBL:D26678 comes from this gene; cDNA EST EMBL:D26681 comes from this gene; cDNA EST EMBL:D26680 comes from this gene; ... >gi_3879468_emb_CAA92978_ (Z68751) predicted using Genefinder; Similarity to Human SNF2alpha protein (PIR Acc. No. S45251); cDNA EST EMBL:D26678 comes from this gene; cDNA EST EMBL:D26681 comes from this gene; cDNA EST EMBL:D26680 comes from this gene;
Seq. No.	53900
Seq. ID	zhf700953337.h1
Method	BLASTX
NCBI GI	g3892709
BLAST score	213
E value	2.0e-17
Match length	48
% identity	79
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]
Seq. No.	53901
Seq. ID	zhf700953352.h1
Method	BLASTX
NCBI GI	g2827141
BLAST score	329
E value	1.0e-34
Match length	82
% identity	89
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	53902
Seq. ID	zhf700953357.h1
Method	BLASTX
NCBI GI	g1173121
BLAST score	178
E value	2.0e-13
Match length	72
% identity	46
NCBI Description	ATP-DEPENDENT RNA HELICASE ROK1 >gi_2131186_pir__S59649 ATP-dependent RNA helicase ROK1 - yeast (Saccharomyces cerevisiae) >gi_607182_emb_CAA84384_ (Z34901) ATP-dependent RNA helicase [Saccharomyces cerevisiae] >gi_971382_emb_CAA59758_ (X85757) putative ATP dependent RNA helicase [Saccharomyces cerevisiae] >gi_1322774_emb_CAA96883_ (Z72693) ORF YGL171w [Saccharomyces cerevisiae]
Seq. No.	53903
Seq. ID	zhf700953361.h1
Method	BLASTX
NCBI GI	g416889
BLAST score	246
E value	2.0e-24
Match length	75
% identity	71

NCBI Description	DEOXYCYTIDYLATE DEAMINASE (DCMP DEAMINASE) >gi_539571_pir__A47288 dCMP deaminase (EC 3.5.4.12) - human >gi_181537 (L12136) deoxycytidylate deaminase [Homo sapiens] >gi_4503277_ref_NP_001912.1_pDCTD_ dCMP deaminase
Seq. No.	53904
Seq. ID	zhf700953364.h1
Method	BLASTX
NCBI GI	g2129740
BLAST score	265
E value	1.0e-23
Match length	63
% identity	79
NCBI Description	small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi_1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]
Seq. No.	53905
Seq. ID	zhf700953366.h1
Method	BLASTX
NCBI GI	g927428
BLAST score	232
E value	1.0e-19
Match length	86
% identity	70
NCBI Description	(X86733) fis1 [Linum usitatissimum]
Seq. No.	53906
Seq. ID	zhf700953416.h1
Method	BLASTX
NCBI GI	g4038055
BLAST score	194
E value	6.0e-27
Match length	82
% identity	72
NCBI Description	(AC005897) putative cytochrome P450 [Arabidopsis thaliana] >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative cytochrome p450 [Arabidopsis thaliana]
Seq. No.	53907
Seq. ID	zhf700953423.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	133
E value	7.0e-69
Match length	248
% identity	92
NCBI Description	Glycine max nodulin-26 mRNA, complete cds
Seq. No.	53908
Seq. ID	zhf700953455.h1
Method	BLASTX
NCBI GI	g2494144
BLAST score	137
E value	1.0e-08

Match length	62
% identity	50
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	53909
Seq. ID	zhf700953457.h1
Method	BLASTX
NCBI GI	g3047082
BLAST score	183
E value	6.0e-14
Match length	44
% identity	64
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	53910
Seq. ID	zhf700953474.h1
Method	BLASTX
NCBI GI	g3287696
BLAST score	198
E value	8.0e-32
Match length	81
% identity	69
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	53911
Seq. ID	zhf700953481.h1
Method	BLASTX
NCBI GI	g3335349
BLAST score	187
E value	2.0e-25
Match length	80
% identity	74
NCBI Description	(AC004512) Similar to gb_U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb_T42908, gb_AA586170 and gb_AA395125 come from this gene. [Arabidopsis thaliana]

Seq. No.	53912
Seq. ID	zhf700953494.h1
Method	BLASTN
NCBI GI	g3449328
BLAST score	32
E value	1.0e-08
Match length	32
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCI2, complete sequence [Arabidopsis thaliana]

Seq. No.	53913
Seq. ID	zhf700953506.h1
Method	BLASTX
NCBI GI	g3122572

BLAST score 284
E value 8.0e-26
Match length 67
% identity 79
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No. 53914
Seq. ID zhf700953513.h1
Method BLASTX
NCBI GI g3860321
BLAST score 162
E value 2.0e-14
Match length 53
% identity 77
NCBI Description (AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No. 53915
Seq. ID zhf700953521.h1
Method BLASTN
NCBI GI g2502086
BLAST score 69
E value 1.0e-30
Match length 117
% identity 90
NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 53916
Seq. ID zhf700953529.h1
Method BLASTX
NCBI GI g4006829
BLAST score 291
E value 1.0e-26
Match length 63
% identity 84
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 53917
Seq. ID zhf700953536.h1
Method BLASTN
NCBI GI g303900
BLAST score 87
E value 2.0e-41
Match length 91
% identity 32
NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 53918
Seq. ID zhf700953551.h1
Method BLASTX
NCBI GI g4206210
BLAST score 142
E value 3.0e-09

Match length	60
% identity	50
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	53919
Seq. ID	zhf700953563.h1
Method	BLASTX
NCBI GI	g3935138
BLAST score	171
E value	1.0e-12
Match length	77
% identity	55
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	53920
Seq. ID	zhf700953566.h1
Method	BLASTX
NCBI GI	g4210330
BLAST score	283
E value	1.0e-25
Match length	78
% identity	69
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	53921
Seq. ID	zhf700953583.h1
Method	BLASTN
NCBI GI	g218325
BLAST score	65
E value	2.0e-28
Match length	93
% identity	92
NCBI Description	Vigna radiata mRNA for invertase, complete cds

Seq. No.	53922
Seq. ID	zhf700953610.h1
Method	BLASTX
NCBI GI	g2160161
BLAST score	174
E value	7.0e-13
Match length	86
% identity	8
NCBI Description	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]

Seq. No.	53923
Seq. ID	zhf700953611.h1
Method	BLASTX
NCBI GI	g3158476
BLAST score	282
E value	2.0e-25
Match length	67
% identity	82
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	53924
Seq. ID	zhf700953617.h1
Method	BLASTX
NCBI GI	g3786009
BLAST score	186
E value	3.0e-14
Match length	40
% identity	90
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	53925
Seq. ID	zhf700953642.h1
Method	BLASTX
NCBI GI	g2262101
BLAST score	180
E value	1.0e-13
Match length	83
% identity	54
NCBI Description	(AC002343) kinesin heavy chain isolog [Arabidopsis thaliana]

Seq. No.	53926
Seq. ID	zhf700953649.h1
Method	BLASTX
NCBI GI	g1491615
BLAST score	186
E value	3.0e-14
Match length	57
% identity	65
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	53927
Seq. ID	zhf700953734.h1
Method	BLASTX
NCBI GI	g3618316
BLAST score	325
E value	1.0e-30
Match length	77
% identity	51
NCBI Description	(AB001886) zinc finger protein [Oryza sativa]

Seq. No.	53928
Seq. ID	zhf700953764.h1
Method	BLASTX
NCBI GI	g3790658
BLAST score	152
E value	3.0e-10
Match length	77
% identity	35
NCBI Description	(AF098999) contains similarity to ABC transporters (Pfam: ABC_tran.hmm, score: 39.76) [Caenorhabditis elegans]

Seq. No.	53929
Seq. ID	zhf700953854.h1
Method	BLASTX
NCBI GI	g4335751

BLAST score	194
E value	3.0e-15
Match length	81
% identity	46
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	53930
Seq. ID	zhf700953882.h1
Method	BLASTN
NCBI GI	g441456
BLAST score	47
E value	2.0e-17
Match length	107
% identity	86
NCBI Description	L.esculentum mRNA for ubiquitin conjugating enzyme E2 >gi_2296161_emb_A39963.1_A39963 Sequence 7 from Patent WO9421794

Seq. No.	53931
Seq. ID	zhf700953907.h1
Method	BLASTX
NCBI GI	g4559388
BLAST score	208
E value	6.0e-17
Match length	69
% identity	51
NCBI Description	(AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53932
Seq. ID	zhf700953927.h1
Method	BLASTX
NCBI GI	g4262161
BLAST score	244
E value	4.0e-21
Match length	66
% identity	67
NCBI Description	(AC005275) SYR1-like syntaxin [Arabidopsis thaliana]

Seq. No.	53933
Seq. ID	zhf700953946.h1
Method	BLASTX
NCBI GI	g1353239
BLAST score	167
E value	4.0e-12
Match length	82
% identity	45
NCBI Description	(U10245) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	53934
Seq. ID	zhf700954134.h1
Method	BLASTX
NCBI GI	g3687237
BLAST score	188
E value	2.0e-14
Match length	76
% identity	50

NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	53935
Seq. ID	zhf700954223.h1
Method	BLASTX
NCBI GI	g2864615
BLAST score	288
E value	3.0e-26
Match length	65
% identity	85
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	53936
Seq. ID	zhf700954226.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	245
E value	1.0e-135
Match length	249
% identity	100
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	53937
Seq. ID	zhf700954242.h1
Method	BLASTX
NCBI GI	g2827516
BLAST score	211
E value	3.0e-17
Match length	48
% identity	77
NCBI Description	(AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana]

Seq. No.	53938
Seq. ID	zhf700954257.h1
Method	BLASTX
NCBI GI	g4406801
BLAST score	137
E value	1.0e-08
Match length	43
% identity	58
NCBI Description	(AC006304) unknown protein [Arabidopsis thaliana]

Seq. No.	53939
Seq. ID	zhf700954331.h1
Method	BLASTX
NCBI GI	g2702279
BLAST score	195
E value	1.0e-15
Match length	43
% identity	79
NCBI Description	(AC003033) putative phosphate transporter [Arabidopsis thaliana] >gi_2780345_dbj_BAA24280_ (AB000093) inorganic phosphate transporter [Arabidopsis thaliana] >gi_2914691 (AC003974) putative phosphate transporter [Arabidopsis

thaliana]

Seq. No.	53940
Seq. ID	zhf700954350.h1
Method	BLASTX
NCBI GI	g3183088
BLAST score	280
E value	3.0e-25
Match length	88
% identity	57
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	53941
Seq. ID	zhf700954361.h1
Method	BLASTX
NCBI GI	g2760844
BLAST score	278
E value	3.0e-25
Match length	89
% identity	67
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53942
Seq. ID	zhf700954363.h1
Method	BLASTX
NCBI GI	g4218120
BLAST score	267
E value	1.0e-23
Match length	65
% identity	71
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	53943
Seq. ID	zhf700954383.h1
Method	BLASTX
NCBI GI	g2289003
BLAST score	227
E value	3.0e-19
Match length	55
% identity	76
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	53944
Seq. ID	zhf700954401.h1
Method	BLASTX
NCBI GI	g2460203
BLAST score	154
E value	1.0e-10
Match length	81
% identity	57
NCBI Description	(AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]

Seq. No.	53945
Seq. ID	zhf700954417.h1
Method	BLASTX
NCBI GI	g3892059
BLAST score	163
E value	1.0e-11
Match length	79
% identity	48
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	53946
Seq. ID	zhf700954426.h1
Method	BLASTX
NCBI GI	g4455171
BLAST score	249
E value	1.0e-21
Match length	75
% identity	59
NCBI Description	(AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53947
Seq. ID	zhf700954440.h1
Method	BLASTX
NCBI GI	g1168654
BLAST score	270
E value	3.0e-24
Match length	69
% identity	68
NCBI Description	BETA-GALACTOSIDASE PRECURSOR (LACTASE) >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) - garden asparagus >gi_452712_emb_CAA54525_ (X77319) beta-galactosidase [Asparagus officinalis]

Seq. No.	53948
Seq. ID	zhf700954457.h1
Method	BLASTX
NCBI GI	g3746060
BLAST score	366
E value	2.0e-35
Match length	81
% identity	79
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]

Seq. No.	53949
Seq. ID	zhf700954471.h1
Method	BLASTX
NCBI GI	g4115538
BLAST score	248
E value	1.0e-21
Match length	81
% identity	64
NCBI Description	(AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No. 53950

Seq. ID	zhf700954485.h1
Method	BLASTX
NCBI GI	g2323344
BLAST score	370
E value	6.0e-36
Match length	79
% identity	84
NCBI Description	(AF014806) alpha-glucosidase 1 [Arabidopsis thaliana]

Seq. No.	53951
Seq. ID	zhf700954535.h1
Method	BLASTN
NCBI GI	g4218186
BLAST score	130
E value	6.0e-67
Match length	134
% identity	99
NCBI Description	Glycine max mRNA for leghemoglobin activating factor

Seq. No.	53952
Seq. ID	zhf700954647.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	248
E value	1.0e-137
Match length	248
% identity	100
NCBI Description	G.max ADR6 mRNA

Seq. No.	53953
Seq. ID	zhf700954714.h1
Method	BLASTN
NCBI GI	g2598586
BLAST score	58
E value	4.0e-24
Match length	118
% identity	87
NCBI Description	Medicago truncatula mRNA for cycloartenol synthase, partial

Seq. No.	53954
Seq. ID	zhf700954822.h1
Method	BLASTN
NCBI GI	g408793
BLAST score	117
E value	3.0e-59
Match length	155
% identity	96
NCBI Description	Glycine soja chloroplast 3-omega faty acid desaturase (Fad3) mRNA, complete cds

Seq. No.	53955
Seq. ID	zhf700954840.h1
Method	BLASTN
NCBI GI	g576506
BLAST score	80
E value	3.0e-37
Match length	251

% identity	83
NCBI Description	Pisum sativum outer membrane protein (IAP75) mRNA, complete cds

Seq. No.	53956
Seq. ID	zhf700954988.h1
Method	BLASTN
NCBI GI	g3184053
BLAST score	43
E value	3.0e-15
Match length	51
% identity	96
NCBI Description	Pisum sativum mRNA for MADS-box transcription factor

Seq. No.	53957
Seq. ID	zhf700955043.h1
Method	BLASTN
NCBI GI	g1256203
BLAST score	34
E value	9.0e-10
Match length	198
% identity	83
NCBI Description	Spinach phosphoserine aminotransferase mRNA, complete cds

Seq. No.	53958
Seq. ID	zhf700955091.h1
Method	BLASTN
NCBI GI	g508303
BLAST score	52
E value	2.0e-20
Match length	164
% identity	83
NCBI Description	Alfalfa bimodular protein (corC) mRNA, complete cds

Seq. No.	53959
Seq. ID	zhf700955152.h1
Method	BLASTN
NCBI GI	g861154
BLAST score	38
E value	4.0e-12
Match length	134
% identity	82
NCBI Description	V.faba VFCWINV1 mRNA for cell wall invertase I

Seq. No.	53960
Seq. ID	zhf700955195.h1
Method	BLASTN
NCBI GI	g3420042
BLAST score	42
E value	1.0e-14
Match length	150
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	53961
Seq. ID	zhf700955317.h1

Method	BLASTN
NCBI GI	g4322939
BLAST score	49
E value	1.0e-18
Match length	93
% identity	88
NCBI Description	Nicotiana tabacum DNA-binding protein 2 (WRKY2) mRNA, complete cds

Seq. No.	53962
Seq. ID	zhf700955425.h1
Method	BLASTN
NCBI GI	g3868723
BLAST score	40
E value	2.0e-13
Match length	68
% identity	90
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	53963
Seq. ID	zhf700955460.h1
Method	BLASTN
NCBI GI	g3869074
BLAST score	32
E value	1.0e-08
Match length	235
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	53964
Seq. ID	zhf700955475.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	258
E value	1.0e-143
Match length	262
% identity	100
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	53965
Seq. ID	zhf700955539.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	250
E value	1.0e-138
Match length	254
% identity	100
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	53966
Seq. ID	zhf700955542.h1
Method	BLASTN
NCBI GI	g4115338
BLAST score	102

E value	2.0e-50
Match length	158
% identity	22
NCBI Description	Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

Seq. No.	53967
Seq. ID	zhf700955604.h1
Method	BLASTN
NCBI GI	g1480346
BLAST score	103
E value	6.0e-51
Match length	151
% identity	92
NCBI Description	P.sativum mRNA for ferrodoxin NADP oxidoreductase

Seq. No.	53968
Seq. ID	zhf700955772.h1
Method	BLASTN
NCBI GI	g4567300
BLAST score	41
E value	6.0e-14
Match length	145
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	53969
Seq. ID	zhf700955817.h1
Method	BLASTN
NCBI GI	g471289
BLAST score	33
E value	3.0e-09
Match length	65
% identity	88
NCBI Description	A.thaliana aha9 gene

Seq. No.	53970
Seq. ID	zhf700955929.h1
Method	BLASTN
NCBI GI	g396638
BLAST score	37
E value	1.0e-11
Match length	89
% identity	85
NCBI Description	P.sativum ribosomal protein S13 mRNA, complete CDS

Seq. No.	53971
Seq. ID	zhf700956003.h1
Method	BLASTN
NCBI GI	g20061
BLAST score	107
E value	2.0e-53
Match length	239
% identity	87
NCBI Description	Oenothera elata subsp. hookeri mRNA for protein kinase C inhibitor homologue

Seq. No.	53972
Seq. ID	zhf700956044.h1
Method	BLASTN
NCBI GI	g515691
BLAST score	162
E value	4.0e-86
Match length	166
% identity	99
NCBI Description	Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds

Seq. No.	53973
Seq. ID	zhf700956060.h1
Method	BLASTN
NCBI GI	g602564
BLAST score	61
E value	7.0e-26
Match length	157
% identity	85
NCBI Description	C.paradisi (Macf) INO1 gene

Seq. No.	53974
Seq. ID	zhf700956133.h1
Method	BLASTN
NCBI GI	g2791833
BLAST score	126
E value	1.0e-64
Match length	190
% identity	92
NCBI Description	Manihot esculenta elongation factor 1-alpha (MeEF1) gene, complete cds

Seq. No.	53975
Seq. ID	zhf700956242.h1
Method	BLASTN
NCBI GI	g2905771
BLAST score	136
E value	1.0e-70
Match length	148
% identity	98
NCBI Description	Glycine max glyceraldehyde-3 phosphate dehydrogenase (GAPDH) mRNA, partial cds

Seq. No.	53976
Seq. ID	zhf700956336.h1
Method	BLASTN
NCBI GI	g170205
BLAST score	56
E value	6.0e-23
Match length	160
% identity	84
NCBI Description	N.plumbaginifolia H+-translocating ATPase mRNA

Seq. No.	53977
Seq. ID	zhf700956361.h1
Method	BLASTN
NCBI GI	g4467131
BLAST score	44

E value	8.0e-16
Match length	148
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	53978
Seq. ID	zhf700956403.h1
Method	BLASTN
NCBI GI	g22073
BLAST score	39
E value	9.0e-13
Match length	57
% identity	92
NCBI Description	Mung bean 25S rRNA - 18S rDNA spacer region

Seq. No.	53979
Seq. ID	zhf700956478.h1
Method	BLASTN
NCBI GI	g1217641
BLAST score	42
E value	1.0e-14
Match length	110
% identity	85
NCBI Description	L.esculentum mRNA for 10kDa polypeptide precursor of photosystem II

Seq. No.	53980
Seq. ID	zhf700956565.h1
Method	BLASTN
NCBI GI	g18662
BLAST score	39
E value	8.0e-13
Match length	55
% identity	93
NCBI Description	Glycine max hsp 70 gene

Seq. No.	53981
Seq. ID	zhf700956625.h1
Method	BLASTN
NCBI GI	g3873174
BLAST score	42
E value	2.0e-14
Match length	110
% identity	85
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	53982
Seq. ID	zhf700956672.h1
Method	BLASTX
NCBI GI	g2281090
BLAST score	289
E value	1.0e-26
Match length	77
% identity	75
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53983
Seq. ID	zhf700956677.h1
Method	BLASTX
NCBI GI	g3176660
BLAST score	334
E value	1.0e-31
Match length	83
% identity	72
NCBI Description	(AC004393) Similar to ERECTA receptor protein kinase gb_U47029 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	53984
Seq. ID	zhf700956709.h1
Method	BLASTX
NCBI GI	g2673918
BLAST score	185
E value	4.0e-14
Match length	63
% identity	60
NCBI Description	(AC002561) unknwon protein [Arabidopsis thaliana]

Seq. No.	53985
Seq. ID	zhf700956765.h1
Method	BLASTX
NCBI GI	g3738301
BLAST score	233
E value	8.0e-20
Match length	62
% identity	31
NCBI Description	(AC005309) putative zinc-finger protein [Arabidopsis thaliana] >gi_4249397 (AC006072) putative zinc-finger protein (B-box zinc finger domain) [Arabidopsis thaliana]

Seq. No.	53986
Seq. ID	zhf700956810.h1
Method	BLASTX
NCBI GI	g1351202
BLAST score	227
E value	3.0e-19
Match length	54
% identity	72
NCBI Description	TUBULIN BETA CHAIN >gi_312989_emb_CAA42777_ (X60216) beta-tubulin [Glycine max]

Seq. No.	53987
Seq. ID	zhf700956994.h1
Method	BLASTN
NCBI GI	g343344
BLAST score	84
E value	7.0e-40
Match length	140
% identity	91
NCBI Description	Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes

Seq. No.	53988

Seq. ID	zhf700957069.h1
Method	BLASTX
NCBI GI	g886100
BLAST score	262
E value	3.0e-23
Match length	55
% identity	85
NCBI Description	(U27347) putative water channel protein; plasmalemma intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No.	53989
Seq. ID	zhf700957084.h1
Method	BLASTX
NCBI GI	g3329368
BLAST score	283
E value	1.0e-25
Match length	85
% identity	62
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	53990
Seq. ID	zhf700957086.h1
Method	BLASTN
NCBI GI	g1173641
BLAST score	67
E value	8.0e-30
Match length	111
% identity	90
NCBI Description	Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No.	53991
Seq. ID	zhf700957087.h1
Method	BLASTX
NCBI GI	g3913008
BLAST score	114
E value	1.0e-08
Match length	64
% identity	64
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No.	53992
Seq. ID	zhf700957202.h1
Method	BLASTX
NCBI GI	g2244956
BLAST score	163
E value	2.0e-16
Match length	75
% identity	50
NCBI Description	(Z97340) strong similarity to pectinesterase [Arabidopsis thaliana]

Seq. No.	53993
Seq. ID	zhf700957207.h1
Method	BLASTX

NCBI GI	g3582328
BLAST score	111
E value	6.0e-12
Match length	75
% identity	49
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	53994
Seq. ID	zhf700957208.h1
Method	BLASTX
NCBI GI	g4567279
BLAST score	162
E value	2.0e-17
Match length	60
% identity	80
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	53995
Seq. ID	zhf700957246.h1
Method	BLASTN
NCBI GI	g886099
BLAST score	61
E value	7.0e-26
Match length	72
% identity	97
NCBI Description	Glycine max putative water channel protein (Pip1) mRNA, complete cds

Seq. No.	53996
Seq. ID	zhf700957319.h1
Method	BLASTX
NCBI GI	g2160756
BLAST score	389
E value	4.0e-38
Match length	85
% identity	79
NCBI Description	(U96879) CLV1 receptor kinase [Arabidopsis thaliana]

Seq. No.	53997
Seq. ID	zhf700957332.h1
Method	BLASTX
NCBI GI	g162629
BLAST score	209
E value	5.0e-17
Match length	70
% identity	64
NCBI Description	(M17029) adrenodoxin oxidoreductase precursor (EC 1.18.1.2) [Bos taurus]

Seq. No.	53998
Seq. ID	zhf700957382.h1
Method	BLASTX
NCBI GI	g3327394
BLAST score	246
E value	2.0e-21
Match length	83

% identity	53
NCBI Description	(AC004483) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	53999
Seq. ID	zhf700957392.h1
Method	BLASTN
NCBI GI	g3860320
BLAST score	127
E value	3.0e-65
Match length	243
% identity	88
NCBI Description	Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-5

Seq. No.	54000
Seq. ID	zhf700957402.h1
Method	BLASTX
NCBI GI	g2108252
BLAST score	171
E value	4.0e-18
Match length	55
% identity	34
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	54001
Seq. ID	zhf700957441.h1
Method	BLASTN
NCBI GI	g3327274
BLAST score	34
E value	9.0e-10
Match length	74
% identity	86
NCBI Description	Ipomoea nil PKn3 (knotted-like gene) mRNA, complete cds

Seq. No.	54002
Seq. ID	zhf700957492.h1
Method	BLASTX
NCBI GI	g2384669
BLAST score	222
E value	1.0e-18
Match length	72
% identity	57
NCBI Description	(AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]

Seq. No.	54003
Seq. ID	zhf700957594.h1
Method	BLASTN
NCBI GI	g3341442
BLAST score	229
E value	1.0e-126
Match length	229
% identity	100
NCBI Description	Glycine max mRNA for root nodule acid phosphatase

Seq. No.	54004
Seq. ID	zhf700957611.h1
Method	BLASTX
NCBI GI	g3201541
BLAST score	356
E value	3.0e-34
Match length	76
% identity	87
NCBI Description	(AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No.	54005
Seq. ID	zhf700957617.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	179
E value	2.0e-96
Match length	183
% identity	99
NCBI Description	G.max ADR6 mRNA

Seq. No.	54006
Seq. ID	zhf700957658.h1
Method	BLASTN
NCBI GI	g1841474
BLAST score	90
E value	3.0e-43
Match length	146
% identity	90
NCBI Description	P.sativum mRNA for Myb-like protein (Myb26)

Seq. No.	54007
Seq. ID	zhf700957675.h1
Method	BLASTX
NCBI GI	g2239262
BLAST score	229
E value	2.0e-19
Match length	76
% identity	59
NCBI Description	(Y13285) pectin methylesterase-like protein [Zea mays]

Seq. No.	54008
Seq. ID	zhf700957701.h1
Method	BLASTX
NCBI GI	g4416302
BLAST score	212
E value	3.0e-17
Match length	68
% identity	62
NCBI Description	(AF105716) copia-type pol polyprotein [Zea mays]

Seq. No.	54009
Seq. ID	zhf700957709.h1
Method	BLASTX
NCBI GI	g2078350
BLAST score	263
E value	2.0e-23

Match length	73
% identity	71
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	54010
Seq. ID	zhf700957723.h1
Method	BLASTX
NCBI GI	g4580395
BLAST score	199
E value	8.0e-16
Match length	82
% identity	46
NCBI Description	(AC007171) putative kinesin-related protein [Arabidopsis thaliana]

Seq. No.	54011
Seq. ID	zhf700957745.h1
Method	BLASTN
NCBI GI	g457569
BLAST score	90
E value	3.0e-43
Match length	136
% identity	94
NCBI Description	Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No.	54012
Seq. ID	zhf700957847.h1
Method	BLASTX
NCBI GI	g3757523
BLAST score	293
E value	8.0e-27
Match length	85
% identity	69
NCBI Description	(AC005167) putative transportin [Arabidopsis thaliana]

Seq. No.	54013
Seq. ID	zhf700957918.h1
Method	BLASTX
NCBI GI	g3492803
BLAST score	142
E value	4.0e-09
Match length	54
% identity	50
NCBI Description	(AJ002479) ENBP1 [Medicago truncatula]

Seq. No.	54014
Seq. ID	zhf700958025.h1
Method	BLASTX
NCBI GI	g1772985
BLAST score	240
E value	1.0e-20
Match length	64
% identity	69
NCBI Description	(Z83835) zeaxanthin epoxidase [Lycopersicon esculentum]

Seq. No.	54015
Seq. ID	zhf700958040.h1

Method	BLASTX
NCBI GI	g4539351
BLAST score	264
E value	2.0e-23
Match length	79
% identity	68
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	54016
Seq. ID	zhf700958048.h1
Method	BLASTX
NCBI GI	g2104534
BLAST score	335
E value	8.0e-32
Match length	81
% identity	77
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54017
Seq. ID	zhf700958113.h1
Method	BLASTX
NCBI GI	g3064245
BLAST score	203
E value	3.0e-16
Match length	71
% identity	54
NCBI Description	(AF039023) Ran-GTP binding protein; RanBP6 [Homo sapiens]

Seq. No.	54018
Seq. ID	zhf700958146.h1
Method	BLASTX
NCBI GI	g2570047
BLAST score	161
E value	2.0e-11
Match length	67
% identity	42
NCBI Description	(Y09234) MSTK2S kinase-like protein [Mus musculus]

Seq. No.	54019
Seq. ID	zhf700958157.h1
Method	BLASTX
NCBI GI	g2245115
BLAST score	146
E value	1.0e-09
Match length	84
% identity	49
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	54020
Seq. ID	zhf700958191.h1
Method	BLASTX
NCBI GI	g3582328
BLAST score	191
E value	7.0e-15
Match length	84
% identity	45
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54021
Seq. ID	zhf700958228.h1
Method	BLASTX
NCBI GI	g2961283
BLAST score	225
E value	7.0e-19
Match length	55
% identity	69
NCBI Description	(Y16848) LG27/30 [Arabidopsis thaliana]

Seq. No.	54022
Seq. ID	zhf700958273.h1
Method	BLASTX
NCBI GI	g4263717
BLAST score	356
E value	3.0e-34
Match length	83
% identity	77
NCBI Description	(AC006223) putative inositol polyphosphate 5-phosphatase [Arabidopsis thaliana]

Seq. No.	54023
Seq. ID	zhf700958302.h1
Method	BLASTN
NCBI GI	g457572
BLAST score	91
E value	9.0e-44
Match length	215
% identity	94
NCBI Description	V.angularis mRNA for endo-xyloglucan transferase, complete cds

Seq. No.	54024
Seq. ID	zhf700958305.h1
Method	BLASTX
NCBI GI	g2462826
BLAST score	205
E value	1.0e-16
Match length	74
% identity	59
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	54025
Seq. ID	zhf700958372.h1
Method	BLASTN
NCBI GI	g4103958
BLAST score	160
E value	5.0e-85
Match length	204
% identity	95
NCBI Description	Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele, complete cds

Seq. No.	54026
Seq. ID	zhf700958415.h1
Method	BLASTX

NCBI GI g4056496
BLAST score 244
E value 5.0e-21
Match length 76
% identity 62
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 54027
Seq. ID zhf700958444.h1
Method BLASTX
NCBI GI g2459408
BLAST score 154
E value 1.0e-10
Match length 35
% identity 86
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana] >gi_2924769 (AC002334) unknown protein [Arabidopsis thaliana]

Seq. No. 54028
Seq. ID zhf700958548.h1
Method BLASTX
NCBI GI g4567286
BLAST score 118
E value 5.0e-12
Match length 65
% identity 65
NCBI Description (AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No. 54029
Seq. ID zhf700958549.h1
Method BLASTN
NCBI GI g2924257
BLAST score 72
E value 2.0e-32
Match length 120
% identity 90
NCBI Description Tobacco chloroplast genome DNA

Seq. No. 54030
Seq. ID zhf700958586.h1
Method BLASTN
NCBI GI g2827299
BLAST score 86
E value 7.0e-41
Match length 158
% identity 89
NCBI Description Medicago sativa MADS-box protein NMH 7 (nmh 7) gene, complete cds

Seq. No. 54031
Seq. ID zhf700958591.h1
Method BLASTX
NCBI GI g3402697
BLAST score 145
E value 1.0e-09

Match length	72
% identity	43
NCBI Description	(AC004261) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	54032
Seq. ID	zhf700958623.h1
Method	BLASTX
NCBI GI	g3779028
BLAST score	184
E value	5.0e-28
Match length	85
% identity	67
NCBI Description	(AC005171) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	54033
Seq. ID	zhf700958657.h1
Method	BLASTX
NCBI GI	g3142292
BLAST score	196
E value	2.0e-15
Match length	46
% identity	78
NCBI Description	(AC002411) Contains similarity to tetratricopeptide repeat protein gb_U46571 from home sapiens. EST gb_Z47802 and gb_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No.	54034
Seq. ID	zhf700958668.h1
Method	BLASTN
NCBI GI	g2315210
BLAST score	75
E value	3.0e-34
Match length	119
% identity	91
NCBI Description	Lycopersicon esculentum mRNA for proteasome, alpha subunit

Seq. No.	54035
Seq. ID	zhf700958740.h1
Method	BLASTN
NCBI GI	g516853
BLAST score	133
E value	7.0e-69
Match length	180
% identity	32
NCBI Description	Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No.	54036
Seq. ID	zhf700958778.h1
Method	BLASTX
NCBI GI	g1708191
BLAST score	126
E value	4.0e-10
Match length	67
% identity	54
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No.	54037
Seq. ID	zhf700958788.h1
Method	BLASTN
NCBI GI	g2149954
BLAST score	95
E value	3.0e-46
Match length	202
% identity	87
NCBI Description	Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA, complete cds

Seq. No.	54038
Seq. ID	zhf700958810.h1
Method	BLASTX
NCBI GI	g3935148
BLAST score	366
E value	2.0e-35
Match length	82
% identity	79
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	54039
Seq. ID	zhf700958835.h1
Method	BLASTX
NCBI GI	g3402718
BLAST score	179
E value	2.0e-13
Match length	82
% identity	44
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54040
Seq. ID	zhf700958860.h1
Method	BLASTX
NCBI GI	g4539383
BLAST score	291
E value	1.0e-26
Match length	79
% identity	73
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	54041
Seq. ID	zhf700958867.h1
Method	BLASTX
NCBI GI	g2129550
BLAST score	308
E value	1.0e-28
Match length	81
% identity	41
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana]

>gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	54042
Seq. ID	zhf700958871.h1
Method	BLASTX
NCBI GI	g2565006
BLAST score	279
E value	3.0e-25
Match length	79
% identity	73
NCBI Description	(AC002983) putative sulfate transporter [Arabidopsis thaliana]

Seq. No.	54043
Seq. ID	zhf700958950.h1
Method	BLASTX
NCBI GI	g2341032
BLAST score	247
E value	2.0e-21
Match length	51
% identity	86
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	54044
Seq. ID	zhf700958957.h1
Method	BLASTX
NCBI GI	g3860247
BLAST score	223
E value	1.0e-18
Match length	79
% identity	63
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	54045
Seq. ID	zhf700959012.h1
Method	BLASTX
NCBI GI	g2088651
BLAST score	193
E value	4.0e-15
Match length	69
% identity	59
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	54046
Seq. ID	zhf700959016.h1
Method	BLASTN
NCBI GI	g1419035
BLAST score	185
E value	1.0e-100
Match length	265
% identity	92
NCBI Description	M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase, P5CS-1

Seq. No.	54047
Seq. ID	zhf700959022.h1
Method	BLASTX
NCBI GI	g1781299
BLAST score	216
E value	8.0e-18
Match length	69
% identity	82
NCBI Description	(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]

Seq. No.	54048
Seq. ID	zhf700959024.h1
Method	BLASTN
NCBI GI	g343348
BLAST score	233
E value	1.0e-128
Match length	258
% identity	97
NCBI Description	Glycine max mitochondrial DNA sequence, transcription initiation motif

Seq. No.	54049
Seq. ID	zhf700959033.h1
Method	BLASTX
NCBI GI	g1685003
BLAST score	276
E value	8.0e-25
Match length	81
% identity	62
NCBI Description	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No.	54050
Seq. ID	zhf700959086.h1
Method	BLASTX
NCBI GI	g4220479
BLAST score	198
E value	3.0e-20
Match length	54
% identity	76
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	54051
Seq. ID	zhf700959130.h1
Method	BLASTX
NCBI GI	g3779218
BLAST score	337
E value	5.0e-32
Match length	80
% identity	85
NCBI Description	(AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No.	54052
Seq. ID	zhf700959155.h1
Method	BLASTX
NCBI GI	g4567319

BLAST score	338
E value	3.0e-32
Match length	77
% identity	78
NCBI Description	(AC005956) putative copper amine oxidase [Arabidopsis thaliana]

Seq. No.	54053
Seq. ID	zhf700959183.h1
Method	BLASTX
NCBI GI	g3063465
BLAST score	206
E value	7.0e-17
Match length	62
% identity	63
NCBI Description	(AC003981) F22O13.27 [Arabidopsis thaliana]

Seq. No.	54054
Seq. ID	zhf700959191.h1
Method	BLASTN
NCBI GI	g18733
BLAST score	217
E value	1.0e-119
Match length	217
% identity	57
NCBI Description	Soybean RPB1-B2 gene for the largest subunit of RNA polymerase II (EC 2.7.7.6)

Seq. No.	54055
Seq. ID	zhf700959213.h1
Method	BLASTX
NCBI GI	g4093155
BLAST score	231
E value	1.0e-19
Match length	78
% identity	58
NCBI Description	(AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No.	54056
Seq. ID	zhf700959225.h1
Method	BLASTX
NCBI GI	g1839214
BLAST score	277
E value	6.0e-25
Match length	85
% identity	60
NCBI Description	(U85835) enolase [unidentified pseudophyllidean]

Seq. No.	54057
Seq. ID	zhf700959264.h1
Method	BLASTX
NCBI GI	g951449
BLAST score	161
E value	2.0e-11
Match length	35
% identity	74

NCBI Description	(L46681) aspartic protease precursor [Lycopersicon esculentum]

Seq. No.	54058
Seq. ID	zhf700959284.h1
Method	BLASTX
NCBI GI	g4176545
BLAST score	176
E value	4.0e-13
Match length	81
% identity	43
NCBI Description	(AL035259) strong similarity to human leukotriene a-4 hydrolase [Schizosaccharomyces pombe]

Seq. No.	54059
Seq. ID	zhf700959328.h1
Method	BLASTX
NCBI GI	g3668118
BLAST score	378
E value	8.0e-37
Match length	82
% identity	58
NCBI Description	(AJ224078) hypothetical protein [Brassica napus]

Seq. No.	54060
Seq. ID	zhf700959422.h1
Method	BLASTX
NCBI GI	g3702323
BLAST score	180
E value	2.0e-28
Match length	85
% identity	75
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	54061
Seq. ID	zhf700959432.h1
Method	BLASTX
NCBI GI	g2244996
BLAST score	165
E value	3.0e-20
Match length	84
% identity	64
NCBI Description	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]

Seq. No.	54062
Seq. ID	zhf700959441.h1
Method	BLASTX
NCBI GI	g3924596
BLAST score	198
E value	2.0e-33
Match length	85
% identity	85
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	54063

Seq. ID	zhf700959522.h1
Method	BLASTX
NCBI GI	g3242785
BLAST score	232
E value	7.0e-20
Match length	63
% identity	70
NCBI Description	(AF055355) respiratory burst oxidase protein C [Arabidopsis thaliana]

Seq. No.	54064
Seq. ID	zhf700959527.h1
Method	BLASTX
NCBI GI	g3894194
BLAST score	266
E value	1.0e-23
Match length	81
% identity	62
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	54065
Seq. ID	zhf700959576.h1
Method	BLASTX
NCBI GI	g2352492
BLAST score	252
E value	4.0e-22
Match length	79
% identity	59
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	54066
Seq. ID	zhf700959579.h1
Method	BLASTX
NCBI GI	g4558683
BLAST score	150
E value	4.0e-10
Match length	46
% identity	48
NCBI Description	(AC006586) putative retrotransposon Tto1 ORF1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	54067
Seq. ID	zhf700959596.h1
Method	BLASTX
NCBI GI	g4455329
BLAST score	137
E value	1.0e-08
Match length	36
% identity	72
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	54068
Seq. ID	zhf700959624.h1

Method	BLASTX
NCBI GI	g2947066
BLAST score	260
E value	4.0e-23
Match length	76
% identity	25
NCBI Description	(AC002521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54069
Seq. ID	zhf700959654.h1
Method	BLASTX
NCBI GI	g4322327
BLAST score	149
E value	4.0e-10
Match length	73
% identity	47
NCBI Description	(AF080545) peptide transporter [Nepenthes alata]

Seq. No.	54070
Seq. ID	zhf700959666.h1
Method	BLASTN
NCBI GI	g169956
BLAST score	99
E value	1.0e-48
Match length	211
% identity	91
NCBI Description	Glycine max G-box binding factor (GBF1) mRNA, complete cds

Seq. No.	54071
Seq. ID	zhf700959668.h1
Method	BLASTX
NCBI GI	g1491931
BLAST score	214
E value	8.0e-18
Match length	72
% identity	90
NCBI Description	(U52078) kinesin-like protein [Nicotiana tabacum]

Seq. No.	54072
Seq. ID	zhf700959705.h1
Method	BLASTX
NCBI GI	g2827621
BLAST score	186
E value	3.0e-14
Match length	86
% identity	47
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	54073
Seq. ID	zhf700959714.h1
Method	BLASTX
NCBI GI	g3063471
BLAST score	232
E value	1.0e-19
Match length	74
% identity	62
NCBI Description	(AC003981) F22O13.33 [Arabidopsis thaliana]

Seq. No.	54074
Seq. ID	zhf700959733.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	94
E value	2.0e-45
Match length	222
% identity	86
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	54075
Seq. ID	zhf700959757.h1
Method	BLASTN
NCBI GI	g2934883
BLAST score	136
E value	1.0e-70
Match length	217
% identity	100
NCBI Description	Glycine max TGACG-motif binding protein (STF1) mRNA, complete cds

Seq. No.	54076
Seq. ID	zhf700959795.h1
Method	BLASTX
NCBI GI	g3522939
BLAST score	342
E value	1.0e-32
Match length	73
% identity	81
NCBI Description	(AC004411) putative squamosa-promoter binding protein [Arabidopsis thaliana]

Seq. No.	54077
Seq. ID	zhf700959810.h1
Method	BLASTX
NCBI GI	g4455283
BLAST score	286
E value	5.0e-26
Match length	82
% identity	63
NCBI Description	(AL035527) L1 specific homeobox gene ATML1/ovule-specific homeobox protein A20 [Arabidopsis thaliana]

Seq. No.	54078
Seq. ID	zhf700959811.h1
Method	BLASTX
NCBI GI	g2129953
BLAST score	296
E value	3.0e-27
Match length	81
% identity	69
NCBI Description	laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542) diphenol oxidase [Nicotiana tabacum]

Seq. No.	54079

Seq. ID	zhf700959817.h1
Method	BLASTX
NCBI GI	g4538624
BLAST score	225
E value	7.0e-19
Match length	82
% identity	52
NCBI Description	(AJ133502) hypothetical protein [Nicotiana tabacum]

Seq. No.	54080
Seq. ID	zhf700959832.h1
Method	BLASTX
NCBI GI	g4115536
BLAST score	141
E value	5.0e-09
Match length	39
% identity	67
NCBI Description	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No.	54081
Seq. ID	zhf700959836.h1
Method	BLASTX
NCBI GI	g3335359
BLAST score	215
E value	1.0e-17
Match length	58
% identity	71
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	54082
Seq. ID	zhf700959857.h1
Method	BLASTX
NCBI GI	g3236261
BLAST score	337
E value	5.0e-32
Match length	80
% identity	74
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	54083
Seq. ID	zhf700959858.h1
Method	BLASTX
NCBI GI	g3093294
BLAST score	389
E value	4.0e-38
Match length	80
% identity	91
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	54084
Seq. ID	zhf700959859.h1
Method	BLASTX
NCBI GI	g3885339
BLAST score	303
E value	5.0e-28

Match length	78
% identity	76
NCBI Description	(AC005623) putative bzip protein [Arabidopsis thaliana]

Seq. No.	54085
Seq. ID	zhf700959908.h1
Method	BLASTX
NCBI GI	g2190548
BLAST score	317
E value	1.0e-29
Match length	83
% identity	69
NCBI Description	(AC001229) EST gb_ATTS1121 comes from this gene. [Arabidopsis thaliana]

Seq. No.	54086
Seq. ID	zhf700959918.h1
Method	BLASTX
NCBI GI	g1431629
BLAST score	183
E value	6.0e-14
Match length	84
% identity	44
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	54087
Seq. ID	zhf700959937.h1
Method	BLASTX
NCBI GI	g4455183
BLAST score	251
E value	6.0e-22
Match length	77
% identity	65
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	54088
Seq. ID	zhf700959956.h1
Method	BLASTX
NCBI GI	g3047123
BLAST score	317
E value	1.0e-29
Match length	81
% identity	67
NCBI Description	(AF058919) similar to the family of glycosyl hydrolases [Arabidopsis thaliana]

Seq. No.	54089
Seq. ID	zhf700960012.h1
Method	BLASTX
NCBI GI	g2760326
BLAST score	234
E value	6.0e-20
Match length	82
% identity	54
NCBI Description	(AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No.	54090

Seq. ID	zhf700960110.h1
Method	BLASTN
NCBI GI	g4159708
BLAST score	35
E value	2.0e-10
Match length	51
% identity	56
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence [Arabidopsis thaliana]

Seq. No.	54091
Seq. ID	zhf700960252.h1
Method	BLASTX
NCBI GI	g2262105
BLAST score	214
E value	2.0e-17
Match length	89
% identity	46
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	54092
Seq. ID	zhf700960266.h1
Method	BLASTX
NCBI GI	g4249385
BLAST score	383
E value	2.0e-37
Match length	72
% identity	92
NCBI Description	(AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No.	54093
Seq. ID	zhf700960270.h1
Method	BLASTX
NCBI GI	g4558664
BLAST score	208
E value	8.0e-17
Match length	88
% identity	11
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54094
Seq. ID	zhf700960318.h1
Method	BLASTX
NCBI GI	g3015488
BLAST score	145
E value	1.0e-17
Match length	86
% identity	48
NCBI Description	(U58474) receptor-like protein kinase [Lycopersicon esculentum]

Seq. No.	54095
Seq. ID	zhf700960328.h1
Method	BLASTX
NCBI GI	g960291
BLAST score	212
E value	2.0e-17

Match length	53
% identity	79
NCBI Description	(L34344) anthranilate synthase alpha subunit [Ruta graveolens]

Seq. No.	54096
Seq. ID	zhf700960331.h1
Method	BLASTX
NCBI GI	g4204263
BLAST score	234
E value	6.0e-20
Match length	71
% identity	51
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	54097
Seq. ID	zhf700960352.h1
Method	BLASTX
NCBI GI	g4220534
BLAST score	182
E value	1.0e-18
Match length	67
% identity	70
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	54098
Seq. ID	zhf700960353.h1
Method	BLASTX
NCBI GI	g2842485
BLAST score	162
E value	2.0e-11
Match length	36
% identity	81
NCBI Description	(AL021749) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54099
Seq. ID	zhf700960431.h1
Method	BLASTN
NCBI GI	g473604
BLAST score	55
E value	3.0e-22
Match length	124
% identity	78
NCBI Description	Zea mays W-22 histone H2B mRNA, complete cds

Seq. No.	54100
Seq. ID	zhf700960465.h1
Method	BLASTX
NCBI GI	g3096919
BLAST score	364
E value	8.0e-39
Match length	87
% identity	88
NCBI Description	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	54101

Seq. ID	zhf700960469.h1
Method	BLASTX
NCBI GI	g1931642
BLAST score	187
E value	2.0e-14
Match length	49
% identity	82
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	54102
Seq. ID	zhf700960478.h1
Method	BLASTX
NCBI GI	g2723486
BLAST score	160
E value	3.0e-11
Match length	80
% identity	40
NCBI Description	(AB003505) BAF60b [Rattus norvegicus]

Seq. No.	54103
Seq. ID	zhf700960507.h1
Method	BLASTX
NCBI GI	g2369714
BLAST score	161
E value	1.0e-11
Match length	52
% identity	54
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	54104
Seq. ID	zhf700960508.h1
Method	BLASTN
NCBI GI	g2687725
BLAST score	59
E value	7.0e-25
Match length	126
% identity	87
NCBI Description	Glycine max mRNA for putative 2-hydroxydihydrodaidzein reductase

Seq. No.	54105
Seq. ID	zhf700960541.h1
Method	BLASTN
NCBI GI	g457569
BLAST score	45
E value	2.0e-16
Match length	97
% identity	87
NCBI Description	Soybean mRNA for endo-xyloglucan transferase, partial cds

Seq. No.	54106
Seq. ID	zhf700960549.h1
Method	BLASTN
NCBI GI	g456713
BLAST score	56
E value	2.0e-23

Match length	103
% identity	27
NCBI Description	Glycine max gene for ubiquitin, complete cds

Seq. No.	54107
Seq. ID	zhf700960601.h1
Method	BLASTN
NCBI GI	g169036
BLAST score	49
E value	1.0e-18
Match length	69
% identity	93
NCBI Description	Pisum sativum L. aldolase gene, 3' end cds

Seq. No.	54108
Seq. ID	zhf700960743.h1
Method	BLASTX
NCBI GI	g1174718
BLAST score	190
E value	5.0e-15
Match length	68
% identity	53
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	54109
Seq. ID	zhf700960745.h1
Method	BLASTN
NCBI GI	g20728
BLAST score	65
E value	2.0e-28
Match length	125
% identity	88
NCBI Description	Pea chloroplast GAPA mRNA encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13)

Seq. No.	54110
Seq. ID	zhf700960749.h1
Method	BLASTX
NCBI GI	g4539351
BLAST score	149
E value	4.0e-10
Match length	57
% identity	53
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	54111
Seq. ID	zhf700960793.h1
Method	BLASTX
NCBI GI	g4455202
BLAST score	191
E value	4.0e-15
Match length	62
% identity	63

NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]
Seq. No.	54112
Seq. ID	zhf700960807.h1
Method	BLASTX
NCBI GI	g2702277
BLAST score	163
E value	8.0e-12
Match length	55
% identity	60
NCBI Description	(AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] >gi_2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]
Seq. No.	54113
Seq. ID	zhf700960825.h1
Method	BLASTX
NCBI GI	g4559391
BLAST score	311
E value	6.0e-29
Match length	85
% identity	71
NCBI Description	(AC006526) putative auxin response factor 1 [Arabidopsis thaliana]
Seq. No.	54114
Seq. ID	zhf700960879.h1
Method	BLASTX
NCBI GI	g4510395
BLAST score	259
E value	7.0e-23
Match length	74
% identity	65
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]
Seq. No.	54115
Seq. ID	zhf700960889.h1
Method	BLASTX
NCBI GI	g4220479
BLAST score	122
E value	2.0e-12
Match length	55
% identity	76
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.	54116
Seq. ID	zhf700960895.h1
Method	BLASTN
NCBI GI	g1778371
BLAST score	36
E value	3.0e-11
Match length	44
% identity	95
NCBI Description	Glycine max asparagine synthetase 1 (AS1) mRNA, complete cds

Seq. No.	54117
Seq. ID	zhf700960910.h1
Method	BLASTX
NCBI GI	g2995340
BLAST score	119
E value	2.0e-15
Match length	84
% identity	49
NCBI Description	(AL022244) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	54118
Seq. ID	zhf700960916.h1
Method	BLASTN
NCBI GI	g1196896
BLAST score	151
E value	1.0e-79
Match length	226
% identity	94
NCBI Description	Glycine max acidic ribosomal protein P0 mRNA, complete cds

Seq. No.	54119
Seq. ID	zhf700960923.h1
Method	BLASTX
NCBI GI	g3249095
BLAST score	210
E value	4.0e-17
Match length	85
% identity	52
NCBI Description	(AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb_L13703 from Schizosaccharomyces pombe. ESTs gb_N37567 and gb_T43002 come from this gene. [Arabidopsis thaliana]

Seq. No.	54120
Seq. ID	zhf700960926.h1
Method	BLASTX
NCBI GI	g2244881
BLAST score	193
E value	2.0e-24
Match length	81
% identity	58
NCBI Description	(Z97338) PDR5-like ABC transporter [Arabidopsis thaliana]

Seq. No.	54121
Seq. ID	zhf700960959.h1
Method	BLASTN
NCBI GI	g170073
BLAST score	245
E value	1.0e-135
Match length	249
% identity	100
NCBI Description	Soybean calmodulin (SCaM-3) mRNA, complete cds

Seq. No.	54122
Seq. ID	zhf700960971.h1
Method	BLASTX
NCBI GI	g1944518

BLAST score	184
E value	3.0e-29
Match length	82
% identity	77
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	54123
Seq. ID	zhf700961030.h1
Method	BLASTN
NCBI GI	g2924653
BLAST score	45
E value	2.0e-16
Match length	105
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	54124
Seq. ID	zhf700961042.h1
Method	BLASTX
NCBI GI	g2244876
BLAST score	410
E value	2.0e-40
Match length	86
% identity	86
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54125
Seq. ID	zhf700961050.h1
Method	BLASTN
NCBI GI	g2605886
BLAST score	34
E value	6.0e-10
Match length	66
% identity	88
NCBI Description	Pisum sativum dormancy-associated protein (DRM1) mRNA, complete cds

Seq. No.	54126
Seq. ID	zhf700961080.h1
Method	BLASTX
NCBI GI	g2351580
BLAST score	282
E value	1.0e-25
Match length	62
% identity	89
NCBI Description	(U82433) thymidine diphospho-glucose 4-6-dehydratase homolog [Prunus armeniaca]

Seq. No.	54127
Seq. ID	zhf700961178.h1
Method	BLASTN
NCBI GI	g609224
BLAST score	60
E value	2.0e-25

Match length	136
% identity	86
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	54128
Seq. ID	zhf700961192.h1
Method	BLASTX
NCBI GI	g3047125
BLAST score	292
E value	7.0e-27
Match length	64
% identity	86
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	54129
Seq. ID	zhf700961217.h1
Method	BLASTX
NCBI GI	g2459421
BLAST score	142
E value	4.0e-09
Match length	33
% identity	67
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	54130
Seq. ID	zhf700961253.h1
Method	BLASTX
NCBI GI	g4510381
BLAST score	146
E value	1.0e-09
Match length	84
% identity	49
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	54131
Seq. ID	zhf700961302.h1
Method	BLASTX
NCBI GI	g2829910
BLAST score	194
E value	3.0e-15
Match length	74
% identity	49
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	54132
Seq. ID	zhf700961314.h1
Method	BLASTN
NCBI GI	g169159
BLAST score	33
E value	3.0e-09
Match length	49
% identity	92
NCBI Description	Pea chloroplastic copper/zinc-superoxide dismutase mRNA,

complete cds

Seq. No.	54133
Seq. ID	zhf700961317.h1
Method	BLASTX
NCBI GI	g584741
BLAST score	156
E value	8.0e-11
Match length	63
% identity	54
NCBI Description	ANKYRIN REPEAT PROTEIN (AKRP) >gi_322461_pir__JQ1729 ankyrin-repeat protein - Arabidopsis thaliana >gi_166744 (M82883) ankyrin repeat-containing protein [Arabidopsis thaliana]

Seq. No.	54134
Seq. ID	zhf700961357.h1
Method	BLASTX
NCBI GI	g2921158
BLAST score	125
E value	5.0e-09
Match length	56
% identity	70
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	54135
Seq. ID	zhf700961370.h1
Method	BLASTX
NCBI GI	g4467148
BLAST score	174
E value	5.0e-13
Match length	75
% identity	53
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	54136
Seq. ID	zhf700961384.h1
Method	BLASTX
NCBI GI	g3935148
BLAST score	350
E value	1.0e-33
Match length	75
% identity	81
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	54137
Seq. ID	zhf700961432.h1
Method	BLASTX
NCBI GI	g3892711
BLAST score	165
E value	8.0e-12
Match length	83
% identity	43
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	54138
Seq. ID	zhf700961437.h1

Method	BLASTX
NCBI GI	g4115914
BLAST score	338
E value	4.0e-32
Match length	84
% identity	70
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1_ (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis thaliana]

Seq. No.	54139
Seq. ID	zhf700961445.h1
Method	BLASTX
NCBI GI	g2905893
BLAST score	253
E value	3.0e-22
Match length	79
% identity	61
NCBI Description	(U66424) fimbrin-like protein [Arabidopsis thaliana]

Seq. No.	54140
Seq. ID	zhf700961469.h1
Method	BLASTX
NCBI GI	g1903347
BLAST score	314
E value	2.0e-29
Match length	81
% identity	72
NCBI Description	(AC000104) EST gb_ATTS5672 comes from this gene. [Arabidopsis thaliana]

Seq. No.	54141
Seq. ID	zhf700961475.h1
Method	BLASTX
NCBI GI	g3063446
BLAST score	337
E value	5.0e-32
Match length	81
% identity	77
NCBI Description	(AC003981) F22O13.8 [Arabidopsis thaliana]

Seq. No.	54142
Seq. ID	zhf700961523.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	183
E value	5.0e-14
Match length	54
% identity	69
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	54143
Seq. ID	zhf700961544.h1
Method	BLASTX
NCBI GI	g2459435

BLAST score	217
E value	5.0e-18
Match length	73
% identity	52
NCBI Description	(AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	54144
Seq. ID	zhf700961560.h1
Method	BLASTX
NCBI GI	g2827709
BLAST score	171
E value	1.0e-12
Match length	66
% identity	48
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	54145
Seq. ID	zhf700961621.h1
Method	BLASTX
NCBI GI	g2739004
BLAST score	217
E value	7.0e-18
Match length	89
% identity	55
NCBI Description	(AF022461) CYP82C1p [Glycine max]

Seq. No.	54146
Seq. ID	zhf700961656.h1
Method	BLASTX
NCBI GI	g2342735
BLAST score	158
E value	6.0e-11
Match length	42
% identity	74
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	54147
Seq. ID	zhf700961668.h1
Method	BLASTX
NCBI GI	g3452263
BLAST score	299
E value	4.0e-33
Match length	85
% identity	88
NCBI Description	(AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No.	54148
Seq. ID	zhf700961705.h1
Method	BLASTX
NCBI GI	g1706822
BLAST score	173
E value	9.0e-13
Match length	64
% identity	53
NCBI Description	FLAVONOL SYNTHASE (FLS) >gi_421946_pir__S33510 flavonol

synthase - garden petunia >gi_311658_emb_CAA80264_ (Z22543) flavonol synthase [Petunia x hybrida]

Seq. No.	54149
Seq. ID	zhf700961727.h1
Method	BLASTX
NCBI GI	g3135253
BLAST score	154
E value	2.0e-10
Match length	83
% identity	41
NCBI Description	(AC003058) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	54150
Seq. ID	zhf700961731.h1
Method	BLASTX
NCBI GI	g4389222
BLAST score	261
E value	4.0e-23
Match length	74
% identity	64
NCBI Description	Chain A, Crystal Structure Of Gdp-4-Keto-6-Deoxy-D-Mannose EpimeraseREDUCTASE FROM ESCHERICHIA COLI A KEY ENZYME IN The Biosynthesis Of Gdp-L-Fucose

Seq. No.	54151
Seq. ID	zhf700961748.h1
Method	BLASTX
NCBI GI	g4406780
BLAST score	252
E value	6.0e-22
Match length	55
% identity	82
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	54152
Seq. ID	zhf700961753.h1
Method	BLASTN
NCBI GI	g257814
BLAST score	105
E value	4.0e-52
Match length	181
% identity	97
NCBI Description	phenylalanine ammonia-lyase [soybeans, mRNA, 1427 nt]

Seq. No.	54153
Seq. ID	zhf700961754.h1
Method	BLASTX
NCBI GI	g3182981
BLAST score	220
E value	3.0e-18
Match length	72
% identity	58
NCBI Description	CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_ (D86494) diminuto [Pisum sativum]

Seq. No.	54154
Seq. ID	zhf700961765.h1
Method	BLASTX
NCBI GI	g1931641
BLAST score	261
E value	4.0e-23
Match length	77
% identity	62
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	54155
Seq. ID	zhf700961836.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	215
E value	1.0e-118
Match length	231
% identity	98
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	54156
Seq. ID	zhf700961896.h1
Method	BLASTX
NCBI GI	g3513727
BLAST score	180
E value	1.0e-13
Match length	64
% identity	67
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	54157
Seq. ID	zhf700961903.h1
Method	BLASTX
NCBI GI	g3335351
BLAST score	275
E value	1.0e-24
Match length	85
% identity	8
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	54158
Seq. ID	zhf700961910.h1
Method	BLASTX
NCBI GI	g2828294
BLAST score	372
E value	4.0e-36
Match length	82
% identity	79
NCBI Description	(AL021687) putatative protein [Arabidopsis thaliana]

Seq. No.	54159
Seq. ID	zhf700961915.h1
Method	BLASTX
NCBI GI	g4056489
BLAST score	168
E value	3.0e-12
Match length	84
% identity	43
NCBI Description	(AC005896) putative white protein [Arabidopsis thaliana]

Seq. No.	54160
Seq. ID	zhf700961924.h1
Method	BLASTX
NCBI GI	g127045
BLAST score	122
E value	7.0e-18
Match length	83
% identity	71
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	54161
Seq. ID	zhf700961949.h1
Method	BLASTX
NCBI GI	g4008006
BLAST score	341
E value	2.0e-32
Match length	82
% identity	82
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	54162
Seq. ID	zhf700961987.h1
Method	BLASTN
NCBI GI	g169980
BLAST score	32
E value	1.0e-08
Match length	76
% identity	87
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	54163
Seq. ID	zhf700962035.h1
Method	BLASTX
NCBI GI	g3850999
BLAST score	172
E value	1.0e-12
Match length	46
% identity	78
NCBI Description	(AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]

Seq. No.	54164
Seq. ID	zhf700962052.h1
Method	BLASTX
NCBI GI	g4454018
BLAST score	183
E value	5.0e-14
Match length	75
% identity	52
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	54165
Seq. ID	zhf700962185.h1
Method	BLASTX
NCBI GI	g4454031
BLAST score	140
E value	4.0e-09
Match length	65
% identity	55
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	54166
Seq. ID	zhf700962203.h1
Method	BLASTX
NCBI GI	g1771162
BLAST score	406
E value	6.0e-40
Match length	96
% identity	76
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	54167
Seq. ID	zhf700962218.h1
Method	BLASTX
NCBI GI	g2980806
BLAST score	153
E value	6.0e-13
Match length	72
% identity	58
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	54168
Seq. ID	zhf700962221.h1
Method	BLASTX
NCBI GI	g2323410
BLAST score	138
E value	1.0e-08
Match length	81
% identity	40
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]

Seq. No.	54169
Seq. ID	zhf700962257.h1
Method	BLASTX
NCBI GI	g3335378

BLAST score	151
E value	4.0e-10
Match length	38
% identity	68
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	54170
Seq. ID	zhf700962265.h1
Method	BLASTX
NCBI GI	g1899175
BLAST score	177
E value	4.0e-13
Match length	87
% identity	43
NCBI Description	(U90262) calcium-dependent calmodulin-independent protein kinase CDPK [Cucurbita pepo]

Seq. No.	54171
Seq. ID	zhf700962277.h1
Method	BLASTX
NCBI GI	g3047106
BLAST score	200
E value	7.0e-16
Match length	90
% identity	49
NCBI Description	(AF058919) Arabidopsis thaliana homeodomain protein AHDP (SP:P93041) [Arabidopsis thaliana]

Seq. No.	54172
Seq. ID	zhf700962283.h1
Method	BLASTX
NCBI GI	g2583123
BLAST score	343
E value	1.0e-32
Match length	88
% identity	76
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	54173
Seq. ID	zhf700962293.h1
Method	BLASTX
NCBI GI	g4335752
BLAST score	222
E value	2.0e-18
Match length	88
% identity	49
NCBI Description	(AC006284) putative myb transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	54174
Seq. ID	zhf700962304.h1
Method	BLASTX
NCBI GI	g3763927
BLAST score	290
E value	2.0e-26

Match length	88
% identity	69
NCBI Description	(AC004450) putative carboxyphosphoenolpyruvate mutase [Arabidopsis thaliana]

Seq. No.	54175
Seq. ID	zhf700962322.h1
Method	BLASTX
NCBI GI	g4455338
BLAST score	362
E value	7.0e-35
Match length	85
% identity	74
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	54176
Seq. ID	zhf700962328.h1
Method	BLASTX
NCBI GI	g3183088
BLAST score	140
E value	7.0e-09
Match length	60
% identity	52
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	54177
Seq. ID	zhf700962337.h1
Method	BLASTN
NCBI GI	g2351062
BLAST score	34
E value	9.0e-10
Match length	74
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	54178
Seq. ID	zhf700962360.h1
Method	BLASTX
NCBI GI	g2367431
BLAST score	204
E value	2.0e-16
Match length	78
% identity	55
NCBI Description	(AF000403) putative cytochrome P450 [Lotus japonicus]

Seq. No.	54179
Seq. ID	zhf700962448.h1
Method	BLASTX
NCBI GI	g1001257
BLAST score	181
E value	1.0e-17
Match length	64
% identity	63

NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]
Seq. No.	54180
Seq. ID	zhf700962451.h1
Method	BLASTN
NCBI GI	g3128166
BLAST score	37
E value	5.0e-12
Match length	53
% identity	49
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	54181
Seq. ID	zhf700962461.h1
Method	BLASTX
NCBI GI	g4140026
BLAST score	137
E value	1.0e-15
Match length	66
% identity	61
NCBI Description	(AB009370) flavonoid 3-O-galactosyl transferase [Vigna mungo]
Seq. No.	54182
Seq. ID	zhf700962506.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	252
E value	1.0e-140
Match length	252
% identity	100
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds
Seq. No.	54183
Seq. ID	zhf700962560.h1
Method	BLASTX
NCBI GI	g2388586
BLAST score	292
E value	9.0e-27
Match length	79
% identity	71
NCBI Description	(AC000098) Similar to Saccharomyces RAD16 (gb_X78993). [Arabidopsis thaliana]
Seq. No.	54184
Seq. ID	zhf700962731.h1
Method	BLASTN
NCBI GI	g170293
BLAST score	102
E value	2.0e-50
Match length	254
% identity	85
NCBI Description	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) mRNA, complete cds
Seq. No.	54185

Seq. ID	zhf700962842.h1
Method	BLASTX
NCBI GI	g3600032
BLAST score	165
E value	6.0e-12
Match length	74
% identity	47
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	54186
Seq. ID	zhf700962892.h1
Method	BLASTX
NCBI GI	g3859659
BLAST score	307
E value	2.0e-28
Match length	79
% identity	70
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	54187
Seq. ID	zhf700962903.h1
Method	BLASTX
NCBI GI	g2462746
BLAST score	285
E value	6.0e-26
Match length	57
% identity	96
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	54188
Seq. ID	zhf700962932.h1
Method	BLASTX
NCBI GI	g285741
BLAST score	144
E value	2.0e-09
Match length	49
% identity	67
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	54189
Seq. ID	zhf700962938.h1
Method	BLASTX
NCBI GI	g2598589
BLAST score	172
E value	1.0e-12
Match length	64
% identity	53
NCBI Description	(Y15367) MtN19 [Medicago truncatula]

Seq. No.	54190
Seq. ID	zhf700962942.h1
Method	BLASTX
NCBI GI	g2344889

BLAST score 146
E value 3.0e-10
Match length 65
% identity 57
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 54191
Seq. ID zhf700962980.h1
Method BLASTX
NCBI GI g629561
BLAST score 162
E value 1.0e-11
Match length 74
% identity 53
NCBI Description SRG1 protein - Arabidopsis thaliana
>gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No. 54192
Seq. ID zhf700963012.h1
Method BLASTX
NCBI GI g3068704
BLAST score 126
E value 1.0e-10
Match length 59
% identity 63
NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 54193
Seq. ID zhf700963039.h1
Method BLASTX
NCBI GI g1518540
BLAST score 263
E value 3.0e-23
Match length 60
% identity 75
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 54194
Seq. ID zhf700963086.h1
Method BLASTX
NCBI GI g3142303
BLAST score 342
E value 2.0e-32
Match length 89
% identity 38
NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No. 54195
Seq. ID zhf700963090.h1
Method BLASTX
NCBI GI g2642153
BLAST score 147
E value 1.0e-09

Match length	35
% identity	77
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	54196
Seq. ID	zhf700963107.h1
Method	BLASTX
NCBI GI	g2501494
BLAST score	184
E value	4.0e-14
Match length	74
% identity	51
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 5) >gi_542015_pir__S41951 UTP-glucose glucosyltransferase - cassava >gi_453249_emb_CAA54612_ (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No.	54197
Seq. ID	zhf700963112.h1
Method	BLASTX
NCBI GI	g2330651
BLAST score	146
E value	8.0e-10
Match length	68
% identity	49
NCBI Description	(Y14559) topoisomerase II [Pisum sativum]

Seq. No.	54198
Seq. ID	zhf700963126.h1
Method	BLASTN
NCBI GI	g1808591
BLAST score	90
E value	3.0e-43
Match length	138
% identity	91
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	54199
Seq. ID	zhf700963128.h1
Method	BLASTX
NCBI GI	g2462746
BLAST score	172
E value	1.0e-12
Match length	46
% identity	74
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	54200
Seq. ID	zhf700963135.h1
Method	BLASTX
NCBI GI	g1495802
BLAST score	154
E value	1.0e-10

Match length	82
% identity	43
NCBI Description	(X96405) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	54201
Seq. ID	zhf700963160.h1
Method	BLASTX
NCBI GI	g4580394
BLAST score	247
E value	2.0e-21
Match length	74
% identity	68
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	54202
Seq. ID	zhf700963162.h1
Method	BLASTX
NCBI GI	g3367519
BLAST score	125
E value	4.0e-10
Match length	69
% identity	54
NCBI Description	(AC004392) Contains similarity to gb_U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	54203
Seq. ID	zhf700963203.h1
Method	BLASTX
NCBI GI	g3269291
BLAST score	157
E value	7.0e-11
Match length	74
% identity	47
NCBI Description	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	54204
Seq. ID	zhf700963211.h1
Method	BLASTX
NCBI GI	g1346769
BLAST score	183
E value	5.0e-14
Match length	68
% identity	49
NCBI Description	PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens] >gi_4506043_ref_NP_002717.1_pPREP_ prolyl endopeptidase

Seq. No.	54205
Seq. ID	zhf700963244.h1
Method	BLASTX
NCBI GI	g3287693
BLAST score	374

E value	2.0e-36
Match length	82
% identity	84
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	54206
Seq. ID	zhf700963249.h1
Method	BLASTX
NCBI GI	g2262104
BLAST score	143
E value	3.0e-09
Match length	42
% identity	62
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	54207
Seq. ID	zhf700963302.h1
Method	BLASTX
NCBI GI	g1935021
BLAST score	170
E value	1.0e-12
Match length	56
% identity	59
NCBI Description	(Z93775) monosaccharid transport protein [Vicia faba]

Seq. No.	54208
Seq. ID	zhf700963303.h1
Method	BLASTX
NCBI GI	g2088647
BLAST score	170
E value	5.0e-15
Match length	76
% identity	49
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	54209
Seq. ID	zhf700963345.h1
Method	BLASTX
NCBI GI	g4432823
BLAST score	174
E value	7.0e-13
Match length	53
% identity	64
NCBI Description	(AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54210
Seq. ID	zhf700963363.h1
Method	BLASTX
NCBI GI	g2829898
BLAST score	187
E value	1.0e-14
Match length	50
% identity	66

NCBI Description	(AC002311) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	54211
Seq. ID	zhf700963383.h1
Method	BLASTN
NCBI GI	g3449327
BLAST score	53
E value	4.0e-21
Match length	189
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	54212
Seq. ID	zhf700963512.h1
Method	BLASTX
NCBI GI	g1770190
BLAST score	211
E value	4.0e-17
Match length	60
% identity	67
NCBI Description	(Y10162) cyclin-D like protein [Chenopodium rubrum]

Seq. No.	54213
Seq. ID	zhf700963537.h1
Method	BLASTX
NCBI GI	g3249105
BLAST score	138
E value	1.0e-08
Match length	90
% identity	38
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	54214
Seq. ID	zhf700963561.h1
Method	BLASTX
NCBI GI	g3850588
BLAST score	214
E value	3.0e-25
Match length	86
% identity	63
NCBI Description	(AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana]

Seq. No.	54215
Seq. ID	zhf700963604.h1
Method	BLASTX
NCBI GI	g3550985
BLAST score	158
E value	6.0e-11
Match length	40
% identity	78
NCBI Description	(AB010740) OsS5a [Oryza sativa]

Seq. No.	54216
Seq. ID	zhf700963626.h1
Method	BLASTX
NCBI GI	g2708745
BLAST score	222
E value	1.0e-31
Match length	77
% identity	95
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	54217
Seq. ID	zhf700963638.h1
Method	BLASTX
NCBI GI	g1771162
BLAST score	165
E value	2.0e-16
Match length	92
% identity	46
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	54218
Seq. ID	zhf700963660.h1
Method	BLASTX
NCBI GI	g3805845
BLAST score	219
E value	8.0e-21
Match length	67
% identity	84
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	54219
Seq. ID	zhf700963721.h1
Method	BLASTX
NCBI GI	g3913366
BLAST score	388
E value	5.0e-38
Match length	83
% identity	86
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi_1597723 (U67422) CRINKLY4 precursor [Zea mays]

Seq. No.	54220
Seq. ID	zhf700963736.h1
Method	BLASTX
NCBI GI	g2245092
BLAST score	211
E value	3.0e-17
Match length	82
% identity	54
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	54221
Seq. ID	zhf700963738.h1
Method	BLASTX

NCBI GI g2853087
BLAST score 429
E value 9.0e-43
Match length 86
% identity 94
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 54222
Seq. ID zhf700963753.h1
Method BLASTX
NCBI GI g3757521
BLAST score 192
E value 5.0e-15
Match length 83
% identity 45
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 54223
Seq. ID zhf700963817.h1
Method BLASTX
NCBI GI g3355474
BLAST score 279
E value 3.0e-25
Match length 85
% identity 64
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 54224
Seq. ID zhf700963825.h1
Method BLASTX
NCBI GI g1944132
BLAST score 319
E value 6.0e-30
Match length 76
% identity 78
NCBI Description (AB002560) CUC2 [Arabidopsis thaliana]

Seq. No. 54225
Seq. ID zhf700963843.h1
Method BLASTX
NCBI GI g2760326
BLAST score 185
E value 3.0e-14
Match length 70
% identity 49
NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana]

Seq. No. 54226
Seq. ID zhf700963849.h1
Method BLASTX
NCBI GI g3046696
BLAST score 176
E value 4.0e-13
Match length 37
% identity 89
NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	54227
Seq. ID	zhf700963889.h1
Method	BLASTN
NCBI GI	g516853
BLAST score	185
E value	1.0e-100
Match length	241
% identity	28
NCBI Description	Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No.	54228
Seq. ID	zhf700963927.h1
Method	BLASTN
NCBI GI	g310560
BLAST score	245
E value	1.0e-135
Match length	249
% identity	100
NCBI Description	Soybean ascorbate peroxidase mRNA, complete cds

Seq. No.	54229
Seq. ID	zhf700963935.h1
Method	BLASTN
NCBI GI	g18551
BLAST score	163
E value	7.0e-87
Match length	187
% identity	97
NCBI Description	Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding protein

Seq. No.	54230
Seq. ID	zhf700963954.h1
Method	BLASTX
NCBI GI	g120676
BLAST score	162
E value	2.0e-11
Match length	49
% identity	65
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82165_pir__C24430 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) C, cytosolic - common tobacco (fragment) >gi_170241 (M14419) glyceraldehyde-3-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No.	54231
Seq. ID	zhf700963981.h1
Method	BLASTX
NCBI GI	g231573
BLAST score	168
E value	3.0e-12
Match length	59
% identity	58
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_99970_pir__S24757 asparaginase (EC 3.5.1.1) - narrow-leaved blue lupine >gi_19135_emb_CAA43099_ (X60691)

developing seed L-asparaginase [Lupinus angustifolius]

Seq. No.	54232
Seq. ID	zhf700963986.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	90
E value	3.0e-43
Match length	166
% identity	89
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	54233
Seq. ID	zhf700964002.h1
Method	BLASTX
NCBI GI	g2129559
BLAST score	170
E value	1.0e-15
Match length	54
% identity	83
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	54234
Seq. ID	zhf700964018.h1
Method	BLASTX
NCBI GI	g3367585
BLAST score	140
E value	7.0e-09
Match length	49
% identity	53
NCBI Description	(AL031135) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	54235
Seq. ID	zhf700964043.h1
Method	BLASTX
NCBI GI	g3355471
BLAST score	186
E value	3.0e-14
Match length	44
% identity	66
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	54236
Seq. ID	zhf700964080.h1
Method	BLASTX
NCBI GI	g3924603
BLAST score	268
E value	7.0e-24
Match length	67

% identity	69
NCBI Description	(AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	54237
Seq. ID	zhf700964115.h1
Method	BLASTX
NCBI GI	g4432827
BLAST score	230
E value	2.0e-19
Match length	62
% identity	37
NCBI Description	(AC006593) putative ADP-ribose polymerase [Arabidopsis thaliana]

Seq. No.	54238
Seq. ID	zhf700964116.h1
Method	BLASTX
NCBI GI	g3924605
BLAST score	149
E value	6.0e-10
Match length	38
% identity	66
NCBI Description	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No.	54239
Seq. ID	zhf700964152.h1
Method	BLASTX
NCBI GI	g2462732
BLAST score	248
E value	1.0e-21
Match length	80
% identity	55
NCBI Description	(AC002292) Hypothetical Protein [Arabidopsis thaliana]

Seq. No.	54240
Seq. ID	zhf700964154.h1
Method	BLASTX
NCBI GI	g1245816
BLAST score	162
E value	2.0e-11
Match length	82
% identity	52
NCBI Description	cyclin A homolog [Medicago falcata=alfalfa, Peptide, 452 aa]

Seq. No.	54241
Seq. ID	zhf700964203.h1
Method	BLASTX
NCBI GI	g3935187
BLAST score	254
E value	3.0e-22
Match length	80
% identity	59
NCBI Description	(AC004557) F17L21.30 [Arabidopsis thaliana]

Seq. No.	54242
Seq. ID	zhf700964215.h1
Method	BLASTX
NCBI GI	g4512703
BLAST score	161
E value	2.0e-11
Match length	47
% identity	60
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	54243
Seq. ID	zhf700964231.h1
Method	BLASTX
NCBI GI	g3540206
BLAST score	155
E value	1.0e-10
Match length	78
% identity	44
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	54244
Seq. ID	zhf700964233.h1
Method	BLASTX
NCBI GI	g4006864
BLAST score	277
E value	6.0e-25
Match length	62
% identity	82
NCBI Description	(Z99707) nucleoporin-like protein [Arabidopsis thaliana]

Seq. No.	54245
Seq. ID	zhf700964241.h1
Method	BLASTX
NCBI GI	g2494111
BLAST score	386
E value	9.0e-38
Match length	80
% identity	88
NCBI Description	(AC002376) Contains similarity to Glycine protein kinase 6 (gb_M67449). [Arabidopsis thaliana]

Seq. No.	54246
Seq. ID	zhf700964271.h1
Method	BLASTX
NCBI GI	g1785622
BLAST score	317
E value	1.0e-29
Match length	81
% identity	70
NCBI Description	(Z84202) ORFc [Arabidopsis thaliana]

Seq. No.	54247
Seq. ID	zhf700964282.h1
Method	BLASTX
NCBI GI	g4336747
BLAST score	232
E value	1.0e-19

Match length 50
% identity 84
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No. 54248
Seq. ID zhf700964295.h1
Method BLASTX
NCBI GI g4538912
BLAST score 152
E value 3.0e-10
Match length 62
% identity 53
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 54249
Seq. ID zhf700964304.h1
Method BLASTX
NCBI GI g2565429
BLAST score 190
E value 9.0e-15
Match length 59
% identity 61
NCBI Description (AF027686) glycine-rich protein [Onobrychis viciifolia]

Seq. No. 54250
Seq. ID zhf700964353.h1
Method BLASTX
NCBI GI g2281092
BLAST score 220
E value 3.0e-18
Match length 55
% identity 80
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 54251
Seq. ID zhf700964355.h1
Method BLASTX
NCBI GI g2335109
BLAST score 375
E value 2.0e-36
Match length 83
% identity 84
NCBI Description (AC002339) putative ABC transporter [Arabidopsis thaliana]

Seq. No. 54252
Seq. ID zhf700964356.h1
Method BLASTX
NCBI GI g4539301
BLAST score 335
E value 9.0e-32
Match length 70
% identity 89
NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 54253
Seq. ID zhf700964368.h1

Method	BLASTX
NCBI GI	g3142300
BLAST score	225
E value	7.0e-19
Match length	79
% identity	57
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	54254
Seq. ID	zhf700964422.h1
Method	BLASTN
NCBI GI	g2815245
BLAST score	47
E value	2.0e-17
Match length	99
% identity	87
NCBI Description	C.arietinum mRNA for class I type 2 metallothionein (clone: CanMT-2)

Seq. No.	54255
Seq. ID	zhf700964445.h1
Method	BLASTX
NCBI GI	g2435519
BLAST score	395
E value	8.0e-39
Match length	82
% identity	90
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	54256
Seq. ID	zhf700964450.h1
Method	BLASTX
NCBI GI	g3643192
BLAST score	248
E value	1.0e-21
Match length	81
% identity	60
NCBI Description	(AF087435) unknown [Arabidopsis thaliana]

Seq. No.	54257
Seq. ID	zhf700964480.h1
Method	BLASTX
NCBI GI	g1946355
BLAST score	147
E value	9.0e-10
Match length	72
% identity	39
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	54258

Seq. ID	zhf700964505.h1
Method	BLASTX
NCBI GI	g2118232
BLAST score	386
E value	8.0e-38
Match length	79
% identity	95
NCBI Description	aha9 protein - Arabidopsis thaliana

Seq. No.	54259
Seq. ID	zhf700964512.h1
Method	BLASTX
NCBI GI	g3668086
BLAST score	209
E value	3.0e-17
Match length	80
% identity	57
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	54260
Seq. ID	zhf700964552.h1
Method	BLASTX
NCBI GI	g2642153
BLAST score	226
E value	5.0e-19
Match length	79
% identity	61
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_2795810 (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	54261
Seq. ID	zhf700964601.h1
Method	BLASTX
NCBI GI	g2760839
BLAST score	269
E value	6.0e-24
Match length	91
% identity	60
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	54262
Seq. ID	zhf700964625.h1
Method	BLASTX
NCBI GI	g2190557
BLAST score	285
E value	7.0e-26
Match length	88
% identity	66
NCBI Description	(AC001229) F5I14.11 [Arabidopsis thaliana]

Seq. No.	54263
Seq. ID	zhf700964662.h1
Method	BLASTX
NCBI GI	g417305
BLAST score	159
E value	4.0e-11

Match length	87
% identity	39
NCBI Description	MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (MAN(9)-ALPHA-MANNOSIDASE) >gi_101195_pir__A39345 alpha-mannosidase MNS1 (EC 3.2.1.-) - yeast (Saccharomyces cerevisiae) >gi_171996 (M63598) alpha-mannosidase [Saccharomyces cerevisiae] >gi_1015864_emb_CAA89662_ (Z49631) ORF YJR131w [Saccharomyces cerevisiae]

Seq. No.	54264
Seq. ID	zhf700964787.h1
Method	BLASTN
NCBI GI	g2661020
BLAST score	202
E value	1.0e-110
Match length	230
% identity	97
NCBI Description	Glycine max catalase (cat4) mRNA, complete cds

Seq. No.	54265
Seq. ID	zhf700964789.h1
Method	BLASTN
NCBI GI	g1143393
BLAST score	46
E value	6.0e-17
Match length	122
% identity	84
NCBI Description	A.thaliana mRNA for vacuolar proton ATPase subunit E

Seq. No.	54266
Seq. ID	zhf700964852.h1
Method	BLASTX
NCBI GI	g4567289
BLAST score	153
E value	2.0e-10
Match length	68
% identity	54
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54267
Seq. ID	zhf700964853.h1
Method	BLASTX
NCBI GI	g4522012
BLAST score	136
E value	9.0e-10
Match length	48
% identity	67
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54268
Seq. ID	zhf700964885.h1
Method	BLASTX
NCBI GI	g2828280
BLAST score	156
E value	1.0e-14
Match length	47
% identity	89

NCBI Description	(AL021687) putative protein [Arabidopsis thaliana] >gi_2832633_emb_CAA16762_ (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	54269
Seq. ID	zhf700964906.h1
Method	BLASTX
NCBI GI	g2914703
BLAST score	160
E value	3.0e-11
Match length	85
% identity	46
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.	54270
Seq. ID	zhf700964920.h1
Method	BLASTX
NCBI GI	g4455330
BLAST score	185
E value	4.0e-14
Match length	83
% identity	47
NCBI Description	(AL035525) contains EST gb:T44002 [Arabidopsis thaliana]
Seq. No.	54271
Seq. ID	zhf700964928.h1
Method	BLASTX
NCBI GI	g1743354
BLAST score	212
E value	3.0e-17
Match length	51
% identity	76
NCBI Description	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
Seq. No.	54272
Seq. ID	zhf700964952.h1
Method	BLASTX
NCBI GI	g1514649
BLAST score	170
E value	2.0e-12
Match length	49
% identity	71
NCBI Description	(X86021) potassium channel [Solanum tuberosum]
Seq. No.	54273
Seq. ID	zhf700964955.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	112
E value	3.0e-56
Match length	204
% identity	89
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds
Seq. No.	54274
Seq. ID	zhf700964961.h1

Method	BLASTX
NCBI GI	g3935147
BLAST score	310
E value	9.0e-29
Match length	88
% identity	70
NCBI Description	(AC005106) T25N20.11 [Arabidopsis thaliana]

Seq. No.	54275
Seq. ID	zhf700964981.h1
Method	BLASTN
NCBI GI	g2665839
BLAST score	40
E value	2.0e-13
Match length	82
% identity	93
NCBI Description	Zea mays putative histone deacetylase RPD3 mRNA, complete cds

Seq. No.	54276
Seq. ID	zhf700964990.h1
Method	BLASTX
NCBI GI	g3885328
BLAST score	179
E value	2.0e-13
Match length	76
% identity	41
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	54277
Seq. ID	zhf700965004.h1
Method	BLASTX
NCBI GI	g2369714
BLAST score	192
E value	7.0e-25
Match length	79
% identity	63
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	54278
Seq. ID	zhf700965016.h1
Method	BLASTX
NCBI GI	g172764
BLAST score	294
E value	6.0e-27
Match length	83
% identity	66
NCBI Description	(M83755) STH1 protein [Saccharomyces cerevisiae]

Seq. No.	54279
Seq. ID	zhf700965021.h1
Method	BLASTX
NCBI GI	g2108252
BLAST score	151
E value	4.0e-19
Match length	81

% identity	33
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.	54280
Seq. ID	zhf700965024.h1
Method	BLASTN
NCBI GI	g217910
BLAST score	44
E value	9.0e-16
Match length	171
% identity	82
NCBI Description	Carrot mRNA for nuclear antigen 21D7
Seq. No.	54281
Seq. ID	zhf700965026.h1
Method	BLASTX
NCBI GI	g3769673
BLAST score	134
E value	5.0e-16
Match length	85
% identity	66
NCBI Description	(AF095285) Tic20 [Pisum sativum]
Seq. No.	54282
Seq. ID	zhf700965032.h1
Method	BLASTX
NCBI GI	g2431769
BLAST score	174
E value	7.0e-13
Match length	49
% identity	63
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]
Seq. No.	54283
Seq. ID	zhf700965159.h1
Method	BLASTX
NCBI GI	g3128168
BLAST score	338
E value	4.0e-32
Match length	80
% identity	75
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]
Seq. No.	54284
Seq. ID	zhf700965175.h1
Method	BLASTN
NCBI GI	g3860320
BLAST score	125
E value	4.0e-64
Match length	256
% identity	88
NCBI Description	Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-5

Seq. No.	54285
Seq. ID	zhf700965214.h1
Method	BLASTX
NCBI GI	g3193291
BLAST score	157
E value	9.0e-12
Match length	48
% identity	77
NCBI Description	(AF069298) Similar to DNA mismatch repair protein; T14P8.6 [Arabidopsis thaliana]

Seq. No.	54286
Seq. ID	zhf700965227.h1
Method	BLASTX
NCBI GI	g4218120
BLAST score	157
E value	6.0e-11
Match length	52
% identity	62
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	54287
Seq. ID	zhf700965264.h1
Method	BLASTX
NCBI GI	g2244965
BLAST score	345
E value	6.0e-33
Match length	81
% identity	84
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No.	54288
Seq. ID	zhf700965266.h1
Method	BLASTN
NCBI GI	g558542
BLAST score	37
E value	1.0e-11
Match length	69
% identity	88
NCBI Description	G.max (Evans) mRNA for zinc-finger protein (C-terminal)

Seq. No.	54289
Seq. ID	zhf700965273.h1
Method	BLASTX
NCBI GI	g629592
BLAST score	297
E value	2.0e-27
Match length	79
% identity	68
NCBI Description	hypothetical protein - rape

Seq. No.	54290
Seq. ID	zhf700965275.h1
Method	BLASTX
NCBI GI	g2632254

BLAST score 156
E value 4.0e-22
Match length 71
% identity 73
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 54291
Seq. ID zlv700807514.h1
Method BLASTX
NCBI GI g4417271
BLAST score 438
E value 9.0e-44
Match length 89
% identity 91
NCBI Description (AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 54292
Seq. ID zlv700807539.h1
Method BLASTX
NCBI GI g3080374
BLAST score 270
E value 7.0e-24
Match length 114
% identity 4
NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 54293
Seq. ID zlv700807560.h1
Method BLASTX
NCBI GI g1946355
BLAST score 202
E value 3.0e-16
Match length 43
% identity 81
NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 54294
Seq. ID zlv700807568.h1
Method BLASTX
NCBI GI g138364
BLAST score 474
E value 8.0e-48
Match length 108
% identity 89
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 54295
Seq. ID zlv700807572.h1
Method BLASTX
NCBI GI g138364
BLAST score 570

E value	4.0e-59
Match length	104
% identity	99
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54296
Seq. ID	zlv700807580.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	432
E value	7.0e-43
Match length	110
% identity	95
NCBI Description	Bean pod mottle virus

Seq. No.	54297
Seq. ID	zlv700807611.h1
Method	BLASTX
NCBI GI	g3201617
BLAST score	149
E value	1.0e-09
Match length	41
% identity	54
NCBI Description	(AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54298
Seq. ID	zlv700807614.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	407
E value	6.0e-40
Match length	98
% identity	84
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54299
Seq. ID	zlv700807631.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	232
E value	2.0e-19
Match length	99
% identity	42
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54300
Seq. ID	zlv700807650.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	500
E value	7.0e-51

Match length	112
% identity	84
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54301
Seq. ID	zlv700807651.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	311
E value	7.0e-37
Match length	102
% identity	80
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54302
Seq. ID	zlv700807675.h1
Method	BLASTX
NCBI GI	g3367576
BLAST score	252
E value	8.0e-22
Match length	95
% identity	52
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	54303
Seq. ID	zpv700756912.h1
Method	BLASTX
NCBI GI	g126398
BLAST score	221
E value	2.0e-18
Match length	68
% identity	72
NCBI Description	SEED LIPOXYGENASE-1 (L-1) >gi_2144382_pir__DASYL2 lipoxygenase (EC 1.13.11.12) 1 - soybean >gi_1000060_pdb_2SBL_B Lipoxygenase-1 (Soybean) (E.C.1.13.11.12) >gi_2392632_pdb_1YGE_ Lipoxygenase-1 (Soybean) At 100k >gi_18675_emb_CAA47717_ (X67304) lipoxygenase [Glycine max] >gi_295118 (J02795) lipoxygenase-1 [Glycine max]

Seq. No.	54304
Seq. ID	zpv700756918.h1
Method	BLASTX
NCBI GI	g4580472
BLAST score	141
E value	6.0e-09
Match length	45
% identity	51
NCBI Description	(AC006081) DNA binding protein;similar to CDC27 and nuclear scaffold proteins [Arabidopsis thaliana]

Seq. No.	54305
Seq. ID	zpv700756934.h1
Method	BLASTX
NCBI GI	g1772308
BLAST score	345
E value	7.0e-33
Match length	81
% identity	81
NCBI Description	(AB000169) glycinin [Glycine max]

Seq. No.	54306
Seq. ID	zpv700756958.h1
Method	BLASTX
NCBI GI	g121282
BLAST score	399
E value	3.0e-39
Match length	87
% identity	92
NCBI Description	BETA-CONGLYCININ, BETA CHAIN PRECURSOR >gi_72290_pir__FWSYCB beta-conglycinin beta chain - soybean >gi_256427_bbs_114632 (S44893) CG4 beta-conglycinin [soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No.	54307
Seq. ID	zpv700756960.h1
Method	BLASTX
NCBI GI	g3107931
BLAST score	333
E value	2.0e-31
Match length	87
% identity	74
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	54308
Seq. ID	zpv700756970.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	304
E value	4.0e-28
Match length	83
% identity	72
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54309
Seq. ID	zpv700756984.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	262
E value	4.0e-23
Match length	76
% identity	68
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54310
Seq. ID	zpv700757001.h1
Method	BLASTX
NCBI GI	g3337356

BLAST score 307
E value 2.0e-28
Match length 61
% identity 95
NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 54311
Seq. ID zpv700757034.h1
Method BLASTX
NCBI GI g3982596
BLAST score 124
E value 5.0e-11
Match length 62
% identity 54
NCBI Description (AF039027) cationic peroxidase 2 [Glycine max]

Seq. No. 54312
Seq. ID zpv700757124.h1
Method BLASTX
NCBI GI g121286
BLAST score 194
E value 7.0e-32
Match length 78
% identity 76
NCBI Description BETA-CONGLYCININ, ALPHA' CHAIN PRECURSOR >gi_81769_pir__B24810 beta-conglycinin alpha chain precursor - soybean >gi_169929 (M13759) beta-conglycinin storage protein [Glycine max]

Seq. No. 54313
Seq. ID zpv700757148.h1
Method BLASTX
NCBI GI g1076488
BLAST score 185
E value 8.0e-20
Match length 78
% identity 69
NCBI Description glycinin A5A4B3 chain - soybean >gi_806556_emb_CAA60533_ (X86970) A5A4B3 subunit [Glycine soja]

Seq. No. 54314
Seq. ID zpv700757167.h1
Method BLASTX
NCBI GI g1076485
BLAST score 230
E value 3.0e-21
Match length 56
% identity 96
NCBI Description SAM-synthetase - chickpea (fragment) >gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer arietinum]

Seq. No. 54315
Seq. ID zpv700757242.h1
Method BLASTX
NCBI GI g3152566

BLAST score 198
E value 1.0e-15
Match length 61
% identity 64
NCBI Description (AC002986) Similar to hypothetical protein YLR002c, gb_Z7314 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No. 54316
Seq. ID zpv700757252.h1
Method BLASTX
NCBI GI g4469008
BLAST score 227
E value 4.0e-19
Match length 80
% identity 54
NCBI Description (AL035602) UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No. 54317
Seq. ID zpv700757304.h1
Method BLASTX
NCBI GI g4097880
BLAST score 333
E value 2.0e-31
Match length 85
% identity 78
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 54318
Seq. ID zpv700757335.h1
Method BLASTX
NCBI GI g126151
BLAST score 131
E value 3.0e-14
Match length 65
% identity 70
NCBI Description LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi_282898_pir__S27365 lectin precursor - soybean >gi_170006 (K00821) lectin prepeptide [Glycine max]

Seq. No. 54319
Seq. ID zpv700757383.h1
Method BLASTX
NCBI GI g121282
BLAST score 291
E value 1.0e-26
Match length 78
% identity 68
NCBI Description BETA-CONGLYCININ, BETA CHAIN PRECURSOR >gi_72290_pir__FWSYCB beta-conglycinin beta chain - soybean >gi_256427_bbs_114632 (S44893) CG4 beta-conglycinin [soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No. 54320
Seq. ID zpv700757475.h1
Method BLASTX
NCBI GI g3582333

BLAST score	373
E value	3.0e-36
Match length	81
% identity	85
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54321
Seq. ID	zpv700757491.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	214
E value	1.0e-17
Match length	63
% identity	65
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54322
Seq. ID	zpv700757579.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	148
E value	8.0e-10
Match length	62
% identity	74
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54323
Seq. ID	zpv700757627.h1
Method	BLASTX
NCBI GI	g121286
BLAST score	391
E value	3.0e-38
Match length	83
% identity	89
NCBI Description	BETA-CONGLYCININ, ALPHA' CHAIN PRECURSOR >gi_81769_pir__B24810 beta-conglycinin alpha chain precursor - soybean >gi_169929 (M13759) beta-conglycinin storage protein [Glycine max]

Seq. No.	54324
Seq. ID	zpv700757641.h1
Method	BLASTX
NCBI GI	g2827715
BLAST score	180
E value	2.0e-13
Match length	62
% identity	63
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	54325
Seq. ID	zpv700757675.h1
Method	BLASTX
NCBI GI	g2196466

BLAST score	115
E value	2.0e-10
Match length	83
% identity	53
NCBI Description	(Y13673) TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	54326
Seq. ID	zpv700757687.h1
Method	BLASTX
NCBI GI	g3891586
BLAST score	263
E value	3.0e-23
Match length	75
% identity	94
NCBI Description	Chain B, Complex Porcine Pancreatic TrypsinSOYBEAN TRYPSIN Inhibitor, Orthorhombic Crystal Form

Seq. No.	54327
Seq. ID	zpv700757731.h1
Method	BLASTX
NCBI GI	g126151
BLAST score	261
E value	2.0e-24
Match length	77
% identity	96
NCBI Description	LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi_282898_pir__S27365 lectin precursor - soybean >gi_170006 (K00821) lectin prepeptide [Glycine max]

Seq. No.	54328
Seq. ID	zpv700757766.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	378
E value	9.0e-37
Match length	78
% identity	94
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54329
Seq. ID	zpv700757796.h1
Method	BLASTX
NCBI GI	g1076488
BLAST score	142
E value	4.0e-19
Match length	77
% identity	69
NCBI Description	glycinin A5A4B3 chain - soybean >gi_806556_emb_CAA60533_ (X86970) A5A4B3 subunit [Glycine soja]

Seq. No.	54330
Seq. ID	zpv700757806.h1
Method	BLASTX

NCBI GI	g4249568
BLAST score	195
E value	2.0e-15
Match length	82
% identity	51
NCBI Description	(AB004062) glycinin [Glycine max]

Seq. No.	54331
Seq. ID	zpv700757857.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	175
E value	6.0e-13
Match length	64
% identity	47
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54332
Seq. ID	zpv700757865.h1
Method	BLASTX
NCBI GI	g121278
BLAST score	302
E value	7.0e-28
Match length	55
% identity	100
NCBI Description	GLYCININ G3 PRECURSOR [CONTAINS: GLYCININ A SUBUNIT; GLYCININ B SUBUNIT] >gi_81778_pir__S04605 glycinin G3 - soybean >gi_18639_emb_CAA33217_ (X15123) glycinin subunit G3 [Glycine max]

Seq. No.	54333
Seq. ID	zpv700757871.h1
Method	BLASTX
NCBI GI	g4191814
BLAST score	225
E value	8.0e-19
Match length	88
% identity	86
NCBI Description	(AB008680) alpha' subunit of beta-conglycinin [Glycine max]

Seq. No.	54334
Seq. ID	zpv700757904.h1
Method	BLASTX
NCBI GI	g4220462
BLAST score	156
E value	6.0e-18
Match length	58
% identity	86
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	54335
Seq. ID	zpv700757905.h1
Method	BLASTX
NCBI GI	g2267567
BLAST score	170

E value	3.0e-12
Match length	49
% identity	67
NCBI Description	(AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum]

Seq. No.	54336
Seq. ID	zpv700757938.h1
Method	BLASTX
NCBI GI	g2664214
BLAST score	122
E value	3.0e-09
Match length	75
% identity	45
NCBI Description	(AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No.	54337
Seq. ID	zpv700757965.h1
Method	BLASTX
NCBI GI	g72296
BLAST score	248
E value	3.0e-42
Match length	92
% identity	99
NCBI Description	glycinin chain A1aBx precursor - soybean >gi_18615_emb_CAA26723_ (X02985) glycinin precursor [Glycine max]

Seq. No.	54338
Seq. ID	zpv700757985.h1
Method	BLASTX
NCBI GI	g121277
BLAST score	206
E value	2.0e-24
Match length	66
% identity	89
NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max] >gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin [Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]

Seq. No.	54339
Seq. ID	zpv700758010.h1
Method	BLASTX
NCBI GI	g2270994
BLAST score	220
E value	3.0e-18
Match length	81
% identity	57
NCBI Description	(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.	54340
Seq. ID	zpv700758019.h1
Method	BLASTX
NCBI GI	g4115377
BLAST score	210
E value	4.0e-17
Match length	85
% identity	49
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	54341
Seq. ID	zpv700758126.h1
Method	BLASTX
NCBI GI	g1076488
BLAST score	244
E value	3.0e-22
Match length	70
% identity	80
NCBI Description	glycinin A5A4B3 chain - soybean >gi_806556_emb_CAA60533_ (X86970) A5A4B3 subunit [Glycine soja]

Seq. No.	54342
Seq. ID	zpv700758127.h1
Method	BLASTX
NCBI GI	g121277
BLAST score	291
E value	1.0e-26
Match length	75
% identity	77
NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max] >gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin [Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]

Seq. No.	54343
Seq. ID	zpv700758133.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	158
E value	5.0e-15
Match length	58
% identity	79
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54344
Seq. ID	zpv700758170.h1
Method	BLASTX
NCBI GI	g121277
BLAST score	221
E value	2.0e-31
Match length	78
% identity	82

NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max] >gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin [Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]

Seq. No.	54345
Seq. ID	zpv700758251.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	346
E value	3.0e-33
Match length	73
% identity	88
NCBI Description	Bean pod mottle virus

Seq. No.	54346
Seq. ID	zpv700758339.h1
Method	BLASTX
NCBI GI	g4191814
BLAST score	239
E value	2.0e-20
Match length	44
% identity	100
NCBI Description	(AB008680) alpha' subunit of beta-conglycinin [Glycine max]

Seq. No.	54347
Seq. ID	zpv700758364.h1
Method	BLASTX
NCBI GI	g2305020
BLAST score	316
E value	1.0e-29
Match length	81
% identity	75
NCBI Description	(AF005030) 2S albumin pre-propeptide [Glycine max] >gi_4097896 (U71195) napin-type 2S albumin 3 [Glycine max]

Seq. No.	54348
Seq. ID	zpv700758434.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	311
E value	7.0e-29
Match length	88
% identity	75
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54349
Seq. ID	zpv700758447.h1
Method	BLASTX

NCBI GI	g72295
BLAST score	251
E value	7.0e-22
Match length	89
% identity	63
NCBI Description	glycinin chain A2B1a precursor - soybean >gi_18609_emb_CAA26575_ (X02806) A2B1a precursor [Glycine max] >gi_224569_prf__1109177A glycinin A2B1A precursor [Glycine max]

Seq. No.	54350
Seq. ID	zpv700758647.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	219
E value	4.0e-18
Match length	104
% identity	64
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54351
Seq. ID	zpv700758656.h1
Method	BLASTX
NCBI GI	g121282
BLAST score	226
E value	6.0e-19
Match length	87
% identity	56
NCBI Description	BETA-CONGLYCININ, BETA CHAIN PRECURSOR >gi_72290_pir__FWSYCB beta-conglycinin beta chain - soybean >gi_256427_bbs_114632 (S44893) CG4 beta-conglycinin [soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No.	54352
Seq. ID	zpv700758667.h1
Method	BLASTX
NCBI GI	g4210948
BLAST score	148
E value	5.0e-10
Match length	35
% identity	83
NCBI Description	(AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.	54353
Seq. ID	zpv700758711.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	222
E value	2.0e-18
Match length	81
% identity	57
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54354
Seq. ID	zpv700758729.h1
Method	BLASTX
NCBI GI	g121279

BLAST score	141
E value	5.0e-09
Match length	73
% identity	47
NCBI Description	GLYCININ G4 PRECURSOR [CONTAINS: GLYCININ A5 SUBUNIT; GLYCININ A4 SUBUNIT; GLYCININ B3 SUBUNIT] >gi_72297_pir__FWSYG5 glycinin chain A5A4B3 precursor - soybean >gi_732706_emb_CAA26478_ (X02626) A5A4B3 subunits precursor (aa -23 to 539) [Glycine max]

Seq. No.	54355
Seq. ID	zpv700758747.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	420
E value	1.0e-41
Match length	99
% identity	83
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54356
Seq. ID	zpv700758769.h1
Method	BLASTX
NCBI GI	g121276
BLAST score	386
E value	1.0e-37
Match length	92
% identity	83
NCBI Description	GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX SUBUNIT] >gi_99907_pir__S10851 glycinin G1 precursor - soybean >gi_255221_bbs_112930 glycinin G1 subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_ (X15121) glycinin subunit G1 [Glycine max] >gi_169973 (M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No.	54357
Seq. ID	zpv700758774.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	201
E value	5.0e-16
Match length	47
% identity	83
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54358
Seq. ID	zpv700758821.h1
Method	BLASTX
NCBI GI	g4415937
BLAST score	272
E value	3.0e-24
Match length	83
% identity	59
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54359
Seq. ID	zpv700758907.h1
Method	BLASTX
NCBI GI	g1334163
BLAST score	400
E value	2.0e-39
Match length	79
% identity	100
NCBI Description	(X06984) aldolase C (AA 1-362) [Rattus norvegicus]

Seq. No.	54360
Seq. ID	zpv700758920.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	299
E value	1.0e-27
Match length	77
% identity	77
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54361
Seq. ID	zpv700758940.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	410
E value	1.0e-40
Match length	79
% identity	97
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54362
Seq. ID	zpv700758963.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	396
E value	5.0e-39
Match length	77
% identity	99
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54363
Seq. ID	zpv700759016.h1
Method	BLASTX
NCBI GI	g121279
BLAST score	208
E value	6.0e-17
Match length	72
% identity	58
NCBI Description	GLYCININ G4 PRECURSOR [CONTAINS: GLYCININ A5 SUBUNIT; GLYCININ A4 SUBUNIT; GLYCININ B3 SUBUNIT] >gi_72297_pir__FWSYG5 glycinin chain A5A4B3 precursor - soybean >gi_732706_emb_CAA26478_ (X02626) A5A4B3 subunits precursor (aa -23 to 539) [Glycine max]

Seq. No.	54364
Seq. ID	zpv700759027.h1

Method	BLASTX
NCBI GI	g121282
BLAST score	163
E value	1.0e-11
Match length	76
% identity	64
NCBI Description	BETA-CONGLYCININ, BETA CHAIN PRECURSOR >gi_72290_pir__FWSYCB beta-conglycinin beta chain - soybean >gi_256427_bbs_114632 (S44893) CG4 beta-conglycinin [soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No.	54365
Seq. ID	zpv700759029.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	293
E value	9.0e-27
Match length	60
% identity	93
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54366
Seq. ID	zpv700759037.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	316
E value	9.0e-31
Match length	86
% identity	76
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54367
Seq. ID	zpv700759066.h1
Method	BLASTX
NCBI GI	g126078
BLAST score	222
E value	2.0e-18
Match length	60
% identity	43
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34) >gi_81554_pir__S04046 embryonic abundant protein gD-34 - upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea protein [Gossypium hirsutum] >gi_167385 (M19389) storage protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea D-34 gene [Saguinus oedipus]

Seq. No.	54368
Seq. ID	zpv700759079.h1
Method	BLASTX
NCBI GI	g121276
BLAST score	313
E value	3.0e-29
Match length	84
% identity	76

NCBI Description	GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX SUBUNIT] >gi_99907_pir__S10851 glycinin G1 precursor - soybean >gi_255221_bbs_112930 glycinin G1 subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_ (X15121) glycinin subunit G1 [Glycine max] >gi_169973 (M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No.	54369
Seq. ID	zpv700759111.h1
Method	BLASTX
NCBI GI	g2305020
BLAST score	185
E value	3.0e-14
Match length	78
% identity	51
NCBI Description	(AF005030) 2S albumin pre-propeptide [Glycine max] >gi_4097896 (U71195) napin-type 2S albumin 3 [Glycine max]

Seq. No.	54370
Seq. ID	zpv700759156.h1
Method	BLASTX
NCBI GI	g1401240
BLAST score	226
E value	5.0e-19
Match length	66
% identity	71
NCBI Description	(U59425) 7S seed globulin precursor [Glycine max]

Seq. No.	54371
Seq. ID	zpv700759162.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	298
E value	1.0e-27
Match length	76
% identity	75
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54372
Seq. ID	zpv700759315.h1
Method	BLASTX
NCBI GI	g3176668
BLAST score	267
E value	3.0e-24
Match length	80
% identity	67
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	54373
Seq. ID	zpv700759326.h1
Method	BLASTX
NCBI GI	g4097880

BLAST score	437
E value	1.0e-43
Match length	87
% identity	95
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54374
Seq. ID	zpv700759451.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	156
E value	6.0e-11
Match length	32
% identity	94
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54375
Seq. ID	zpv700759469.h1
Method	BLASTX
NCBI GI	g121282
BLAST score	208
E value	4.0e-17
Match length	57
% identity	65
NCBI Description	BETA-CONGLYCININ, BETA CHAIN PRECURSOR >gi_72290_pir__FWSYCB beta-conglycinin beta chain - soybean >gi_256427_bbs_114632 (S44893) CG4 beta-conglycinin [soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No.	54376
Seq. ID	zpv700759473.h1
Method	BLASTX
NCBI GI	g121282
BLAST score	214
E value	6.0e-28
Match length	83
% identity	82
NCBI Description	BETA-CONGLYCININ, BETA CHAIN PRECURSOR >gi_72290_pir__FWSYCB beta-conglycinin beta chain - soybean >gi_256427_bbs_114632 (S44893) CG4 beta-conglycinin [soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No.	54377
Seq. ID	zpv700759479.h1
Method	BLASTX
NCBI GI	g121277
BLAST score	226
E value	5.0e-19
Match length	57
% identity	82
NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max] >gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin

[Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]

Seq. No.	54378
Seq. ID	zpv700759504.h1
Method	BLASTX
NCBI GI	g3080420
BLAST score	183
E value	5.0e-14
Match length	69
% identity	57
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	54379
Seq. ID	zpv700759526.h1
Method	BLASTX
NCBI GI	g121282
BLAST score	346
E value	5.0e-33
Match length	84
% identity	86
NCBI Description	BETA-CONGLYCININ, BETA CHAIN PRECURSOR >gi_72290_pir__FWSYCB beta-conglycinin beta chain - soybean >gi_256427_bbs_114632 (S44893) CG4 beta-conglycinin [soybeans, Forrest and Dare, Peptide, 439 aa] [Glycine max]

Seq. No.	54380
Seq. ID	zpv700759527.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	234
E value	6.0e-20
Match length	72
% identity	62
NCBI Description	Bean pod mottle virus

Seq. No.	54381
Seq. ID	zpv700759539.h1
Method	BLASTX
NCBI GI	g3600033
BLAST score	260
E value	5.0e-23
Match length	80
% identity	66
NCBI Description	(AF080119) contains similarity to the N terminal domain of the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis thaliana]

Seq. No.	54382
Seq. ID	zpv700759544.h1
Method	BLASTX
NCBI GI	g729442
BLAST score	245
E value	3.0e-21
Match length	81
% identity	42

NCBI Description	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi_166380 (M80235) glucose-regulated endoplasmic reticular protein precursor [Medicago sativa]

Seq. No.	54383
Seq. ID	zpv700759555.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	178
E value	3.0e-13
Match length	78
% identity	62
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54384
Seq. ID	zpv700759584.h1
Method	BLASTX
NCBI GI	g4249566
BLAST score	181
E value	6.0e-14
Match length	50
% identity	72
NCBI Description	(AB003680) glycinin [Glycine max]

Seq. No.	54385
Seq. ID	zpv700759588.h1
Method	BLASTX
NCBI GI	g3176709
BLAST score	158
E value	5.0e-11
Match length	73
% identity	41
NCBI Description	(AC002392) putative anthranilate N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis thaliana]

Seq. No.	54386
Seq. ID	zpv700759642.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	357
E value	1.0e-34
Match length	71
% identity	96
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54387
Seq. ID	zpv700759745.h1
Method	BLASTX
NCBI GI	g4191814
BLAST score	138
E value	1.0e-08
Match length	47
% identity	64

NCBI Description	(AB008680) alpha' subunit of beta-conglycinin [Glycine max]

Seq. No.	54388
Seq. ID	zpv700759793.h1
Method	BLASTX
NCBI GI	g2317900
BLAST score	449
E value	4.0e-45
Match length	86
% identity	100
NCBI Description	(U89693) Sali3-2 [Glycine max]

Seq. No.	54389
Seq. ID	zpv700759813.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	328
E value	7.0e-31
Match length	63
% identity	97
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54390
Seq. ID	zpv700759833.h1
Method	BLASTX
NCBI GI	g992917
BLAST score	232
E value	7.0e-20
Match length	44
% identity	98
NCBI Description	(L42814) acetyl CoA carboxylase [Glycine max]

Seq. No.	54391
Seq. ID	zpv700759858.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	252
E value	4.0e-22
Match length	89
% identity	63
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54392
Seq. ID	zpv700759874.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	248
E value	2.0e-21
Match length	74
% identity	65
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54393
Seq. ID	zpv700759882.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	274

E value	8.0e-25
Match length	67
% identity	84
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54394
Seq. ID	zpv700759978.h1
Method	BLASTX
NCBI GI	g121276
BLAST score	298
E value	2.0e-27
Match length	60
% identity	95
NCBI Description	GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX SUBUNIT] >gi_99907_pir__S10851 glycinin G1 precursor - soybean >gi_255221_bbs_112930 glycinin G1 subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_ (X15121) glycinin subunit G1 [Glycine max] >gi_169973 (M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No.	54395
Seq. ID	zpv700760001.h1
Method	BLASTX
NCBI GI	g3250687
BLAST score	200
E value	7.0e-16
Match length	69
% identity	57
NCBI Description	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]

Seq. No.	54396
Seq. ID	zpv700760010.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	207
E value	7.0e-17
Match length	65
% identity	72
NCBI Description	Bean pod mottle virus

Seq. No.	54397
Seq. ID	zpv700760075.h1
Method	BLASTX
NCBI GI	g1771160
BLAST score	188
E value	1.0e-14
Match length	55
% identity	67
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	54398
Seq. ID	zpv700760087.h1
Method	BLASTX
NCBI GI	g4097880

BLAST score	182
E value	5.0e-14
Match length	35
% identity	100
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54399
Seq. ID	zpv700760090.h1
Method	BLASTX
NCBI GI	g1076488
BLAST score	114
E value	6.0e-14
Match length	66
% identity	73
NCBI Description	glycinin A5A4B3 chain - soybean >gi_806556_emb_CAA60533_ (X86970) A5A4B3 subunit [Glycine soja]

Seq. No.	54400
Seq. ID	zpv700760110.h1
Method	BLASTX
NCBI GI	g736002
BLAST score	368
E value	1.0e-35
Match length	84
% identity	83
NCBI Description	(X79467) A3B4 subunit [Glycine soja]

Seq. No.	54401
Seq. ID	zpv700760117.h1
Method	BLASTX
NCBI GI	g1197636
BLAST score	153
E value	2.0e-10
Match length	55
% identity	56
NCBI Description	(U46838) p105MCM [Homo sapiens]

Seq. No.	54402
Seq. ID	zpv700760273.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	462
E value	1.0e-46
Match length	90
% identity	97
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54403
Seq. ID	zpv700760275.h1
Method	BLASTX
NCBI GI	g434061
BLAST score	318
E value	1.0e-29
Match length	78
% identity	78
NCBI Description	(D16107) basic 7S globulin [Glycine max]

Seq. No.	54404
Seq. ID	zpv700760282.h1
Method	BLASTX
NCBI GI	g99909
BLAST score	327
E value	9.0e-31
Match length	60
% identity	100
NCBI Description	glycinin G3 precursor - soybean >gi_255223_bbs_112932 glycinin G3 subunit [soybeans, Peptide, 484 aa]

Seq. No.	54405
Seq. ID	zpv700760302.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	203
E value	1.0e-26
Match length	93
% identity	89
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54406
Seq. ID	zpv700760348.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	268
E value	7.0e-24
Match length	53
% identity	94
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54407
Seq. ID	zpv700760364.h1
Method	BLASTX
NCBI GI	g736002
BLAST score	351
E value	1.0e-33
Match length	74
% identity	85
NCBI Description	(X79467) A3B4 subunit [Glycine soja]

Seq. No.	54408
Seq. ID	zpv700760432.h1
Method	BLASTX
NCBI GI	g121277
BLAST score	350
E value	2.0e-33
Match length	78
% identity	86
NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max]

	>gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin [Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]
Seq. No.	54409
Seq. ID	zpv700760504.h1
Method	BLASTX
NCBI GI	g112857
BLAST score	403
E value	1.0e-39
Match length	91
% identity	96
NCBI Description	BASIC 7S GLOBULIN PRECURSOR >gi_81766_pir__S06750 basic 7S globulin precursor - soybean >gi_18543_emb_CAA34489_ (X16469) precursor (AA -24 to 403) [Glycine max]
Seq. No.	54410
Seq. ID	zpv700760540.h1
Method	BLASTX
NCBI GI	g4249566
BLAST score	263
E value	3.0e-23
Match length	73
% identity	73
NCBI Description	(AB003680) glycinin [Glycine max]
Seq. No.	54411
Seq. ID	zpv700760551.h1
Method	BLASTX
NCBI GI	g3108053
BLAST score	164
E value	6.0e-12
Match length	64
% identity	67
NCBI Description	(AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea mays]
Seq. No.	54412
Seq. ID	zpv700760561.h1
Method	BLASTX
NCBI GI	g282901
BLAST score	176
E value	2.0e-13
Match length	37
% identity	89
NCBI Description	maturation-associated protein MAT9 - soybean >gi_170024 (M94012) maturation-associated protein [Glycine max]
Seq. No.	54413
Seq. ID	zpv700760605.h1
Method	BLASTX
NCBI GI	g4006895
BLAST score	173
E value	1.0e-12
Match length	45
% identity	69

NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	54414
Seq. ID	zpv700760610.h1
Method	BLASTX
NCBI GI	g3738289
BLAST score	156
E value	5.0e-14
Match length	90
% identity	49
NCBI Description	(AC005309) Not56-like protein [Arabidopsis thaliana]
Seq. No.	54415
Seq. ID	zpv700760632.h1
Method	BLASTX
NCBI GI	g99910
BLAST score	305
E value	4.0e-28
Match length	82
% identity	72
NCBI Description	glycinin G4 precursor - soybean >gi_255224_bbs_112933 glycinin G4 subunit [soybeans, Peptide, 560 aa]
Seq. No.	54416
Seq. ID	zpv700760640.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	241
E value	4.0e-38
Match length	91
% identity	90
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]
Seq. No.	54417
Seq. ID	zpv700760651.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	269
E value	5.0e-24
Match length	83
% identity	67
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]
Seq. No.	54418
Seq. ID	zpv700760659.h1
Method	BLASTX
NCBI GI	g719291
BLAST score	369
E value	1.0e-35
Match length	86
% identity	83
NCBI Description	(U19134) unknown [Arabidopsis thaliana] >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]

Seq. No.	54419
Seq. ID	zpv700760679.h1
Method	BLASTX
NCBI GI	g4263717
BLAST score	171
E value	8.0e-17
Match length	56
% identity	79
NCBI Description	(AC006223) putative inositol polyphosphate 5-phosphatase [Arabidopsis thaliana]

Seq. No.	54420
Seq. ID	zpv700760766.h1
Method	BLASTX
NCBI GI	g2980762
BLAST score	203
E value	3.0e-16
Match length	56
% identity	66
NCBI Description	(AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54421
Seq. ID	zpv700760813.h1
Method	BLASTX
NCBI GI	g4210504
BLAST score	157
E value	4.0e-11
Match length	49
% identity	55
NCBI Description	(AC002392) putative cadmium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	54422
Seq. ID	zpv700760922.h1
Method	BLASTX
NCBI GI	g121286
BLAST score	205
E value	1.0e-16
Match length	56
% identity	75
NCBI Description	BETA-CONGLYCININ, ALPHA' CHAIN PRECURSOR >gi_81769_pir__B24810 beta-conglycinin alpha chain precursor - soybean >gi_169929 (M13759) beta-conglycinin storage protein [Glycine max]

Seq. No.	54423
Seq. ID	zpv700760935.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	176
E value	4.0e-17
Match length	82
% identity	62
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54424
Seq. ID	zpv700760964.h1

Method	BLASTX
NCBI GI	g4097880
BLAST score	199
E value	1.0e-27
Match length	76
% identity	87
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54425
Seq. ID	zpv700760975.h1
Method	BLASTX
NCBI GI	g2317900
BLAST score	301
E value	5.0e-28
Match length	62
% identity	90
NCBI Description	(U89693) Sali3-2 [Glycine max]

Seq. No.	54426
Seq. ID	zpv700760982.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	210
E value	4.0e-17
Match length	53
% identity	81
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54427
Seq. ID	zpv700761002.h1
Method	BLASTX
NCBI GI	g82114
BLAST score	152
E value	3.0e-10
Match length	63
% identity	56
NCBI Description	wound-induced protein - tomato (fragment) >gi_19320_emb_CAA42537_ (X59882) wound induced protein [Lycopersicon esculentum]

Seq. No.	54428
Seq. ID	zpv700761005.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	230
E value	1.0e-19
Match length	48
% identity	88
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54429
Seq. ID	zpv700761030.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	380
E value	5.0e-37
Match length	87

% identity	87
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54430
Seq. ID	zpv700761088.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	426
E value	2.0e-42
Match length	86
% identity	100
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54431
Seq. ID	zpv700761113.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	273
E value	2.0e-24
Match length	84
% identity	63
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54432
Seq. ID	zpv700761173.h1
Method	BLASTX
NCBI GI	g2605510
BLAST score	340
E value	2.0e-32
Match length	82
% identity	87
NCBI Description	(AB008678) alpha subunit of beta conglycinin [Glycine max]

Seq. No.	54433
Seq. ID	zpv700761183.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	307
E value	2.0e-28
Match length	70
% identity	79
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54434
Seq. ID	zpv700761235.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	128
E value	1.0e-10
Match length	84
% identity	40
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No. 54435

Seq. ID	zpv700761316.h1
Method	BLASTX
NCBI GI	g434061
BLAST score	201
E value	5.0e-16
Match length	71
% identity	62
NCBI Description	(D16107) basic 7S globulin [Glycine max]

Seq. No.	54436
Seq. ID	zpv700761348.h1
Method	BLASTX
NCBI GI	g1076678
BLAST score	343
E value	9.0e-33
Match length	70
% identity	99
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	54437
Seq. ID	zpv700761360.h1
Method	BLASTX
NCBI GI	g4539340
BLAST score	221
E value	2.0e-18
Match length	45
% identity	84
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	54438
Seq. ID	zpv700761361.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	399
E value	3.0e-39
Match length	83
% identity	90
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54439
Seq. ID	zpv700761394.h1
Method	BLASTX
NCBI GI	g3097321
BLAST score	255
E value	2.0e-22
Match length	54
% identity	91
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54440
Seq. ID	zpv700761521.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	239

E value	1.0e-20
Match length	63
% identity	71
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54441
Seq. ID	zpv700761573.h1
Method	BLASTX
NCBI GI	g225651
BLAST score	361
E value	9.0e-35
Match length	69
% identity	97
NCBI Description	Glycinin A1aBx [Glycine max]

Seq. No.	54442
Seq. ID	zpv700761656.h1
Method	BLASTX
NCBI GI	g2129753
BLAST score	328
E value	6.0e-31
Match length	76
% identity	83
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	54443
Seq. ID	zpv700761690.h1
Method	BLASTX
NCBI GI	g2305020
BLAST score	378
E value	8.0e-37
Match length	81
% identity	89
NCBI Description	(AF005030) 2S albumin pre-propeptide [Glycine max] >gi_4097896 (U71195) napin-type 2S albumin 3 [Glycine max]

Seq. No.	54444
Seq. ID	zpv700761727.h1
Method	BLASTX
NCBI GI	g68821
BLAST score	344
E value	1.0e-32
Match length	93
% identity	62
NCBI Description	trypsin inhibitor C (Kunitz) - soybean >gi_354136_prf__1108235C inhibitor Tic,trypsin [Glycine max]

Seq. No.	54445
Seq. ID	zpv700761968.h1
Method	BLASTX
NCBI GI	g736002
BLAST score	389
E value	3.0e-38
Match length	76

% identity	97
NCBI Description	(X79467) A3B4 subunit [Glycine soja]

Seq. No.	54446
Seq. ID	zpv700761974.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	393
E value	1.0e-38
Match length	77
% identity	97
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54447
Seq. ID	zpv700762016.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	471
E value	1.0e-47
Match length	90
% identity	99
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54448
Seq. ID	zpv700762072.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	371
E value	5.0e-36
Match length	78
% identity	95
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54449
Seq. ID	zpv700762082.h1
Method	BLASTX
NCBI GI	g2623298
BLAST score	182
E value	8.0e-14
Match length	37
% identity	92
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	54450
Seq. ID	zpv700762120.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	409
E value	2.0e-40
Match length	79
% identity	99
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54451
Seq. ID	zpv700762123.h1
Method	BLASTX

NCBI GI	g99889
BLAST score	239
E value	1.0e-20
Match length	63
% identity	71
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54452
Seq. ID	zpv700762169.h1
Method	BLASTX
NCBI GI	g3319357
BLAST score	283
E value	8.0e-26
Match length	76
% identity	74
NCBI Description	(AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

Seq. No.	54453
Seq. ID	zpv700762182.h1
Method	BLASTX
NCBI GI	g548900
BLAST score	200
E value	5.0e-16
Match length	63
% identity	41
NCBI Description	SUCROSE-BINDING PROTEIN PRECURSOR (SBP) >gi_322691_pir__JQ1730 62K sucrose-binding protein precursor - soybean >gi_170064 (L06038) glucose binding protein [Glycine max]

Seq. No.	54454
Seq. ID	zpv700762218.h1
Method	BLASTX
NCBI GI	g2605512
BLAST score	160
E value	9.0e-22
Match length	58
% identity	97
NCBI Description	(AB008679) beta subunit of beta conglycinin [Glycine max]

Seq. No.	54455
Seq. ID	zpv700762223.h1
Method	BLASTX
NCBI GI	g549316
BLAST score	175
E value	9.0e-20
Match length	75
% identity	64
NCBI Description	GENOME POLYPROTEIN B (CONTAINS: PROTEASE COFACTOR, MEMBRANE BINDING PROTEIN, VPG, PROTEASE , RNA POLYMERASE >gi_419503_pir__A44214 genome polyprotein 1 - cowpea severe mosaic virus

Seq. No.	54456
Seq. ID	zpv700762282.h1
Method	BLASTX

NCBI GI	g138364
BLAST score	138
E value	7.0e-12
Match length	73
% identity	72
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54457
Seq. ID	zpv700762284.h1
Method	BLASTX
NCBI GI	g2305020
BLAST score	239
E value	5.0e-28
Match length	75
% identity	88
NCBI Description	(AF005030) 2S albumin pre-propeptide [Glycine max] >gi_4097896 (U71195) napin-type 2S albumin 3 [Glycine max]

Seq. No.	54458
Seq. ID	zpv700762294.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	192
E value	2.0e-18
Match length	64
% identity	65
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54459
Seq. ID	zpv700762350.h1
Method	BLASTX
NCBI GI	g2369714
BLAST score	149
E value	4.0e-10
Match length	37
% identity	84
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	54460
Seq. ID	zpv700762355.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	236
E value	3.0e-20
Match length	74
% identity	62
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54461
Seq. ID	zpv700762391.h1
Method	BLASTX
NCBI GI	g2605510
BLAST score	211
E value	2.0e-17

Match length	61
% identity	77
NCBI Description	(AB008678) alpha subunit of beta conglycinin [Glycine max]

Seq. No.	54462
Seq. ID	zpv700762429.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	189
E value	9.0e-17
Match length	62
% identity	66
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54463
Seq. ID	zpv700762490.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	202
E value	1.0e-33
Match length	79
% identity	95
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54464
Seq. ID	zpv700762503.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	203
E value	3.0e-16
Match length	74
% identity	73
NCBI Description	Bean pod mottle virus

Seq. No.	54465
Seq. ID	zpv700762533.h1
Method	BLASTX
NCBI GI	g434061
BLAST score	216
E value	7.0e-18
Match length	65
% identity	68
NCBI Description	(D16107) basic 7S globulin [Glycine max]

Seq. No.	54466
Seq. ID	zpv700762549.h1
Method	BLASTX
NCBI GI	g3132476
BLAST score	182
E value	5.0e-14
Match length	46
% identity	72
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]

Seq. No.	54467
Seq. ID	zpv700762591.h1
Method	BLASTX

NCBI GI	g121276
BLAST score	239
E value	1.0e-20
Match length	64
% identity	70
NCBI Description	GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX SUBUNIT] >gi_99907_pir__S10851 glycinin G1 precursor - soybean >gi_255221_bbs_112930 glycinin G1 subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_ (X15121) glycinin subunit G1 [Glycine max] >gi_169973 (M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No.	54468
Seq. ID	zpv700762667.h1
Method	BLASTX
NCBI GI	g3924603
BLAST score	162
E value	1.0e-11
Match length	47
% identity	77
NCBI Description	(AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	54469
Seq. ID	zpv700762762.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	143
E value	6.0e-16
Match length	54
% identity	73
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54470
Seq. ID	zpv700762856.h1
Method	BLASTX
NCBI GI	g121276
BLAST score	307
E value	2.0e-28
Match length	72
% identity	81
NCBI Description	GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX SUBUNIT] >gi_99907_pir__S10851 glycinin G1 precursor - soybean >gi_255221_bbs_112930 glycinin G1 subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_ (X15121) glycinin subunit G1 [Glycine max] >gi_169973 (M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No.	54471
Seq. ID	zpv700762865.h1
Method	BLASTX
NCBI GI	g3176072
BLAST score	356
E value	3.0e-34

Match length	80
% identity	89
NCBI Description	(AJ002485) protein phosphatase 1, catalytic beta subunit [Medicago sativa]

Seq. No.	54472
Seq. ID	zpv700762905.h1
Method	BLASTX
NCBI GI	g121277
BLAST score	350
E value	2.0e-33
Match length	85
% identity	81
NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max] >gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin [Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]

Seq. No.	54473
Seq. ID	zpv700762906.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	347
E value	4.0e-33
Match length	82
% identity	84
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54474
Seq. ID	zpv700762909.h1
Method	BLASTX
NCBI GI	g4191814
BLAST score	343
E value	1.0e-32
Match length	64
% identity	100
NCBI Description	(AB008680) alpha' subunit of beta-conglycinin [Glycine max]

Seq. No.	54475
Seq. ID	zpv700762915.h1
Method	BLASTX
NCBI GI	g121286
BLAST score	393
E value	2.0e-38
Match length	82
% identity	90
NCBI Description	BETA-CONGLYCININ, ALPHA' CHAIN PRECURSOR >gi_81769_pir__B24810 beta-conglycinin alpha chain precursor - soybean >gi_169929 (M13759) beta-conglycinin

storage protein [Glycine max]

Seq. No.	54476
Seq. ID	zpv700762949.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	218
E value	5.0e-18
Match length	91
% identity	57
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54477
Seq. ID	zpv700762954.h1
Method	BLASTX
NCBI GI	g1173198
BLAST score	217
E value	3.0e-19
Match length	70
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal protein S13.e - garden pea >gi_396639_emb_CAA80974_ (Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.	54478
Seq. ID	zpv700762962.h1
Method	BLASTX
NCBI GI	g66009
BLAST score	374
E value	3.0e-36
Match length	76
% identity	89
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH (AA 1-337) [Zea mays]

Seq. No.	54479
Seq. ID	zpv700762965.h1
Method	BLASTX
NCBI GI	g1076488
BLAST score	305
E value	3.0e-28
Match length	73
% identity	85
NCBI Description	glycinin A5A4B3 chain - soybean >gi_806556_emb_CAA60533_ (X86970) A5A4B3 subunit [Glycine soja]

Seq. No.	54480
Seq. ID	zpv700763045.h1
Method	BLASTX
NCBI GI	g3763928
BLAST score	205
E value	2.0e-16
Match length	86
% identity	45
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54481
Seq. ID	zpv700763067.h1
Method	BLASTX
NCBI GI	g99889
BLAST score	286
E value	5.0e-26
Match length	82
% identity	67
NCBI Description	beta-conglycinin alpha chain precursor - soybean

Seq. No.	54482
Seq. ID	zpv700763108.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	198
E value	1.0e-15
Match length	39
% identity	97
NCBI Description	Bean pod mottle virus

Seq. No.	54483
Seq. ID	zpv700763171.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	391
E value	2.0e-38
Match length	81
% identity	96
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54484
Seq. ID	zpv700763172.h1
Method	BLASTX
NCBI GI	g2317900
BLAST score	389
E value	4.0e-38
Match length	76
% identity	95
NCBI Description	(U89693) Sali3-2 [Glycine max]

Seq. No.	54485
Seq. ID	zpv700763196.h1
Method	BLASTX
NCBI GI	g2104908
BLAST score	176
E value	3.0e-13
Match length	57
% identity	56
NCBI Description	(Y07632) potassium channel [Zea mays]

Seq. No.	54486
Seq. ID	zpv700763237.h1
Method	BLASTX
NCBI GI	g138364

BLAST score	151
E value	5.0e-19
Match length	74
% identity	86
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54487
Seq. ID	zpv700763250.h1
Method	BLASTX
NCBI GI	g736002
BLAST score	177
E value	1.0e-27
Match length	86
% identity	77
NCBI Description	(X79467) A3B4 subunit [Glycine soja]

Seq. No.	54488
Seq. ID	zpv700763253.h1
Method	BLASTX
NCBI GI	g121276
BLAST score	225
E value	6.0e-24
Match length	57
% identity	87
NCBI Description	GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX SUBUNIT] >gi_99907_pir__S10851 glycinin G1 precursor - soybean >gi_255221_bbs_112930 glycinin G1 subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_ (X15121) glycinin subunit G1 [Glycine max] >gi_169973 (M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No.	54489
Seq. ID	zpv700763273.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	431
E value	5.0e-43
Match length	88
% identity	99
NCBI Description	Bean pod mottle virus

Seq. No.	54490
Seq. ID	zpv700763312.h1
Method	BLASTX
NCBI GI	g4097880
BLAST score	489
E value	9.0e-50
Match length	92
% identity	99
NCBI Description	(U70866) polyprotein [Bean pod mottle virus]

Seq. No.	54491
Seq. ID	zpv700763322.h1
Method	BLASTX

NCBI GI	g3236351
BLAST score	207
E value	1.0e-16
Match length	75
% identity	57
NCBI Description	(AF033663) PRP4 protein kinase homolog [Mus musculus]

Seq. No.	54492
Seq. ID	zpv700763351.h1
Method	BLASTX
NCBI GI	g4262240
BLAST score	320
E value	6.0e-30
Match length	76
% identity	41
NCBI Description	(AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No.	54493
Seq. ID	zpv700763371.h1
Method	BLASTX
NCBI GI	g2305020
BLAST score	411
E value	1.0e-40
Match length	88
% identity	89
NCBI Description	(AF005030) 2S albumin pre-propeptide [Glycine max] >gi_4097896 (U71195) napin-type 2S albumin 3 [Glycine max]

Seq. No.	54494
Seq. ID	zpv700763376.h1
Method	BLASTX
NCBI GI	g4544383
BLAST score	205
E value	2.0e-16
Match length	57
% identity	67
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54495
Seq. ID	zpv700763388.h1
Method	BLASTX
NCBI GI	g1942405
BLAST score	326
E value	1.0e-30
Match length	77
% identity	80
NCBI Description	Lipoxygenase-3(Soybean) Non-Heme Fe(Ii) Metalloprotein >gi_4388888_pdb_1BYT_ Lipoxygenase-3(Soybean) Complex With 4-Nitrocatechol >gi_1794172 (U50081) lipoxygenase-3 [Glycine max]

Seq. No.	54496
Seq. ID	zpv700763412.h1
Method	BLASTX
NCBI GI	g121277
BLAST score	372
E value	5.0e-36

Match length	72
% identity	97
NCBI Description	GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] >gi_99908_pir__S11002 glycinin G2 precursor - soybean >gi_255222_bbs_112931 glycinin G2 subunit [soybeans, Peptide, 485 aa] >gi_18637_emb_CAA33216_ (X15122) glycinin subunit G2 [Glycine max] >gi_218265_dbj_BAA00154_ (D00216) glycinin A2B1a subunit [Glycine max] >gi_295800_emb_CAA68460_ (Y00398) glycinin [Glycine max] >gi_225863_prf__1402179A glycinin A2B1a [Glycine max]

Seq. No.	54497
Seq. ID	zpv700763422.h1
Method	BLASTX
NCBI GI	g3420050
BLAST score	329
E value	5.0e-31
Match length	89
% identity	65
NCBI Description	(AC004680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54498
Seq. ID	zpv700763429.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	168
E value	4.0e-21
Match length	81
% identity	88
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54499
Seq. ID	zpv700763445.h1
Method	BLASTX
NCBI GI	g225651
BLAST score	229
E value	3.0e-19
Match length	45
% identity	98
NCBI Description	Glycinin A1aBx [Glycine max]

Seq. No.	54500
Seq. ID	zpv700763452.h1
Method	BLASTX
NCBI GI	g4249568
BLAST score	235
E value	6.0e-20
Match length	74
% identity	64
NCBI Description	(AB004062) glycinin [Glycine max]

Seq. No.	54501
Seq. ID	zpv700763517.h1

Method	BLASTX
NCBI GI	g3097321
BLAST score	260
E value	5.0e-23
Match length	78
% identity	67
NCBI Description	(AB013289) Bd 30K [Glycine max]

Seq. No.	54502
Seq. ID	zpv700763565.h1
Method	BLASTX
NCBI GI	g229708
BLAST score	451
E value	2.0e-45
Match length	82
% identity	98
NCBI Description	Bean pod mottle virus

Seq. No.	54503
Seq. ID	zpv700763628.h1
Method	BLASTX
NCBI GI	g2506470
BLAST score	195
E value	5.0e-30
Match length	91
% identity	78
NCBI Description	ALPHA-1,4 GLUCAN PHOSPHORYLASE, L ISOFORM PRECURSOR (STARCH PHOSPHORYLASE L) >gi_1616637_emb_CAA85354_ (Z36880) alpha-1,4 Glucan Phosphorylase, L isoform precursor [Vicia faba]

Seq. No.	54504
Seq. ID	zpv700763631.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	229
E value	1.0e-27
Match length	84
% identity	71
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54505
Seq. ID	zpv700763634.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	239
E value	3.0e-38
Match length	87
% identity	95
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54506
Seq. ID	zpv700763642.h1
Method	BLASTX
NCBI GI	g3982596
BLAST score	283
E value	8.0e-34
Match length	77
% identity	87
NCBI Description	(AF039027) cationic peroxidase 2 [Glycine max]

Seq. No.	54507
Seq. ID	zpv700763650.h1
Method	BLASTX
NCBI GI	g121276
BLAST score	254
E value	3.0e-22
Match length	80
% identity	72
NCBI Description	GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; GLYCININ BX SUBUNIT] >gi_99907_pir__S10851 glycinin G1 precursor - soybean >gi_255221_bbs_112930 glycinin G1 subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_ (X15121) glycinin subunit G1 [Glycine max] >gi_169973 (M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No.	54508
Seq. ID	zpv700763670.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	214
E value	2.0e-17
Match length	88
% identity	35
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54509
Seq. ID	zpv700763685.h1
Method	BLASTX
NCBI GI	g138364
BLAST score	278
E value	1.0e-27
Match length	80
% identity	91
NCBI Description	GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No.	54510
Seq. ID	zpv700763686.h1
Method	BLASTX
NCBI GI	g124033
BLAST score	287
E value	4.0e-26

Match length	56
% identity	88
NCBI Description	BOWMAN-BIRK TYPE PROTEINASE INHIBITOR D-II PRECURSOR (IV) >gi_99951_pir__S07941 proteinase inhibitor IV - soybean >gi_169947 (M20733) protease inhibitor IV [Glycine max]

Seq. No.	54511
Seq. ID	zsg701117318.h1
Method	BLASTN
NCBI GI	g1808591
BLAST score	69
E value	1.0e-30
Match length	157
% identity	86
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	54512
Seq. ID	zsg701117329.h1
Method	BLASTX
NCBI GI	g4510348
BLAST score	281
E value	3.0e-25
Match length	98
% identity	56
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	54513
Seq. ID	zsg701117419.h1
Method	BLASTX
NCBI GI	g1326161
BLAST score	221
E value	2.0e-18
Match length	62
% identity	81
NCBI Description	(U54703) dehydrin [Phaseolus vulgaris]

Seq. No.	54514
Seq. ID	zsg701117467.h1
Method	BLASTN
NCBI GI	g1399449
BLAST score	92
E value	2.0e-44
Match length	160
% identity	89
NCBI Description	Lupinus albus beta-tubulin 2 (TubB2) gene, complete cds

Seq. No.	54515
Seq. ID	zsg701117476.h1
Method	BLASTX
NCBI GI	g3513727
BLAST score	179
E value	2.0e-13
Match length	52
% identity	67
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis

thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	54516
Seq. ID	zsg701117492.h1
Method	BLASTN
NCBI GI	g296408
BLAST score	235
E value	1.0e-129
Match length	267
% identity	97
NCBI Description	G.max ADR12 mRNA

Seq. No.	54517
Seq. ID	zsg701117603.h1
Method	BLASTX
NCBI GI	g4455181
BLAST score	239
E value	2.0e-20
Match length	70
% identity	70
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	54518
Seq. ID	zsg701117609.h1
Method	BLASTN
NCBI GI	g2264316
BLAST score	53
E value	4.0e-21
Match length	109
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	54519
Seq. ID	zsg701117612.h1
Method	BLASTX
NCBI GI	g541943
BLAST score	269
E value	5.0e-25
Match length	71
% identity	80
NCBI Description	metallothionein - soybean >gi_228682_prf__1808316A metallothionein-like protein [Glycine max]

Seq. No.	54520
Seq. ID	zsg701117625.h1
Method	BLASTX
NCBI GI	g4544464
BLAST score	306
E value	3.0e-28
Match length	90
% identity	68
NCBI Description	(AC006580) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	54521

Seq. ID	zsg701117634.h1
Method	BLASTN
NCBI GI	g1421750
BLAST score	35
E value	2.0e-10
Match length	55
% identity	91
NCBI Description	Pisum sativum S-adenosylmethionine decarboxylase mRNA, complete cds

Seq. No.	54522
Seq. ID	zsg701117713.h2
Method	BLASTX
NCBI GI	g1710551
BLAST score	141
E value	3.0e-09
Match length	36
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_ (X95458) ribosomal protein L39 [Zea mays]

Seq. No.	54523
Seq. ID	zsg701117746.h2
Method	BLASTX
NCBI GI	g3738297
BLAST score	162
E value	1.0e-24
Match length	79
% identity	16
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	54524
Seq. ID	zsg701117748.h2
Method	BLASTX
NCBI GI	g2244771
BLAST score	348
E value	3.0e-33
Match length	82
% identity	80
NCBI Description	(Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No.	54525
Seq. ID	zsg701117785.h2
Method	BLASTX
NCBI GI	g4455255
BLAST score	296
E value	3.0e-27
Match length	77
% identity	73
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	54526
Seq. ID	zsg701117846.h2
Method	BLASTN
NCBI GI	g1778822
BLAST score	47
E value	1.0e-17

Match length	79
% identity	90
NCBI Description	Glycine max early light-induced protein (ELIP) mRNA, complete cds

Seq. No.	54527
Seq. ID	zsg701117902.h2
Method	BLASTX
NCBI GI	g3928083
BLAST score	172
E value	1.0e-12
Match length	28
% identity	96
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	54528
Seq. ID	zsg701117917.h2
Method	BLASTN
NCBI GI	g849135
BLAST score	129
E value	2.0e-66
Match length	201
% identity	92
NCBI Description	Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete cds

Seq. No.	54529
Seq. ID	zsg701117929.h2
Method	BLASTX
NCBI GI	g3776567
BLAST score	229
E value	3.0e-19
Match length	85
% identity	59
NCBI Description	(AC005388) Strong similarity to F21B7.33 gi_2809264 from A. thaliana BAC gb_AC002560. EST gb_N65119 comes from this gene. [Arabidopsis thaliana]

Seq. No.	54530
Seq. ID	zsg701117952.h2
Method	BLASTX
NCBI GI	g3249105
BLAST score	408
E value	3.0e-40
Match length	82
% identity	90
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	54531
Seq. ID	zsg701117958.h2
Method	BLASTX
NCBI GI	g4455169
BLAST score	217
E value	7.0e-18
Match length	84
% identity	50

NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	54532
Seq. ID	zsg701117969.h2
Method	BLASTN
NCBI GI	g927504
BLAST score	66
E value	6.0e-29
Match length	170
% identity	85
NCBI Description	P.sativum mRNA for fructose-1, 6-biphosphate aldolase (clone aldcyt2)

Seq. No.	54533
Seq. ID	zsg701118037.h2
Method	BLASTX
NCBI GI	g4490704
BLAST score	257
E value	1.0e-22
Match length	75
% identity	64
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	54534
Seq. ID	zsg701118134.h1
Method	BLASTX
NCBI GI	g3152619
BLAST score	173
E value	6.0e-13
Match length	54
% identity	59
NCBI Description	(AC004482) putative (s)-acetone-cyanohydrin lyase ((s)-hydroxynitrilase), 3'partial [Arabidopsis thaliana]

Seq. No.	54535
Seq. ID	zsg701118146.h1
Method	BLASTX
NCBI GI	g4056495
BLAST score	153
E value	2.0e-10
Match length	88
% identity	47
NCBI Description	(AC005896) putative TKRP125 [Arabidopsis thaliana]

Seq. No.	54536
Seq. ID	zsg701118167.h1
Method	BLASTN
NCBI GI	g2687434
BLAST score	98
E value	4.0e-48
Match length	174
% identity	91
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	54537

Seq. ID	zsg701118335.h1
Method	BLASTX
NCBI GI	g2494165
BLAST score	338
E value	5.0e-32
Match length	92
% identity	71
NCBI Description	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No.	54538
Seq. ID	zsg701118337.h1
Method	BLASTX
NCBI GI	g3687239
BLAST score	256
E value	2.0e-22
Match length	63
% identity	90
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	54539
Seq. ID	zsg701118381.h1
Method	BLASTX
NCBI GI	g4455033
BLAST score	200
E value	7.0e-16
Match length	86
% identity	47
NCBI Description	(AF116237) pseudouridine synthase 1 [Mus musculus]

Seq. No.	54540
Seq. ID	zsg701118405.h1
Method	BLASTX
NCBI GI	g836954
BLAST score	149
E value	9.0e-16
Match length	81
% identity	52
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]

Seq. No.	54541
Seq. ID	zsg701118484.h1
Method	BLASTN
NCBI GI	g19497
BLAST score	49
E value	1.0e-18
Match length	89
% identity	89
NCBI Description	L.polyphyllus pPLB07 mRNA

Seq. No.	54542
Seq. ID	zsg701118501.h1
Method	BLASTX
NCBI GI	g2245131

BLAST score	151
E value	5.0e-10
Match length	91
% identity	52
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54543
Seq. ID	zsg701118503.h1
Method	BLASTN
NCBI GI	g3985957
BLAST score	37
E value	2.0e-11
Match length	57
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	54544
Seq. ID	zsg701118509.h1
Method	BLASTN
NCBI GI	g2264307
BLAST score	40
E value	3.0e-13
Match length	91
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	54545
Seq. ID	zsg701118551.h1
Method	BLASTN
NCBI GI	g3175989
BLAST score	83
E value	6.0e-39
Match length	243
% identity	89
NCBI Description	Cicer arietinum mRNA for GDP dissociation inhibitor (gdi)

Seq. No.	54546
Seq. ID	zsg701118560.h1
Method	BLASTX
NCBI GI	g2980790
BLAST score	168
E value	5.0e-12
Match length	64
% identity	48
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54547
Seq. ID	zsg701118562.h1
Method	BLASTX
NCBI GI	g2853078
BLAST score	149
E value	6.0e-10
Match length	47
% identity	53
NCBI Description	(AL021768) TMV resistance protein N-like [Arabidopsis

thaliana]

Seq. No.	54548
Seq. ID	zsg701118576.h1
Method	BLASTX
NCBI GI	g3924602
BLAST score	251
E value	7.0e-22
Match length	88
% identity	57
NCBI Description	(AF069442) predicted OR23 protein of unknown function [Arabidopsis thaliana]

Seq. No.	54549
Seq. ID	zsg701118589.h1
Method	BLASTN
NCBI GI	g3204133
BLAST score	33
E value	4.0e-09
Match length	101
% identity	88
NCBI Description	Cicer arietinum mRNA for beta-galactosidase, partial

Seq. No.	54550
Seq. ID	zsg701118592.h1
Method	BLASTX
NCBI GI	g4538992
BLAST score	212
E value	3.0e-17
Match length	79
% identity	58
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	54551
Seq. ID	zsg701118596.h1
Method	BLASTX
NCBI GI	g3068704
BLAST score	415
E value	5.0e-41
Match length	94
% identity	44
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	54552
Seq. ID	zsg701118608.h1
Method	BLASTX
NCBI GI	g4406764
BLAST score	164
E value	5.0e-18
Match length	70
% identity	73
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	54553
Seq. ID	zsg701118680.h1
Method	BLASTN

NCBI GI	g169980
BLAST score	105
E value	4.0e-52
Match length	200
% identity	89
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	54554
Seq. ID	zsg701118693.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	47
E value	1.0e-17
Match length	142
% identity	84
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	54555
Seq. ID	zsg701118737.h1
Method	BLASTX
NCBI GI	g460932
BLAST score	151
E value	4.0e-10
Match length	80
% identity	39
NCBI Description	(U07157) ISRE-binding protein [Mus musculus]

Seq. No.	54556
Seq. ID	zsg701118764.h1
Method	BLASTN
NCBI GI	g21012
BLAST score	79
E value	1.0e-36
Match length	137
% identity	95
NCBI Description	Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase (GS,EC 6.3.1.2)

Seq. No.	54557
Seq. ID	zsg701118792.h1
Method	BLASTX
NCBI GI	g629528
BLAST score	267
E value	9.0e-24
Match length	76
% identity	68
NCBI Description	hypothetical protein - Arabidopsis thaliana >gi_1076335_pir__S51580 hypothetical protein 1 - Arabidopsis thaliana >gi_499167_emb_CAA56144_ (X79707) ORF [Arabidopsis thaliana]

Seq. No.	54558
Seq. ID	zsg701118793.h1
Method	BLASTX
NCBI GI	g4539401
BLAST score	298

E value	2.0e-27
Match length	79
% identity	80
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	54559
Seq. ID	zsg701118826.h1
Method	BLASTX
NCBI GI	g100226
BLAST score	105
E value	9.0e-11
Match length	58
% identity	64
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	54560
Seq. ID	zsg701118832.h1
Method	BLASTX
NCBI GI	g3549639
BLAST score	246
E value	3.0e-21
Match length	57
% identity	84
NCBI Description	(AJ005194) receiver-like protein 3 [Arabidopsis thaliana]

Seq. No.	54561
Seq. ID	zsg701118848.h1
Method	BLASTX
NCBI GI	g1808692
BLAST score	92
E value	4.0e-09
Match length	46
% identity	57
NCBI Description	(Y10786) hypothetical protein [Sporobolus stapfianus]

Seq. No.	54562
Seq. ID	zsg701118866.h1
Method	BLASTX
NCBI GI	g2493910
BLAST score	321
E value	4.0e-30
Match length	88
% identity	65
NCBI Description	CULLIN HOMOLOG 4B (CUL-4B) >gi_1381150 (U58091) Hs-CUL-4B [Homo sapiens]

Seq. No.	54563
Seq. ID	zsg701118871.h1
Method	BLASTX
NCBI GI	g423902
BLAST score	209
E value	5.0e-17
Match length	70
% identity	51

NCBI Description	luciferase - southern Russian firefly >gi_409317_bbs_133113 (S61961) luciferase [Luciola mingrelica=East European fireflies, Peptide, 548 aa] [Luciola mingrelica]

Seq. No.	54564
Seq. ID	zsg701118915.h1
Method	BLASTX
NCBI GI	g3033391
BLAST score	332
E value	3.0e-31
Match length	80
% identity	72
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	54565
Seq. ID	zsg701118955.h1
Method	BLASTN
NCBI GI	g402752
BLAST score	116
E value	9.0e-59
Match length	144
% identity	95
NCBI Description	G.max gene fusA

Seq. No.	54566
Seq. ID	zsg701118965.h1
Method	BLASTX
NCBI GI	g3056594
BLAST score	224
E value	1.0e-18
Match length	93
% identity	47
NCBI Description	(AC004255) T1F9.15 [Arabidopsis thaliana]

Seq. No.	54567
Seq. ID	zsg701119051.h1
Method	BLASTX
NCBI GI	g2653885
BLAST score	337
E value	5.0e-32
Match length	83
% identity	75
NCBI Description	(AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis thaliana]

Seq. No.	54568
Seq. ID	zsg701119062.h1
Method	BLASTX
NCBI GI	g2129651
BLAST score	345
E value	6.0e-33
Match length	82
% identity	78
NCBI Description	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis thaliana]

Seq. No.	54569
Seq. ID	zsg701119077.h1
Method	BLASTX
NCBI GI	g1084336
BLAST score	182
E value	7.0e-14
Match length	40
% identity	82
NCBI Description	chlorophyll a/b-binding protein type II - Arabidopsis thaliana >gi_541565 (U03395) PSI type II chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	54570
Seq. ID	zsg701119114.h1
Method	BLASTN
NCBI GI	g1813328
BLAST score	52
E value	2.0e-20
Match length	128
% identity	89
NCBI Description	Canavalia gladiata mRNA for HMG-1, complete cds

Seq. No.	54571
Seq. ID	zsg701119125.h1
Method	BLASTN
NCBI GI	g313723
BLAST score	43
E value	4.0e-15
Match length	91
% identity	87
NCBI Description	P.sativum hemC mRNA for hydroxymethylbilane synthase

Seq. No.	54572
Seq. ID	zsg701119212.h1
Method	BLASTX
NCBI GI	g2341042
BLAST score	178
E value	2.0e-13
Match length	90
% identity	46
NCBI Description	(AC000104) F19P19.26 [Arabidopsis thaliana]

Seq. No.	54573
Seq. ID	zsg701119253.h1
Method	BLASTX
NCBI GI	g3242710
BLAST score	213
E value	2.0e-17
Match length	90
% identity	48
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54574
Seq. ID	zsg701119261.h1
Method	BLASTX
NCBI GI	g1237250

BLAST score 188
E value 2.0e-14
Match length 83
% identity 68
NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No. 54575
Seq. ID zsg701119276.h1
Method BLASTX
NCBI GI g2618704
BLAST score 364
E value 4.0e-35
Match length 83
% identity 80
NCBI Description (AC002510) putative thioredoxin reductase [Arabidopsis thaliana]

Seq. No. 54576
Seq. ID zsg701119314.h1
Method BLASTX
NCBI GI g1354849
BLAST score 218
E value 6.0e-18
Match length 93
% identity 47
NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No. 54577
Seq. ID zsg701119318.h1
Method BLASTN
NCBI GI g170067
BLAST score 110
E value 5.0e-55
Match length 110
% identity 100
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3) gene, complete cds

Seq. No. 54578
Seq. ID zsg701119333.h1
Method BLASTX
NCBI GI g2961384
BLAST score 304
E value 2.0e-29
Match length 92
% identity 74
NCBI Description (AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No. 54579
Seq. ID zsg701119418.h1
Method BLASTN
NCBI GI g1438878
BLAST score 145
E value 5.0e-76
Match length 169
% identity 97

NCBI Description	Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No.	54580
Seq. ID	zsg701119548.h1
Method	BLASTN
NCBI GI	g3219360
BLAST score	56
E value	4.0e-23
Match length	110
% identity	92
NCBI Description	Glycine max biotin carboxylase precursor (accC-3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	54581
Seq. ID	zsg701119567.h1
Method	BLASTX
NCBI GI	g2494144
BLAST score	167
E value	4.0e-12
Match length	72
% identity	28
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	54582
Seq. ID	zsg701119607.h1
Method	BLASTX
NCBI GI	g4469020
BLAST score	261
E value	5.0e-23
Match length	63
% identity	75
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	54583
Seq. ID	zsg701119621.h1
Method	BLASTN
NCBI GI	g20892
BLAST score	56
E value	4.0e-23
Match length	124
% identity	87
NCBI Description	Pea U2 snRNA (clone pPSU2.1)

Seq. No.	54584
Seq. ID	zsg701119626.h1
Method	BLASTX
NCBI GI	g3426039
BLAST score	141
E value	5.0e-09
Match length	78
% identity	44
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	54585
Seq. ID	zsg701119655.h1

Method	BLASTN
NCBI GI	g287563
BLAST score	33
E value	4.0e-09
Match length	37
% identity	97
NCBI Description	Vigna radiata arg2 mRNA

Seq. No.	54586
Seq. ID	zsg701119656.h1
Method	BLASTX
NCBI GI	g1076634
BLAST score	183
E value	6.0e-14
Match length	60
% identity	55
NCBI Description	protein-serine/threonine kinase NPK15 - common tobacco >gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine kinase [Nicotiana tabacum]

Seq. No.	54587
Seq. ID	zsg701119774.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	74
E value	1.0e-33
Match length	128
% identity	90
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	54588
Seq. ID	zsg701119780.h1
Method	BLASTX
NCBI GI	g2183221
BLAST score	143
E value	2.0e-09
Match length	30
% identity	73
NCBI Description	(AF001954) p33ING1 [Homo sapiens]

Seq. No.	54589
Seq. ID	zsg701119788.h1
Method	BLASTX
NCBI GI	g3928862
BLAST score	142
E value	2.0e-09
Match length	63
% identity	38
NCBI Description	(AF089710) disease resistance protein RPP8 [Arabidopsis thaliana]

Seq. No.	54590
Seq. ID	zsg701119807.h1
Method	BLASTN
NCBI GI	g2052028
BLAST score	70

E value	3.0e-31
Match length	74
% identity	99
NCBI Description	G.max mRNA for glutathione transferase

Seq. No.	54591
Seq. ID	zsg701119822.h1
Method	BLASTX
NCBI GI	g2347189
BLAST score	259
E value	8.0e-23
Match length	53
% identity	89
NCBI Description	(AC002338) hypothetical protein [Arabidopsis thaliana] >gi_3150399 (AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54592
Seq. ID	zsg701119834.h1
Method	BLASTX
NCBI GI	g4432814
BLAST score	152
E value	3.0e-10
Match length	42
% identity	64
NCBI Description	(AC006593) unknown protein [Arabidopsis thaliana]

Seq. No.	54593
Seq. ID	zsg701119863.h1
Method	BLASTX
NCBI GI	g3024871
BLAST score	215
E value	1.0e-17
Match length	86
% identity	50
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	54594
Seq. ID	zsg701119893.h1
Method	BLASTX
NCBI GI	g4115371
BLAST score	171
E value	1.0e-12
Match length	89
% identity	47
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	54595
Seq. ID	zsg701119923.h1
Method	BLASTX
NCBI GI	g1658197
BLAST score	138
E value	1.0e-08
Match length	80
% identity	41

NCBI Description	(U74630) calreticulin [Ricinus communis] >gi_1763297 (U74631) calreticulin [Ricinus communis]

Seq. No.	54596
Seq. ID	zsg701119927.h1
Method	BLASTX
NCBI GI	g4309760
BLAST score	158
E value	5.0e-11
Match length	58
% identity	66
NCBI Description	(AC006217) unknown protein [Arabidopsis thaliana]

Seq. No.	54597
Seq. ID	zsg701119934.h1
Method	BLASTX
NCBI GI	g3540178
BLAST score	338
E value	4.0e-32
Match length	88
% identity	75
NCBI Description	(AC004122) calcium-transporting ATPase [Arabidopsis thaliana]

Seq. No.	54598
Seq. ID	zsg701120030.h1
Method	BLASTX
NCBI GI	g400790
BLAST score	172
E value	2.0e-12
Match length	63
% identity	52
NCBI Description	GLYCOGEN PHOSPHORYLASE 1 (GP1) >gi_478597_pir__S20595 glycogen phosphorylase (EC 2.4.1.1) 1 - slime mold (Dictyostelium discoideum)

Seq. No.	54599
Seq. ID	zsg701120054.h1
Method	BLASTX
NCBI GI	g3790441
BLAST score	112
E value	1.0e-11
Match length	74
% identity	57
NCBI Description	(AF030515) chaperonin 60 alpha subunit [Canavalia lineata]

Seq. No.	54600
Seq. ID	zsg701120105.h1
Method	BLASTX
NCBI GI	g2827516
BLAST score	239
E value	2.0e-20
Match length	91
% identity	55
NCBI Description	(AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana]

Seq. No.	54601
Seq. ID	zsg701120130.h1
Method	BLASTN
NCBI GI	g3378649
BLAST score	93
E value	6.0e-45
Match length	193
% identity	87
NCBI Description	M.sativa mRNA translated from abscisic activated gene

Seq. No.	54602
Seq. ID	zsg701120178.h1
Method	BLASTX
NCBI GI	g3046696
BLAST score	210
E value	2.0e-17
Match length	59
% identity	71
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	54603
Seq. ID	zsg701120238.h1
Method	BLASTX
NCBI GI	g2979547
BLAST score	216
E value	9.0e-18
Match length	87
% identity	51
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	54604
Seq. ID	zsg701120246.h1
Method	BLASTX
NCBI GI	g2576255
BLAST score	203
E value	3.0e-16
Match length	62
% identity	63
NCBI Description	(AJ001729) TH65 protein [Arabidopsis thaliana]

Seq. No.	54605
Seq. ID	zsg701120252.h1
Method	BLASTN
NCBI GI	g2304954
BLAST score	264
E value	1.0e-147
Match length	272
% identity	99
NCBI Description	Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No.	54606
Seq. ID	zsg701120263.h1
Method	BLASTX
NCBI GI	g2496731
BLAST score	199
E value	1.0e-15

Match length	74
% identity	57
NCBI Description	HYPOTHETICAL 30.2 KD PROTEIN Y4OV >gi_2182566 (AE000089) Y4oV [Rhizobium sp. NGR234]

Seq. No.	54607
Seq. ID	zsg701120288.h1
Method	BLASTX
NCBI GI	g3033386
BLAST score	175
E value	6.0e-13
Match length	83
% identity	43
NCBI Description	(AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No.	54608
Seq. ID	zsg701120318.h1
Method	BLASTN
NCBI GI	g170091
BLAST score	72
E value	1.0e-32
Match length	120
% identity	90
NCBI Description	Glycine max vegetative storage protein (vspB) gene, complete cds

Seq. No.	54609
Seq. ID	zsg701120356.h1
Method	BLASTX
NCBI GI	g2088658
BLAST score	192
E value	6.0e-15
Match length	57
% identity	65
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	54610
Seq. ID	zsg701120358.h1
Method	BLASTX
NCBI GI	g4510398
BLAST score	147
E value	1.0e-09
Match length	27
% identity	93
NCBI Description	(AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54611
Seq. ID	zsg701120371.h1
Method	BLASTX
NCBI GI	g3738325
BLAST score	381
E value	4.0e-37
Match length	88
% identity	82
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No.	54612
Seq. ID	zsg701120408.h1
Method	BLASTX
NCBI GI	g3916230
BLAST score	152
E value	3.0e-10
Match length	59
% identity	54
NCBI Description	(AF073883) myotubularin related protein 2 [Danio rerio]

Seq. No.	54613
Seq. ID	zsg701120419.h1
Method	BLASTX
NCBI GI	g4376203
BLAST score	197
E value	2.0e-15
Match length	88
% identity	39
NCBI Description	(U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]

Seq. No.	54614
Seq. ID	zsg701120443.h1
Method	BLASTX
NCBI GI	g4455356
BLAST score	292
E value	1.0e-26
Match length	84
% identity	73
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	54615
Seq. ID	zsg701120514.h1
Method	BLASTN
NCBI GI	g169922
BLAST score	43
E value	4.0e-15
Match length	43
% identity	100
NCBI Description	Soybean beta-1,3-endoglucanase mRNA, complete cds

Seq. No.	54616
Seq. ID	zsg701120519.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	243
E value	1.0e-134
Match length	271
% identity	99
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	54617
Seq. ID	zsg701120540.h1
Method	BLASTX
NCBI GI	g2462837
BLAST score	240

E value	1.0e-20
Match length	61
% identity	79
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54618
Seq. ID	zsg701120593.h1
Method	BLASTX
NCBI GI	g267069
BLAST score	185
E value	3.0e-14
Match length	50
% identity	66
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	54619
Seq. ID	zsg701120613.h1
Method	BLASTX
NCBI GI	g4417287
BLAST score	313
E value	4.0e-29
Match length	93
% identity	62
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	54620
Seq. ID	zsg701120619.h1
Method	BLASTX
NCBI GI	g2829887
BLAST score	299
E value	2.0e-27
Match length	94
% identity	64
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	54621
Seq. ID	zsg701120626.h1
Method	BLASTX
NCBI GI	g3540206
BLAST score	398
E value	5.0e-39
Match length	93
% identity	72
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	54622
Seq. ID	zsg701120642.h1
Method	BLASTN
NCBI GI	g303838
BLAST score	34
E value	1.0e-09
Match length	38
% identity	97
NCBI Description	Rice mRNA for 40S subunit ribosomal protein, complete cds

Seq. No.	54623
Seq. ID	zsg701120684.h1
Method	BLASTX
NCBI GI	g3461813
BLAST score	213
E value	2.0e-17
Match length	80
% identity	60
NCBI Description	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]

Seq. No.	54624
Seq. ID	zsg701120712.h1
Method	BLASTX
NCBI GI	g2244806
BLAST score	200
E value	2.0e-16
Match length	79
% identity	59
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54625
Seq. ID	zsg701120736.h1
Method	BLASTN
NCBI GI	g530086
BLAST score	68
E value	2.0e-30
Match length	75
% identity	99
NCBI Description	Glycine max aminoalcoholphosphotransferase (AAPT1) mRNA, complete cds

Seq. No.	54626
Seq. ID	zsg701120778.h1
Method	BLASTN
NCBI GI	g2104674
BLAST score	59
E value	1.0e-24
Match length	123
% identity	87
NCBI Description	V.faba mRNA for transcription factor containing bZIP

Seq. No.	54627
Seq. ID	zsg701120785.h1
Method	BLASTN
NCBI GI	g170059
BLAST score	53
E value	2.0e-21
Match length	105
% identity	88
NCBI Description	Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete cds

Seq. No.	54628
Seq. ID	zsg701120786.h1
Method	BLASTX

NCBI GI	g3421104
BLAST score	202
E value	6.0e-23
Match length	70
% identity	81
NCBI Description	(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]

Seq. No.	54629
Seq. ID	zsg701120821.h1
Method	BLASTX
NCBI GI	g3789911
BLAST score	145
E value	1.0e-09
Match length	55
% identity	51
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No.	54630
Seq. ID	zsg701120847.h1
Method	BLASTX
NCBI GI	g3004563
BLAST score	223
E value	2.0e-18
Match length	67
% identity	61
NCBI Description	(AC003673) similar to APG (non proline-rich region) [Arabidopsis thaliana] >gi_3176703 (AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	54631
Seq. ID	zsg701120851.h1
Method	BLASTX
NCBI GI	g2829895
BLAST score	152
E value	3.0e-10
Match length	39
% identity	77
NCBI Description	(AC002311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54632
Seq. ID	zsg701120878.h1
Method	BLASTX
NCBI GI	g1351271
BLAST score	154
E value	2.0e-10
Match length	50
% identity	64
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	54633
Seq. ID	zsg701120885.h1

Method	BLASTX
NCBI GI	g3135251
BLAST score	288
E value	4.0e-26
Match length	94
% identity	59
NCBI Description	(AC003058) putative receptor protein kinase [Arabidopsis thaliana] >gi_3176719 (AC002392) putative protein kinase [Arabidopsis thaliana]

Seq. No.	54634
Seq. ID	zsg701120965.h1
Method	BLASTX
NCBI GI	g4468984
BLAST score	229
E value	3.0e-19
Match length	89
% identity	46
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	54635
Seq. ID	zsg701120991.h1
Method	BLASTX
NCBI GI	g2181190
BLAST score	145
E value	2.0e-09
Match length	80
% identity	39
NCBI Description	(Y12531) serine/threonine kinase [Brassica oleracea]

Seq. No.	54636
Seq. ID	zsg701121009.h1
Method	BLASTX
NCBI GI	g2980806
BLAST score	196
E value	2.0e-15
Match length	42
% identity	83
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	54637
Seq. ID	zsg701121031.h1
Method	BLASTN
NCBI GI	g2687434
BLAST score	59
E value	1.0e-24
Match length	124
% identity	91
NCBI Description	Eucryphia lucida large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	54638
Seq. ID	zsg701121039.h1
Method	BLASTX
NCBI GI	g2624328
BLAST score	167
E value	5.0e-12

Match length	74
% identity	46
NCBI Description	(AJ002894) OsGRP2 [Oryza sativa]

Seq. No.	54639
Seq. ID	zsg701121087.h1
Method	BLASTX
NCBI GI	g4139230
BLAST score	355
E value	4.0e-34
Match length	88
% identity	81
NCBI Description	(AF109243) mismatch repair protein [Arabidopsis thaliana]

Seq. No.	54640
Seq. ID	zsg701121104.h1
Method	BLASTN
NCBI GI	g3702734
BLAST score	38
E value	4.0e-12
Match length	70
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	54641
Seq. ID	zsg701121147.h1
Method	BLASTX
NCBI GI	g4160298
BLAST score	125
E value	2.0e-15
Match length	63
% identity	75
NCBI Description	(AJ011892) cyclin D2.1 protein [Nicotiana tabacum]

Seq. No.	54642
Seq. ID	zsg701121160.h1
Method	BLASTN
NCBI GI	g256142
BLAST score	190
E value	1.0e-103
Match length	265
% identity	93
NCBI Description	cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No.	54643
Seq. ID	zsg701121174.h1
Method	BLASTX
NCBI GI	g541943
BLAST score	272
E value	3.0e-24
Match length	53
% identity	91
NCBI Description	metallothionein - soybean >gi_228682_prf__1808316A metallothionein-like protein [Glycine max]

Seq. No.	54644
Seq. ID	zsg701121226.h1
Method	BLASTX
NCBI GI	g2244826
BLAST score	154
E value	3.0e-15
Match length	60
% identity	77
NCBI Description	(Z97336) replication control protein homolog [Arabidopsis thaliana]

Seq. No.	54645
Seq. ID	zsg701121259.h1
Method	BLASTX
NCBI GI	g2369766
BLAST score	242
E value	4.0e-21
Match length	66
% identity	70
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	54646
Seq. ID	zsg701121265.h1
Method	BLASTN
NCBI GI	g2746231
BLAST score	35
E value	3.0e-10
Match length	75
% identity	87
NCBI Description	Gossypium hirsutum glutathione peroxidase mRNA, partial cds

Seq. No.	54647
Seq. ID	zsg701121276.h1
Method	BLASTX
NCBI GI	g2911077
BLAST score	204
E value	2.0e-16
Match length	66
% identity	56
NCBI Description	(AL021960) gibberellin 20-oxidase - like protein [Arabidopsis thaliana]

Seq. No.	54648
Seq. ID	zsg701121281.h1
Method	BLASTX
NCBI GI	g2462758
BLAST score	148
E value	9.0e-10
Match length	35
% identity	80
NCBI Description	(AC002292) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	54649
Seq. ID	zsg701121304.h1
Method	BLASTX
NCBI GI	g3551960

BLAST score	337
E value	7.0e-32
Match length	96
% identity	70
NCBI Description	(AF082033) senescence-associated protein 15 [Hemerocallis hybrid cultivar]

Seq. No.	54650
Seq. ID	zsg701121308.h1
Method	BLASTX
NCBI GI	g2980789
BLAST score	166
E value	3.0e-19
Match length	94
% identity	55
NCBI Description	(AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54651
Seq. ID	zsg701121429.h1
Method	BLASTX
NCBI GI	g2981439
BLAST score	179
E value	1.0e-13
Match length	86
% identity	44
NCBI Description	(AF051853) t-SNARE SED5 [Arabidopsis thaliana]

Seq. No.	54652
Seq. ID	zsg701121493.h1
Method	BLASTX
NCBI GI	g3548802
BLAST score	323
E value	3.0e-30
Match length	85
% identity	80
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	54653
Seq. ID	zsg701121511.h1
Method	BLASTX
NCBI GI	g266731
BLAST score	257
E value	2.0e-22
Match length	66
% identity	76
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303 phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea >gi_217980_dbj_BAA00885_ (D10001) phenylalanine ammonia-lyase [Pisum sativum] >gi_217982_dbj_BAA00886_ (D10002) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No.	54654
Seq. ID	zsg701121513.h1
Method	BLASTX
NCBI GI	g3378650

BLAST score	260
E value	6.0e-23
Match length	75
% identity	72
NCBI Description	(X97606) abscisic acid activated [Medicago sativa]

Seq. No.	54655
Seq. ID	zsg701121545.h1
Method	BLASTX
NCBI GI	g3641845
BLAST score	380
E value	5.0e-37
Match length	90
% identity	44
NCBI Description	(AJ223358) stelar K+ outward rectifying channel [Arabidopsis thaliana]

Seq. No.	54656
Seq. ID	zsg701121563.h1
Method	BLASTX
NCBI GI	g2980765
BLAST score	298
E value	2.0e-32
Match length	89
% identity	71
NCBI Description	(AL022198) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54657
Seq. ID	zsg701121605.h1
Method	BLASTX
NCBI GI	g3702340
BLAST score	190
E value	1.0e-14
Match length	75
% identity	49
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54658
Seq. ID	zsg701121617.h1
Method	BLASTX
NCBI GI	g2708752
BLAST score	290
E value	2.0e-26
Match length	92
% identity	65
NCBI Description	(AC003952) putative histidine kinase [Arabidopsis thaliana]

Seq. No.	54659
Seq. ID	zsg701121630.h1
Method	BLASTX
NCBI GI	g2244998
BLAST score	234
E value	7.0e-20
Match length	46
% identity	83
NCBI Description	(Z97341) similarity to probable transcriptional adaptor ADA2 [Arabidopsis thaliana]

Seq. No.	54660
Seq. ID	zsg701121679.h1
Method	BLASTX
NCBI GI	g4151321
BLAST score	309
E value	1.0e-28
Match length	84
% identity	75
NCBI Description	(AF089085) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]

Seq. No.	54661
Seq. ID	zsg701121732.h1
Method	BLASTN
NCBI GI	g310575
BLAST score	110
E value	3.0e-55
Match length	204
% identity	91
NCBI Description	Glycine max nodulin-26 mRNA, complete cds

Seq. No.	54662
Seq. ID	zsg701121769.h1
Method	BLASTX
NCBI GI	g3281858
BLAST score	171
E value	1.0e-12
Match length	63
% identity	60
NCBI Description	(AL031004) ribosomal protein S6 - like [Arabidopsis thaliana]

Seq. No.	54663
Seq. ID	zsg701121773.h1
Method	BLASTN
NCBI GI	g18761
BLAST score	172
E value	4.0e-92
Match length	196
% identity	96
NCBI Description	Soybean stem mRNA for 31 kD glycoprotein

Seq. No.	54664
Seq. ID	zsg701121803.h1
Method	BLASTN
NCBI GI	g479144
BLAST score	117
E value	1.0e-59
Match length	125
% identity	98
NCBI Description	G.max mRNA for ATP synthase subunit

Seq. No.	54665
Seq. ID	zsg701121816.h1
Method	BLASTX
NCBI GI	g3859659

BLAST score	141
E value	6.0e-09
Match length	82
% identity	41
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	54666
Seq. ID	zsg701121852.h1
Method	BLASTN
NCBI GI	g169980
BLAST score	81
E value	9.0e-38
Match length	212
% identity	84
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	54667
Seq. ID	zsg701121858.h1
Method	BLASTX
NCBI GI	g2444178
BLAST score	161
E value	1.0e-11
Match length	69
% identity	46
NCBI Description	(U94784) unconventional myosin [Helianthus annuus]

Seq. No.	54668
Seq. ID	zsg701121878.h1
Method	BLASTN
NCBI GI	g3158475
BLAST score	72
E value	2.0e-32
Match length	188
% identity	85
NCBI Description	Samanea saman aquaporin 2 (Aqp2) mRNA, complete cds

Seq. No.	54669
Seq. ID	zsg701122067.h1
Method	BLASTN
NCBI GI	g1370197
BLAST score	99
E value	1.0e-48
Match length	147
% identity	93
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAB8E

Seq. No.	54670
Seq. ID	zsg701122152.h1
Method	BLASTX
NCBI GI	g1706947
BLAST score	401
E value	2.0e-39
Match length	84
% identity	93
NCBI Description	(U43528) RAD51 homolog AtRad51 [Arabidopsis thaliana] >gi_1706949 (U43652) AtRAD51 [Arabidopsis thaliana]

>gi_2388778_emb_CAA04529_ (AJ001100) Rad51-like protein [Arabidopsis thaliana]

Seq. No.	54671
Seq. ID	zsg701122161.h1
Method	BLASTX
NCBI GI	g4490736
BLAST score	385
E value	1.0e-37
Match length	88
% identity	44
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	54672
Seq. ID	zsg701122248.h1
Method	BLASTX
NCBI GI	g4115931
BLAST score	286
E value	9.0e-35
Match length	85
% identity	85
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	54673
Seq. ID	zsg701122255.h1
Method	BLASTN
NCBI GI	g623585
BLAST score	36
E value	6.0e-11
Match length	68
% identity	88
NCBI Description	Nicotiana tabacum SR1 Nt-rab6 mRNA, complete cds

Seq. No.	54674
Seq. ID	zsg701122257.h1
Method	BLASTX
NCBI GI	g3292824
BLAST score	359
E value	1.0e-34
Match length	82
% identity	84
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	54675
Seq. ID	zsg701122290.h1
Method	BLASTX
NCBI GI	g4454567
BLAST score	203
E value	3.0e-16
Match length	68
% identity	54
NCBI Description	(AF128407) lipase homolog [Arabidopsis thaliana]

Seq. No.	54676
Seq. ID	zsg701122296.h1
Method	BLASTX

NCBI GI	g3395938
BLAST score	154
E value	9.0e-11
Match length	39
% identity	74
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	54677
Seq. ID	zsg701122328.h1
Method	BLASTN
NCBI GI	g1813328
BLAST score	38
E value	2.0e-12
Match length	174
% identity	86
NCBI Description	Canavalia gladiata mRNA for HMG-1, complete cds

Seq. No.	54678
Seq. ID	zsg701122358.h1
Method	BLASTX
NCBI GI	g466160
BLAST score	157
E value	8.0e-11
Match length	38
% identity	92
NCBI Description	HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No.	54679
Seq. ID	zsg701122513.h1
Method	BLASTX
NCBI GI	g2980767
BLAST score	282
E value	2.0e-25
Match length	91
% identity	60
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	54680
Seq. ID	zsg701122544.h1
Method	BLASTX
NCBI GI	g1698548
BLAST score	144
E value	1.0e-09
Match length	47
% identity	64
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	54681
Seq. ID	zsg701122562.h1
Method	BLASTX
NCBI GI	g2213602
BLAST score	168
E value	4.0e-12

Match length	88
% identity	49
NCBI Description	(AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No.	54682
Seq. ID	zsg701122637.h1
Method	BLASTX
NCBI GI	g4115388
BLAST score	237
E value	4.0e-20
Match length	76
% identity	57
NCBI Description	(AC005967) putative prolylcarboxypeptidase [Arabidopsis thaliana]

Seq. No.	54683
Seq. ID	zsg701122667.h1
Method	BLASTX
NCBI GI	g2435395
BLAST score	456
E value	7.0e-46
Match length	93
% identity	89
NCBI Description	(U63550) pectate lyase [Fragaria x ananassa]

Seq. No.	54684
Seq. ID	zsg701122681.h1
Method	BLASTN
NCBI GI	g2345147
BLAST score	66
E value	8.0e-29
Match length	170
% identity	91
NCBI Description	Pisum sativum developmentally regulated GTP binding protein (PsDRG1) mRNA, complete cds

Seq. No.	54685
Seq. ID	zsg701122715.h1
Method	BLASTX
NCBI GI	g3395440
BLAST score	151
E value	2.0e-10
Match length	40
% identity	60
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54686
Seq. ID	zsg701122726.h1
Method	BLASTX
NCBI GI	g4510395
BLAST score	302
E value	8.0e-28
Match length	67
% identity	78
NCBI Description	(AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

Seq. No.	54687
Seq. ID	zsg701122761.h1
Method	BLASTN
NCBI GI	g1381085
BLAST score	70
E value	3.0e-31
Match length	106
% identity	92
NCBI Description	Pisum sativum imidazoleglycerol-phosphate dehydratase (PSHIS3) mRNA, complete cds

Seq. No.	54688
Seq. ID	zsg701122770.h1
Method	BLASTX
NCBI GI	g4406769
BLAST score	160
E value	2.0e-19
Match length	77
% identity	75
NCBI Description	(AC006836) putative translin [Arabidopsis thaliana]

Seq. No.	54689
Seq. ID	zsg701122781.h1
Method	BLASTX
NCBI GI	g3355471
BLAST score	162
E value	2.0e-11
Match length	67
% identity	42
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	54690
Seq. ID	zsg701122826.h1
Method	BLASTN
NCBI GI	g857396
BLAST score	95
E value	4.0e-46
Match length	259
% identity	84
NCBI Description	Glycine max mRNA for mitotic cyclin a2-type, complete cds

Seq. No.	54691
Seq. ID	zsg701122841.h1
Method	BLASTN
NCBI GI	g1369847
BLAST score	34
E value	1.0e-09
Match length	34
% identity	100
NCBI Description	Mkilua fragrans 18S ribosomal RNA (18S rDNA) gene

Seq. No.	54692
Seq. ID	zsg701122896.h1
Method	BLASTX
NCBI GI	g1350742
BLAST score	170

E value	2.0e-12
Match length	41
% identity	68
NCBI Description	PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA yk64g1

Seq. No.	54693
Seq. ID	zsg701122934.h1
Method	BLASTX
NCBI GI	g3805851
BLAST score	217
E value	5.0e-20
Match length	75
% identity	67
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	54694
Seq. ID	zsg701122944.h1
Method	BLASTX
NCBI GI	g282873
BLAST score	334
E value	1.0e-31
Match length	90
% identity	69
NCBI Description	transforming protein (myb) homolog - Arabidopsis thaliana >gi_217859_dbj_BAA01730_ (D10936) ATMYB1 protein [Arabidopsis thaliana]

Seq. No.	54695
Seq. ID	zsg701122990.h1
Method	BLASTX
NCBI GI	g3152572
BLAST score	237
E value	3.0e-20
Match length	87
% identity	54
NCBI Description	(AC002986) Contains homology to DNAJ heatshock protein gb_U32803 from Haemophilus influenzae. [Arabidopsis thaliana]

Seq. No.	54696
Seq. ID	zsg701123044.h1
Method	BLASTX
NCBI GI	g1168518
BLAST score	353
E value	7.0e-34
Match length	84
% identity	79
NCBI Description	APURINIC ENDONUCLEASE-REDOX PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE) >gi_472869_emb_CAA54234_ (X76912) ARP protein [Arabidopsis thaliana]

Seq. No.	54697

Seq. ID	zsg701123055.h1
Method	BLASTX
NCBI GI	g3786025
BLAST score	228
E value	3.0e-19
Match length	78
% identity	60
NCBI Description	(AC005499) putative DNA-binding protein, 5' partial [Arabidopsis thaliana]

Seq. No.	54698
Seq. ID	zsg701123089.h1
Method	BLASTX
NCBI GI	g4263718
BLAST score	229
E value	2.0e-19
Match length	55
% identity	85
NCBI Description	(AC006223) putative DNA topoisomerase III beta [Arabidopsis thaliana]

Seq. No.	54699
Seq. ID	zsg701123152.h1
Method	BLASTX
NCBI GI	g1304599
BLAST score	208
E value	6.0e-17
Match length	77
% identity	48
NCBI Description	(U41315) ZNF127-Xp [Homo sapiens]

Seq. No.	54700
Seq. ID	zsg701123158.h1
Method	BLASTN
NCBI GI	g2213537
BLAST score	33
E value	3.0e-09
Match length	85
% identity	85
NCBI Description	P.sativum mRNA encoding DNA-binding protein PD2

Seq. No.	54701
Seq. ID	zsg701123183.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	64
E value	1.0e-27
Match length	156
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	54702
Seq. ID	zsg701123191.h1
Method	BLASTX
NCBI GI	g2384673

BLAST score	319
E value	6.0e-30
Match length	80
% identity	72
NCBI Description	(AF012658) putative potassium transporter AtKT3p [Arabidopsis thaliana]

Seq. No.	54703
Seq. ID	zsg701123245.h1
Method	BLASTX
NCBI GI	g2766740
BLAST score	230
E value	2.0e-19
Match length	61
% identity	64
NCBI Description	(AF039487) beta-glucosidase [Thermotoga neapolitana]

Seq. No.	54704
Seq. ID	zsg701123249.h1
Method	BLASTN
NCBI GI	g288187
BLAST score	80
E value	3.0e-37
Match length	96
% identity	96
NCBI Description	V.unguiculata cysteine proteinase inhibitor mRNA

Seq. No.	54705
Seq. ID	zsg701123265.h1
Method	BLASTN
NCBI GI	g343348
BLAST score	81
E value	9.0e-38
Match length	138
% identity	88
NCBI Description	Glycine max mitochondrial DNA sequence, transcription initiation motif

Seq. No.	54706
Seq. ID	zsg701123276.h1
Method	BLASTX
NCBI GI	g3337361
BLAST score	186
E value	3.0e-14
Match length	59
% identity	54
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	54707
Seq. ID	zsg701123296.h1
Method	BLASTX
NCBI GI	g3298498
BLAST score	225
E value	9.0e-19
Match length	68
% identity	59
NCBI Description	(AB013301) ethylene responsive element binding factor

[Arabidopsis thaliana]

Seq. No.	54708
Seq. ID	zsg701123313.h1
Method	BLASTX
NCBI GI	g4006829
BLAST score	186
E value	3.0e-14
Match length	69
% identity	52
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	54709
Seq. ID	zsg701123317.h1
Method	BLASTN
NCBI GI	g3869087
BLAST score	144
E value	2.0e-75
Match length	204
% identity	93
NCBI Description	Nicotiana paniculata mRNA for elongation factor-1 alpha, complete cds

Seq. No.	54710
Seq. ID	zsg701123333.h1
Method	BLASTX
NCBI GI	g3183088
BLAST score	275
E value	1.0e-24
Match length	64
% identity	75
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	54711
Seq. ID	zsg701123350.h1
Method	BLASTX
NCBI GI	g82306
BLAST score	141
E value	5.0e-09
Match length	39
% identity	62
NCBI Description	myb protein 305 - garden snapdragon

Seq. No.	54712
Seq. ID	zsg701123380.h1
Method	BLASTX
NCBI GI	g2245060
BLAST score	184
E value	5.0e-14
Match length	60
% identity	60
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No. 54713

Seq. ID	zsg701123390.h1
Method	BLASTX
NCBI GI	g3947735
BLAST score	171
E value	2.0e-12
Match length	80
% identity	45
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	54714
Seq. ID	zsg701123394.h1
Method	BLASTX
NCBI GI	g4204095
BLAST score	203
E value	3.0e-16
Match length	54
% identity	67
NCBI Description	(AF030260) CYP94A1 [Vicia sativa]

Seq. No.	54715
Seq. ID	zsg701123406.h1
Method	BLASTN
NCBI GI	g2921315
BLAST score	109
E value	1.0e-54
Match length	123
% identity	98
NCBI Description	Glycine max beta-1,3-glucanase 2 (SGlu2) gene, partial sequence

Seq. No.	54716
Seq. ID	zsg701123409.h1
Method	BLASTX
NCBI GI	g3135270
BLAST score	352
E value	1.0e-33
Match length	89
% identity	76
NCBI Description	(AC003058) putative protein kinase [Arabidopsis thaliana]

Seq. No.	54717
Seq. ID	zsg701123494.h1
Method	BLASTX
NCBI GI	g3461835
BLAST score	200
E value	7.0e-16
Match length	86
% identity	50
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	54718
Seq. ID	zsg701123550.h1
Method	BLASTX
NCBI GI	g3608479
BLAST score	273

E value	8.0e-34
Match length	86
% identity	88
NCBI Description	(AF088912) ribosomal protein L15 [Petunia x hybrida]

Seq. No.	54719
Seq. ID	zsg701123570.h1
Method	BLASTX
NCBI GI	g3249068
BLAST score	138
E value	1.0e-08
Match length	83
% identity	45
NCBI Description	(AC004473) Contains similarity to zinc-binding protein (PWA33) gb_L04190 from Pleurodeles waltlii. [Arabidopsis thaliana]

Seq. No.	54720
Seq. ID	zsg701123577.h1
Method	BLASTX
NCBI GI	g2245109
BLAST score	354
E value	5.0e-34
Match length	84
% identity	82
NCBI Description	(Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]

Seq. No.	54721
Seq. ID	zsg701123581.h1
Method	BLASTX
NCBI GI	g4210330
BLAST score	147
E value	1.0e-09
Match length	42
% identity	62
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	54722
Seq. ID	zsg701123582.h1
Method	BLASTX
NCBI GI	g2780192
BLAST score	187
E value	2.0e-14
Match length	84
% identity	45
NCBI Description	(AJ222713) unnamed protein product [Arabidopsis thaliana]

Seq. No.	54723
Seq. ID	zsg701123591.h1
Method	BLASTX
NCBI GI	g1706282
BLAST score	181
E value	1.0e-13
Match length	63
% identity	62

NCBI Description	DISEASE RESISTANCE RESPONSE PROTEIN 206 >gi_508844 (U11716) disease resistance response protein 206-d [Pisum sativum]

Seq. No.	54724
Seq. ID	zsg701123596.h1
Method	BLASTX
NCBI GI	g1350956
BLAST score	255
E value	2.0e-22
Match length	58
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	54725
Seq. ID	zsg701123638.h1
Method	BLASTX
NCBI GI	g3702340
BLAST score	199
E value	4.0e-18
Match length	81
% identity	60
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54726
Seq. ID	zsg701123664.h1
Method	BLASTX
NCBI GI	g2827561
BLAST score	299
E value	2.0e-27
Match length	87
% identity	68
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292809_emb_CAA19799_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	54727
Seq. ID	zsg701123740.h1
Method	BLASTX
NCBI GI	g3047082
BLAST score	369
E value	1.0e-35
Match length	85
% identity	80
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	54728
Seq. ID	zsg701123743.h1
Method	BLASTX
NCBI GI	g4510369
BLAST score	201
E value	5.0e-16
Match length	84
% identity	49
NCBI Description	(AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54729

Seq. ID	zsg701123836.h1
Method	BLASTX
NCBI GI	g3023216
BLAST score	155
E value	1.0e-10
Match length	56
% identity	57
NCBI Description	14-3-3-LIKE PROTEIN GF14 MU >gi_1531629 (U60444) GF14 mu [Arabidopsis thaliana]

Seq. No.	54730
Seq. ID	zsg701123845.h1
Method	BLASTX
NCBI GI	g4467159
BLAST score	363
E value	5.0e-35
Match length	86
% identity	79
NCBI Description	(AL035540) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54731
Seq. ID	zsg701123847.h1
Method	BLASTX
NCBI GI	g1856971
BLAST score	254
E value	3.0e-22
Match length	52
% identity	90
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	54732
Seq. ID	zsg701123917.h1
Method	BLASTX
NCBI GI	g3334409
BLAST score	150
E value	6.0e-10
Match length	32
% identity	94
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2129765_pir__S71261 V-type proton-ATPase - Arabidopsis thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type proton-ATPase [Arabidopsis thaliana]

Seq. No.	54733
Seq. ID	zsg701123936.h1
Method	BLASTX
NCBI GI	g3033384
BLAST score	213
E value	2.0e-17
Match length	71
% identity	56
NCBI Description	(AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No.	54734
Seq. ID	zsg701123944.h1

Method	BLASTX
NCBI GI	g4038035
BLAST score	141
E value	6.0e-09
Match length	37
% identity	78
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	54735
Seq. ID	zsg701123950.h1
Method	BLASTX
NCBI GI	g1946355
BLAST score	357
E value	3.0e-34
Match length	92
% identity	68
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	54736
Seq. ID	zsg701123958.h1
Method	BLASTX
NCBI GI	g3510251
BLAST score	272
E value	2.0e-24
Match length	88
% identity	50
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	54737
Seq. ID	zsg701123978.h1
Method	BLASTX
NCBI GI	g3236235
BLAST score	222
E value	2.0e-18
Match length	59
% identity	66
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana] >gi_4056501 (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	54738
Seq. ID	zsg701123986.h1
Method	BLASTX
NCBI GI	g3702335
BLAST score	148
E value	8.0e-10
Match length	38
% identity	66
NCBI Description	(AC005397) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	54739
Seq. ID	zsg701123993.h1
Method	BLASTX

NCBI GI	g465514
BLAST score	143
E value	3.0e-09
Match length	83
% identity	40
NCBI Description	HYPOTHETICAL 47.4 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION >gi_542308_pir__S39833 hypothetical protein YBL055c - yeast (Saccharomyces cerevisiae) >gi_313743_emb_CAA80792_ (Z23261) YBL0511 [Saccharomyces cerevisiae] >gi_536084_emb_CAA84875_ (Z35816) ORF YBL055c [Saccharomyces cerevisiae]

Seq. No.	54740
Seq. ID	zsg701124029.h1
Method	BLASTX
NCBI GI	g4512667
BLAST score	162
E value	2.0e-11
Match length	63
% identity	52
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	54741
Seq. ID	zsg701124084.h1
Method	BLASTX
NCBI GI	g4093157
BLAST score	137
E value	1.0e-08
Match length	69
% identity	52
NCBI Description	(AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana]

Seq. No.	54742
Seq. ID	zsg701124086.h1
Method	BLASTX
NCBI GI	g4467124
BLAST score	201
E value	3.0e-16
Match length	40
% identity	90
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54743
Seq. ID	zsg701124109.h1
Method	BLASTX
NCBI GI	g3738288
BLAST score	277
E value	2.0e-27
Match length	81
% identity	73
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	54744
Seq. ID	zsg701124153.h1
Method	BLASTX

NCBI GI	g2632252
BLAST score	186
E value	3.0e-14
Match length	82
% identity	40
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	54745
Seq. ID	zsg701124172.h1
Method	BLASTX
NCBI GI	g3738320
BLAST score	138
E value	1.0e-08
Match length	80
% identity	34
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	54746
Seq. ID	zsg701124256.h1
Method	BLASTN
NCBI GI	g2267582
BLAST score	38
E value	4.0e-12
Match length	65
% identity	91
NCBI Description	Gossypium hirsutum vacuolar H+-ATPase subunit E mRNA, complete cds

Seq. No.	54747
Seq. ID	zsg701124260.h1
Method	BLASTX
NCBI GI	g4572671
BLAST score	151
E value	3.0e-10
Match length	74
% identity	46
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	54748
Seq. ID	zsg701124312.h1
Method	BLASTX
NCBI GI	g112564
BLAST score	180
E value	2.0e-13
Match length	73
% identity	53
NCBI Description	beta-glucosidase (EC 3.2.1.21) - cassava >gi_249262_bbs_101989 (S35175) linamarase=beta-glucosidase [Manihot esculenta=cassava, Cranz, Peptide, 531 aa] [Manihot esculenta]

Seq. No.	54749
Seq. ID	zsg701124318.h1
Method	BLASTN
NCBI GI	g475599

BLAST score	138
E value	7.0e-72
Match length	161
% identity	98
NCBI Description	Glycine max Century 84 BiP isoform B mRNA, complete cds

Seq. No.	54750
Seq. ID	zsg701124349.h1
Method	BLASTX
NCBI GI	g3914940
BLAST score	183
E value	2.0e-19
Match length	64
% identity	78
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_2529376 (L76556) sedoheptulose-1,7-bisphosphatase [Spinacia oleracea]

Seq. No.	54751
Seq. ID	zsg701124378.h1
Method	BLASTN
NCBI GI	g4104973
BLAST score	46
E value	6.0e-17
Match length	66
% identity	92
NCBI Description	Pisum sativum spermidine synthase 2 (SPDSYN2) mRNA, complete cds

Seq. No.	54752
Seq. ID	zsg701124406.h1
Method	BLASTN
NCBI GI	g2052028
BLAST score	119
E value	2.0e-60
Match length	254
% identity	87
NCBI Description	G.max mRNA for glutathione transferase

Seq. No.	54753
Seq. ID	zsg701124438.h1
Method	BLASTN
NCBI GI	g2052028
BLAST score	156
E value	1.0e-82
Match length	212
% identity	94
NCBI Description	G.max mRNA for glutathione transferase

Seq. No.	54754
Seq. ID	zsg701124504.h1
Method	BLASTX
NCBI GI	g2623297
BLAST score	147
E value	1.0e-09
Match length	68

% identity	49
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana]

Seq. No.	54755
Seq. ID	zsg701124539.h1
Method	BLASTX
NCBI GI	g1825727
BLAST score	131
E value	1.0e-16
Match length	79
% identity	56
NCBI Description	(U88308) C32E8.5 gene product [Caenorhabditis elegans]

Seq. No.	54756
Seq. ID	zsg701124570.h1
Method	BLASTX
NCBI GI	g4406808
BLAST score	268
E value	7.0e-24
Match length	89
% identity	57
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	54757
Seq. ID	zsg701124582.h1
Method	BLASTX
NCBI GI	g2853081
BLAST score	275
E value	1.0e-24
Match length	67
% identity	79
NCBI Description	(AL021768) ATP binding protein - like [Arabidopsis thaliana]

Seq. No.	54758
Seq. ID	zsg701124606.h1
Method	BLASTX
NCBI GI	g3548806
BLAST score	168
E value	3.0e-12
Match length	41
% identity	71
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	54759
Seq. ID	zsg701124674.h1
Method	BLASTN
NCBI GI	g3176097
BLAST score	110
E value	4.0e-55
Match length	206
% identity	88
NCBI Description	Medicago truncatula mRNA for annexin

Seq. No.	54760

Seq. ID	zsg701124682.h1
Method	BLASTX
NCBI GI	g728938
BLAST score	368
E value	1.0e-35
Match length	80
% identity	90
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472) inorganic pyrophosphatse ase' [Hordeum vulgare]

Seq. No.	54761
Seq. ID	zsg701124695.h1
Method	BLASTX
NCBI GI	g2829890
BLAST score	283
E value	9.0e-26
Match length	79
% identity	35
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	54762
Seq. ID	zsg701124709.h1
Method	BLASTX
NCBI GI	g2760323
BLAST score	391
E value	2.0e-38
Match length	82
% identity	89
NCBI Description	(AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No.	54763
Seq. ID	zsg701124726.h1
Method	BLASTN
NCBI GI	g2224730
BLAST score	88
E value	5.0e-42
Match length	116
% identity	94
NCBI Description	Vigna radiata mRNA for Aux22d, complete cds

Seq. No.	54764
Seq. ID	zsg701124761.h1
Method	BLASTX
NCBI GI	g4538903
BLAST score	321
E value	4.0e-30
Match length	78
% identity	77
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	54765
Seq. ID	zsg701124762.h1
Method	BLASTN
NCBI GI	g3097265

BLAST score	81
E value	8.0e-38
Match length	149
% identity	89
NCBI Description	Pisum sativum mRNA for translation initiation factor

Seq. No.	54766
Seq. ID	zsg701124782.h1
Method	BLASTX
NCBI GI	g1899188
BLAST score	189
E value	1.0e-14
Match length	82
% identity	19
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	54767
Seq. ID	zsg701124817.h1
Method	BLASTN
NCBI GI	g3687388
BLAST score	50
E value	2.0e-19
Match length	174
% identity	83
NCBI Description	Lycopersicon esculentum mRNA for putative cullin protein

Seq. No.	54768
Seq. ID	zsg701124874.h1
Method	BLASTX
NCBI GI	g3402675
BLAST score	151
E value	3.0e-10
Match length	78
% identity	42
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54769
Seq. ID	zsg701124879.h1
Method	BLASTX
NCBI GI	g2244792
BLAST score	243
E value	1.0e-29
Match length	84
% identity	71
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	54770
Seq. ID	zsg701124880.h1
Method	BLASTN
NCBI GI	g18751
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	Soybean Soychs gene for chalcone synthase (EC 2.3.1.74)

Seq. No.	54771

Seq. ID	zsg701124944.h1
Method	BLASTN
NCBI GI	g169932
BLAST score	183
E value	1.0e-98
Match length	242
% identity	94
NCBI Description	Soybean light-harvesting chlorophyll a/b-binding protein (LHCPII) mRNA, 3' end

Seq. No.	54772
Seq. ID	zsg701124951.h1
Method	BLASTX
NCBI GI	g2613143
BLAST score	200
E value	5.0e-16
Match length	68
% identity	59
NCBI Description	(AF030548) tubulin [Oryza sativa]

Seq. No.	54773
Seq. ID	zsg701124978.h1
Method	BLASTN
NCBI GI	g4185510
BLAST score	50
E value	2.0e-19
Match length	121
% identity	86
NCBI Description	Arabidopsis thaliana actin depolymerizing factor 4 (ADF4) mRNA, complete cds

Seq. No.	54774
Seq. ID	zsg701125040.h1
Method	BLASTX
NCBI GI	g2398529
BLAST score	274
E value	2.0e-24
Match length	75
% identity	75
NCBI Description	(Y13724) Transcription factor [Arabidopsis thaliana]

Seq. No.	54775
Seq. ID	zsg701125081.h1
Method	BLASTX
NCBI GI	g416869
BLAST score	315
E value	2.0e-29
Match length	91
% identity	66
NCBI Description	CYSTEINE SYNTHASE CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_303902_dbj_BAA03542_ (D14722) cysteine synthase [Spinacia oleracea]

Seq. No.	54776
Seq. ID	zsg701125094.h1
Method	BLASTX

NCBI GI	g3641845
BLAST score	215
E value	1.0e-18
Match length	61
% identity	80
NCBI Description	(AJ223358) stelar K+ outward rectifying channel [Arabidopsis thaliana]

Seq. No.	54777
Seq. ID	zsg701125105.h1
Method	BLASTX
NCBI GI	g3819710
BLAST score	262
E value	4.0e-23
Match length	59
% identity	80
NCBI Description	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]

Seq. No.	54778
Seq. ID	zsg701125106.h1
Method	BLASTX
NCBI GI	g3063473
BLAST score	163
E value	2.0e-11
Match length	90
% identity	51
NCBI Description	(AC003981) F22O13.35 [Arabidopsis thaliana]

Seq. No.	54779
Seq. ID	zsg701125157.h1
Method	BLASTX
NCBI GI	g4262140
BLAST score	236
E value	4.0e-20
Match length	56
% identity	79
NCBI Description	(AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]

Seq. No.	54780
Seq. ID	zsg701125193.h1
Method	BLASTX
NCBI GI	g3914052
BLAST score	137
E value	9.0e-09
Match length	37
% identity	84
NCBI Description	DNA MISMATCH REPAIR PROTEIN MSH6 >gi_2104549 (AF001535) AGAA.3 [Arabidopsis thaliana]

Seq. No.	54781
Seq. ID	zsg701125266.h1
Method	BLASTN
NCBI GI	g516853
BLAST score	245
E value	1.0e-135
Match length	257

% identity	36
NCBI Description	Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No.	54782
Seq. ID	zsg701125296.h1
Method	BLASTX
NCBI GI	g3913239
BLAST score	256
E value	9.0e-29
Match length	78
% identity	83
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No.	54783
Seq. ID	zsg701125308.h1
Method	BLASTX
NCBI GI	g2982303
BLAST score	354
E value	5.0e-34
Match length	83
% identity	77
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	54784
Seq. ID	zsg701125351.h1
Method	BLASTX
NCBI GI	g4454039
BLAST score	266
E value	1.0e-23
Match length	83
% identity	61
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	54785
Seq. ID	zsg701125361.h1
Method	BLASTN
NCBI GI	g169980
BLAST score	201
E value	1.0e-109
Match length	241
% identity	96
NCBI Description	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.	54786
Seq. ID	zsg701125455.h1
Method	BLASTX
NCBI GI	g3426039
BLAST score	389
E value	5.0e-38
Match length	87
% identity	83
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 54787

Seq. ID	zsg701125479.h1
Method	BLASTN
NCBI GI	g1369851
BLAST score	55
E value	3.0e-22
Match length	123
% identity	86
NCBI Description	Solanum tuberosum kinesin heavy chain-like protein mRNA, complete cds

Seq. No.	54788
Seq. ID	zsg701125490.h1
Method	BLASTX
NCBI GI	g4220474
BLAST score	157
E value	7.0e-11
Match length	66
% identity	65
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	54789
Seq. ID	zsg701125671.h1
Method	BLASTN
NCBI GI	g166419
BLAST score	131
E value	1.0e-67
Match length	191
% identity	92
NCBI Description	Medicago sativa S-adenosyl-L-methionine: caffeic acid 3-0-methyltransferase mRNA, complete cds

Seq. No.	54790
Seq. ID	zsg701125684.h1
Method	BLASTX
NCBI GI	g2781436
BLAST score	157
E value	7.0e-11
Match length	84
% identity	40
NCBI Description	(AF035483) phospholipase D2 [Homo sapiens] >gi_4505875_ref_NP_002654.1_pPLD2_ phospholipase D2

Seq. No.	54791
Seq. ID	zsg701125688.h1
Method	BLASTN
NCBI GI	g402635
BLAST score	132
E value	3.0e-68
Match length	240
% identity	89
NCBI Description	L.albus gene for beta-tubulin

Seq. No.	54792
Seq. ID	zsg701125710.h1
Method	BLASTX
NCBI GI	g4510400

BLAST score	348
E value	3.0e-33
Match length	89
% identity	71
NCBI Description	(AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis thaliana]

Seq. No.	54793
Seq. ID	zsg701125770.h1
Method	BLASTX
NCBI GI	g3377797
BLAST score	214
E value	2.0e-17
Match length	89
% identity	56
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	54794
Seq. ID	zsg701125801.h1
Method	BLASTN
NCBI GI	g2055227
BLAST score	195
E value	1.0e-106
Match length	263
% identity	94
NCBI Description	Glycine max mRNA for SRC1, complete cds

Seq. No.	54795
Seq. ID	zsg701125808.h1
Method	BLASTN
NCBI GI	g1431628
BLAST score	104
E value	2.0e-51
Match length	139
% identity	94
NCBI Description	V.radiata mRNA for pectinacetylesterase

Seq. No.	54796
Seq. ID	zsg701125826.h1
Method	BLASTX
NCBI GI	g4204275
BLAST score	139
E value	9.0e-09
Match length	60
% identity	48
NCBI Description	(AC004146) Unknown protein [Arabidopsis thaliana]

Seq. No.	54797
Seq. ID	zsg701125848.h1
Method	BLASTN
NCBI GI	g218088
BLAST score	96
E value	9.0e-47

Match length	235
% identity	86
NCBI Description	Rice mRNA for ribosomal protein 117 (249 gene), partial sequence

Seq. No.	54798
Seq. ID	zsg701125869.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	101
E value	9.0e-50
Match length	145
% identity	92
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	54799
Seq. ID	zsg701125875.h1
Method	BLASTX
NCBI GI	g1841355
BLAST score	157
E value	7.0e-11
Match length	37
% identity	73
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	54800
Seq. ID	zsg701125888.h1
Method	BLASTX
NCBI GI	g3047109
BLAST score	164
E value	1.0e-11
Match length	54
% identity	63
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	54801
Seq. ID	zsg701125903.h1
Method	BLASTX
NCBI GI	g2288988
BLAST score	154
E value	1.0e-10
Match length	68
% identity	50
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54802
Seq. ID	zsg701125910.h1
Method	BLASTX
NCBI GI	g2245115
BLAST score	174
E value	7.0e-13
Match length	66
% identity	53
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	54803
Seq. ID	zsg701125921.h1
Method	BLASTX
NCBI GI	g4512705
BLAST score	273
E value	2.0e-24
Match length	75
% identity	75
NCBI Description	(AC006569) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	54804
Seq. ID	zsg701125957.h1
Method	BLASTX
NCBI GI	g3021348
BLAST score	209
E value	5.0e-17
Match length	46
% identity	89
NCBI Description	(AJ004961) ribosomal protein L18 [Cicer arietinum]

Seq. No.	54805
Seq. ID	zsg701125973.h1
Method	BLASTX
NCBI GI	g1856971
BLAST score	278
E value	4.0e-25
Match length	79
% identity	70
NCBI Description	(D26058) This gene is specifically expressed at the S phase during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus]

Seq. No.	54806
Seq. ID	zsg701126004.h1
Method	BLASTN
NCBI GI	g2970653
BLAST score	60
E value	3.0e-25
Match length	124
% identity	94
NCBI Description	Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	54807
Seq. ID	zsg701126013.h1
Method	BLASTN
NCBI GI	g2160155
BLAST score	42
E value	2.0e-14
Match length	94
% identity	86
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	54808

Seq. ID	zsg701126040.h1
Method	BLASTN
NCBI GI	g1663536
BLAST score	62
E value	2.0e-26
Match length	162
% identity	85
NCBI Description	Glycine max clone RLG1 disease resistance protein homolog gene, partial cds

Seq. No.	54809
Seq. ID	zsg701126043.h1
Method	BLASTX
NCBI GI	g2833378
BLAST score	172
E value	1.0e-12
Match length	55
% identity	65
NCBI Description	HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis thaliana] >gi_1582383_prf__2118367A hexokinase [Arabidopsis thaliana]

Seq. No.	54810
Seq. ID	zsg701126066.h1
Method	BLASTN
NCBI GI	g2791947
BLAST score	39
E value	4.0e-13
Match length	71
% identity	89
NCBI Description	Lupinus luteus mRNA for ribosomal protein L13a

Seq. No.	54811
Seq. ID	zsg701126078.h1
Method	BLASTX
NCBI GI	g3860255
BLAST score	173
E value	1.0e-12
Match length	52
% identity	73
NCBI Description	(AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54812
Seq. ID	zsg701126113.h1
Method	BLASTN
NCBI GI	g4191760
BLAST score	45
E value	2.0e-16
Match length	85
% identity	88
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	54813
Seq. ID	zsg701126222.h1
Method	BLASTX
NCBI GI	g4567271

BLAST score	196
E value	1.0e-15
Match length	73
% identity	68
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	54814
Seq. ID	zsg701126224.h1
Method	BLASTX
NCBI GI	g629562
BLAST score	326
E value	6.0e-31
Match length	67
% identity	90
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	54815
Seq. ID	zsg701126225.h1
Method	BLASTX
NCBI GI	g3643609
BLAST score	349
E value	1.0e-33
Match length	70
% identity	77
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	54816
Seq. ID	zsg701126258.h1
Method	BLASTN
NCBI GI	g169956
BLAST score	50
E value	3.0e-19
Match length	50
% identity	100
NCBI Description	Glycine max G-box binding factor (GBF1) mRNA, complete cds

Seq. No.	54817
Seq. ID	zsg701126296.h1
Method	BLASTX
NCBI GI	g2920839
BLAST score	173
E value	8.0e-13
Match length	57
% identity	56
NCBI Description	(U95136) Os-FIERG2 gene product [Oryza sativa]

Seq. No.	54818
Seq. ID	zsg701126335.h1

Method	BLASTN
NCBI GI	g310562
BLAST score	145
E value	5.0e-76
Match length	203
% identity	95
NCBI Description	Glycine max calmodulin (SCaM-5) mRNA, complete cds

Seq. No.	54819
Seq. ID	zsg701126378.h1
Method	BLASTX
NCBI GI	g584825
BLAST score	206
E value	9.0e-17
Match length	57
% identity	89
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	54820
Seq. ID	zsg701126388.h1
Method	BLASTN
NCBI GI	g1841869
BLAST score	41
E value	5.0e-14
Match length	77
% identity	95
NCBI Description	Pimpinella brachycarpa elongation factor 1-beta (EF-1-beta) mRNA, complete cds

Seq. No.	54821
Seq. ID	zsg701126408.h1
Method	BLASTX
NCBI GI	g4006902
BLAST score	301
E value	1.0e-27
Match length	88
% identity	64
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	54822
Seq. ID	zsg701126439.h1
Method	BLASTX
NCBI GI	g2245060
BLAST score	199
E value	9.0e-16
Match length	83
% identity	47
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No.	54823
Seq. ID	zsg701126455.h1
Method	BLASTX
NCBI GI	g4220489
BLAST score	355
E value	4.0e-34

Match length	86
% identity	76
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54824
Seq. ID	zsg701126469.h1
Method	BLASTX
NCBI GI	g1076715
BLAST score	290
E value	2.0e-26
Match length	85
% identity	55
NCBI Description	abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare]

Seq. No.	54825
Seq. ID	zsg701126504.h1
Method	BLASTN
NCBI GI	g170059
BLAST score	269
E value	1.0e-150
Match length	281
% identity	99
NCBI Description	Soybean (G.max L.) beta-tubulin (S-beta-1) gene, complete cds

Seq. No.	54826
Seq. ID	zsg701126524.h1
Method	BLASTX
NCBI GI	g1076668
BLAST score	207
E value	7.0e-17
Match length	64
% identity	67
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	54827
Seq. ID	zsg701126530.h1
Method	BLASTX
NCBI GI	g4544453
BLAST score	279
E value	4.0e-25
Match length	65
% identity	78
NCBI Description	(AC006592) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54828
Seq. ID	zsg701126583.h1
Method	BLASTX
NCBI GI	g2351374
BLAST score	197
E value	2.0e-15
Match length	90
% identity	80
NCBI Description	(U54560) putative 26S proteasome subunit athMOV34

[Arabidopsis thaliana]

Seq. No.	54829
Seq. ID	zsg701126588.h1
Method	BLASTX
NCBI GI	g2842490
BLAST score	148
E value	8.0e-10
Match length	53
% identity	58
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	54830
Seq. ID	zsg701126594.h1
Method	BLASTN
NCBI GI	g402635
BLAST score	86
E value	1.0e-40
Match length	230
% identity	88
NCBI Description	L.albus gene for beta-tubulin

Seq. No.	54831
Seq. ID	zsg701126648.h1
Method	BLASTX
NCBI GI	g2435519
BLAST score	193
E value	3.0e-17
Match length	80
% identity	79
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	54832
Seq. ID	zsg701126651.h1
Method	BLASTX
NCBI GI	g134810
BLAST score	142
E value	4.0e-09
Match length	81
% identity	36
NCBI Description	SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY) >gi_66609_pir__SYECSD spermidine synthase (EC 2.5.1.16) - Escherichia coli >gi_147852 (J02804) spermidine synthase [Escherichia coli] >gi_473788_dbj_BAA05577_ (D26562) 'spermidine synthase' [Escherichia coli] >gi_1786312 (AE000121) spermidine synthase = putrescine aminopropyltransferase [Escherichia coli]

Seq. No.	54833
Seq. ID	zsg701126677.h1
Method	BLASTX
NCBI GI	g4512663
BLAST score	168
E value	4.0e-12
Match length	82

% identity	18
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544470_gb_AAD22377.1_AC006580_9 (AC006580) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54834
Seq. ID	zsg701126704.h1
Method	BLASTX
NCBI GI	g2660670
BLAST score	196
E value	1.0e-21
Match length	85
% identity	68
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	54835
Seq. ID	zsg701126792.h1
Method	BLASTX
NCBI GI	g3914052
BLAST score	102
E value	3.0e-09
Match length	53
% identity	66
NCBI Description	DNA MISMATCH REPAIR PROTEIN MSH6 >gi_2104549 (AF001535) AGAA.3 [Arabidopsis thaliana]

Seq. No.	54836
Seq. ID	zsg701126823.h1
Method	BLASTX
NCBI GI	g3068705
BLAST score	148
E value	7.0e-10
Match length	43
% identity	63
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	54837
Seq. ID	zsg701126912.h1
Method	BLASTX
NCBI GI	g2342690
BLAST score	139
E value	6.0e-09
Match length	44
% identity	48
NCBI Description	(AC000106) Similar to Homo copine I (gb_U83246). [Arabidopsis thaliana]

Seq. No.	54838
Seq. ID	zsg701126920.h1
Method	BLASTX
NCBI GI	g4006878
BLAST score	277
E value	6.0e-25
Match length	83
% identity	60
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	54839
Seq. ID	zsg701126925.h1
Method	BLASTN
NCBI GI	g12545
BLAST score	36
E value	5.0e-11
Match length	48
% identity	94
NCBI Description	Cucurbita sp. pMCPN60-2 mRNA for chaperonin

Seq. No.	54840
Seq. ID	zsg701126939.h1
Method	BLASTX
NCBI GI	g4314365
BLAST score	141
E value	4.0e-09
Match length	61
% identity	51
NCBI Description	(AC006340) putative copia-like retrotransposon Hopscotch [Arabidopsis thaliana]

Seq. No.	54841
Seq. ID	zsg701126940.h1
Method	BLASTN
NCBI GI	g1498371
BLAST score	81
E value	8.0e-38
Match length	137
% identity	90
NCBI Description	Solanum tuberosum actin (Pot79) gene, partial cds

Seq. No.	54842
Seq. ID	zsg701126948.h1
Method	BLASTN
NCBI GI	g4104973
BLAST score	122
E value	3.0e-62
Match length	194
% identity	91
NCBI Description	Pisum sativum spermidine synthase 2 (SPDSYN2) mRNA, complete cds

Seq. No.	54843
Seq. ID	zsg701126951.h1
Method	BLASTN
NCBI GI	g849135
BLAST score	33
E value	2.0e-09
Match length	123
% identity	87
NCBI Description	Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete cds

Seq. No.	54844
Seq. ID	zsg701127089.h1
Method	BLASTX

NCBI GI g4105798
BLAST score 160
E value 3.0e-11
Match length 37
% identity 62
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 54845
Seq. ID zsg701127093.h1
Method BLASTX
NCBI GI g3451067
BLAST score 162
E value 1.0e-12
Match length 56
% identity 68
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 54846
Seq. ID zsg701127167.h1
Method BLASTN
NCBI GI g927504
BLAST score 97
E value 2.0e-47
Match length 196
% identity 88
NCBI Description P.sativum mRNA for fructose-1, 6-biphosphate aldolase (clone aldcyt2)

Seq. No. 54847
Seq. ID zsg701127225.h1
Method BLASTX
NCBI GI g2160690
BLAST score 263
E value 2.0e-23
Match length 66
% identity 74
NCBI Description (U73526) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No. 54848
Seq. ID zsg701127318.h1
Method BLASTX
NCBI GI g3021267
BLAST score 201
E value 5.0e-16
Match length 53
% identity 75
NCBI Description (AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No. 54849
Seq. ID zsg701127327.h1
Method BLASTN
NCBI GI g2564044
BLAST score 35
E value 2.0e-10
Match length 51

% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	54850
Seq. ID	zsg701127336.h1
Method	BLASTN
NCBI GI	g2598656
BLAST score	149
E value	2.0e-78
Match length	236
% identity	91
NCBI Description	Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.	54851
Seq. ID	zsg701127358.h1
Method	BLASTX
NCBI GI	g2252844
BLAST score	153
E value	2.0e-10
Match length	44
% identity	61
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	54852
Seq. ID	zsg701127368.h1
Method	BLASTN
NCBI GI	g4165549
BLAST score	60
E value	3.0e-25
Match length	110
% identity	93
NCBI Description	Malus domestica mRNA for phosphoglyceromutase, complete cds

Seq. No.	54853
Seq. ID	zsg701127376.h1
Method	BLASTX
NCBI GI	g3738089
BLAST score	154
E value	2.0e-10
Match length	90
% identity	42
NCBI Description	(AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana] >gi_4314372_gb_AAD15583_ (AC006340) putative symbiotic ammonium transporter SAT1 [Arabidopsis thaliana]

Seq. No.	54854
Seq. ID	zsg701127395.h1
Method	BLASTX
NCBI GI	g285741
BLAST score	139
E value	1.0e-08
Match length	94
% identity	38
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	54855
Seq. ID	zsg701127490.h1
Method	BLASTX
NCBI GI	g1707010
BLAST score	172
E value	1.0e-12
Match length	40
% identity	78
NCBI Description	(U78721) mitochondrial carrier protein isolog [Arabidopsis thaliana]

Seq. No.	54856
Seq. ID	zsg701127544.h1
Method	BLASTN
NCBI GI	g4468976
BLAST score	37
E value	2.0e-11
Match length	92
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	54857
Seq. ID	zsg701127545.h1
Method	BLASTX
NCBI GI	g3831451
BLAST score	205
E value	2.0e-16
Match length	43
% identity	91
NCBI Description	(AC005700) putative O-GlcNAc transferase [Arabidopsis thaliana]

Seq. No.	54858
Seq. ID	zsg701127546.h1
Method	BLASTX
NCBI GI	g2443329
BLAST score	170
E value	2.0e-12
Match length	63
% identity	38
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	54859
Seq. ID	zsg701127575.h1
Method	BLASTX
NCBI GI	g4559304
BLAST score	470
E value	2.0e-47
Match length	92
% identity	91
NCBI Description	(AF127021) T7-like RNA polymerase [Zea mays]

Seq. No.	54860
Seq. ID	zsg701127586.h1
Method	BLASTX

NCBI GI	g3559816
BLAST score	176
E value	4.0e-17
Match length	66
% identity	74
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	54861
Seq. ID	zsg701127680.h1
Method	BLASTX
NCBI GI	g585416
BLAST score	348
E value	3.0e-33
Match length	89
% identity	71
NCBI Description	LIPOXYGENASE >gi_467565_emb_CAA50483_ (X71344) lipoxygenase [Lens culinaris]

Seq. No.	54862
Seq. ID	zsg701127690.h1
Method	BLASTN
NCBI GI	g506628
BLAST score	204
E value	1.0e-111
Match length	232
% identity	97
NCBI Description	Glycine max cv. Dare photosystem II type I chlorophyll a/b-binding protein (lhcb1*7) gene, complete cds

Seq. No.	54863
Seq. ID	zsg701127692.h1
Method	BLASTX
NCBI GI	g4530126
BLAST score	303
E value	6.0e-28
Match length	88
% identity	67
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	54864
Seq. ID	zsg701127703.h1
Method	BLASTN
NCBI GI	g170053
BLAST score	189
E value	1.0e-102
Match length	189
% identity	100
NCBI Description	Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.	54865
Seq. ID	zsg701127713.h1
Method	BLASTX
NCBI GI	g4544440
BLAST score	221
E value	2.0e-18
Match length	75

% identity	56
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]

Seq. No.	54866
Seq. ID	zsg701127833.h1
Method	BLASTN
NCBI GI	g2564045
BLAST score	36
E value	6.0e-11
Match length	118
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	54867
Seq. ID	zsg701127849.h1
Method	BLASTN
NCBI GI	g4406529
BLAST score	33
E value	3.0e-09
Match length	53
% identity	91
NCBI Description	Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No.	54868
Seq. ID	zsg701127862.h1
Method	BLASTX
NCBI GI	g4455296
BLAST score	365
E value	3.0e-35
Match length	85
% identity	73
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54869
Seq. ID	zsg701127863.h1
Method	BLASTX
NCBI GI	g3860333
BLAST score	199
E value	9.0e-16
Match length	68
% identity	62
NCBI Description	(AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No.	54870
Seq. ID	zsg701127880.h1
Method	BLASTN
NCBI GI	g166379
BLAST score	114
E value	2.0e-57
Match length	226
% identity	88
NCBI Description	Alfalfa glucose-regulated endoplasmic reticular protein mRNA, complete cds

Seq. No.	54871

Seq. ID	zsg701127904.h1
Method	BLASTN
NCBI GI	g170046
BLAST score	39
E value	1.0e-12
Match length	63
% identity	90
NCBI Description	Glycine max protein kinase (PK6) mRNA, complete cds

Seq. No.	54872
Seq. ID	zsg701127927.h1
Method	BLASTN
NCBI GI	g1928978
BLAST score	32
E value	5.0e-09
Match length	36
% identity	97
NCBI Description	Vigna unguiculata phospholipase D mRNA, complete cds

Seq. No.	54873
Seq. ID	zsg701127954.h1
Method	BLASTN
NCBI GI	g609224
BLAST score	73
E value	5.0e-33
Match length	173
% identity	86
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	54874
Seq. ID	zsg701128019.h1
Method	BLASTX
NCBI GI	g3980378
BLAST score	153
E value	1.0e-10
Match length	33
% identity	82
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	54875
Seq. ID	zsg701128076.h1
Method	BLASTN
NCBI GI	g2920665
BLAST score	153
E value	7.0e-81
Match length	188
% identity	96
NCBI Description	Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No.	54876
Seq. ID	zsg701128115.h1
Method	BLASTX
NCBI GI	g3287270

BLAST score	246
E value	2.0e-21
Match length	59
% identity	75
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No.	54877
Seq. ID	zsg701128181.h1
Method	BLASTX
NCBI GI	g625990
BLAST score	155
E value	9.0e-11
Match length	76
% identity	45
NCBI Description	porin, plastid - garden pea

Seq. No.	54878
Seq. ID	zsg701128195.h1
Method	BLASTX
NCBI GI	g2129698
BLAST score	333
E value	6.0e-32
Match length	80
% identity	90
NCBI Description	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi_1054633_emb_CAA63387_ (X92728) protein kinase [Arabidopsis thaliana]

Seq. No.	54879
Seq. ID	zsg701128201.h1
Method	BLASTN
NCBI GI	g510545
BLAST score	57
E value	8.0e-24
Match length	89
% identity	91
NCBI Description	P.sativum mRNA for starch branching enzyme I

Seq. No.	54880
Seq. ID	zsg701128212.h1
Method	BLASTX
NCBI GI	g629693
BLAST score	229
E value	3.0e-19
Match length	88
% identity	50
NCBI Description	probable integrase - common tobacco (fragment) >gi_530742_emb_CAA56791_ (X80830) integrase [Nicotiana tabacum]

Seq. No.	54881
Seq. ID	zsg701128223.h1
Method	BLASTN
NCBI GI	g2920665
BLAST score	89
E value	1.0e-42
Match length	161

% identity	89
NCBI Description	Glycine max 2,4-D inducible glutathione S-transferase (GSTa) mRNA, complete cds

Seq. No.	54882
Seq. ID	zsg701128440.h1
Method	BLASTN
NCBI GI	g870783
BLAST score	42
E value	2.0e-14
Match length	66
% identity	91
NCBI Description	Sesamum indicum omega-3 fatty acid desaturase mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	54883
Seq. ID	zsg701128521.h1
Method	BLASTX
NCBI GI	g4185312
BLAST score	144
E value	5.0e-18
Match length	91
% identity	65
NCBI Description	(AF090446) copia protein [Zea mays]

Seq. No.	54884
Seq. ID	zsg701128523.h1
Method	BLASTX
NCBI GI	g3970797
BLAST score	151
E value	2.0e-10
Match length	52
% identity	56
NCBI Description	(Y13766) polynucleotide phosphorylase [Staphylococcus aureus]

Seq. No.	54885
Seq. ID	zsg701128528.h1
Method	BLASTX
NCBI GI	g2239229
BLAST score	145
E value	1.0e-09
Match length	33
% identity	79
NCBI Description	(Z97210) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	54886
Seq. ID	zsg701128549.h1
Method	BLASTN
NCBI GI	g313147
BLAST score	120
E value	5.0e-61
Match length	276
% identity	89
NCBI Description	A.medicago MSK-3 mRNA for protein kinase

Seq. No.	54887

Seq. ID	zsg701128556.h1
Method	BLASTN
NCBI GI	g4102689
BLAST score	68
E value	2.0e-30
Match length	113
% identity	90
NCBI Description	Glycine max 24 kDa seed maturation protein mRNA, complete cds

Seq. No.	54888
Seq. ID	zsg701128609.h1
Method	BLASTX
NCBI GI	g3183088
BLAST score	279
E value	4.0e-25
Match length	87
% identity	57
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	54889
Seq. ID	zsg701128647.h1
Method	BLASTX
NCBI GI	g1076344
BLAST score	224
E value	6.0e-19
Match length	71
% identity	61
NCBI Description	kinase-associated protein phosphatase precursor - Arabidopsis thaliana

Seq. No.	54890
Seq. ID	zsg701128657.h1
Method	BLASTN
NCBI GI	g310568
BLAST score	153
E value	9.0e-81
Match length	212
% identity	92
NCBI Description	Glycine max homeobox-containing (Sbh1) mRNA, complete cds

Seq. No.	54891
Seq. ID	zsg701128696.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	72
E value	2.0e-32
Match length	186
% identity	85
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	54892
Seq. ID	zsg701128738.h1

Method	BLASTX
NCBI GI	g3033399
BLAST score	162
E value	1.0e-11
Match length	61
% identity	46
NCBI Description	(AC004238) hypothetical protein [Arabidopsis thaliana]

Seq. No.	54893
Seq. ID	zsg701128804.h1
Method	BLASTX
NCBI GI	g1345132
BLAST score	250
E value	1.0e-21
Match length	91
% identity	56
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	54894
Seq. ID	zsg701128820.h1
Method	BLASTX
NCBI GI	g4218991
BLAST score	215
E value	1.0e-17
Match length	50
% identity	78
NCBI Description	(AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	54895
Seq. ID	zsg701128840.h1
Method	BLASTN
NCBI GI	g3900979
BLAST score	37
E value	2.0e-11
Match length	57
% identity	91
NCBI Description	Eichhornia crassipes mRNA for metallothionein-like protein, clone A

Seq. No.	54896
Seq. ID	zsg701128901.h1
Method	BLASTN
NCBI GI	g189311
BLAST score	297
E value	1.0e-166
Match length	297
% identity	100
NCBI Description	Human nucleolar protein (B23) mRNA, complete cds

Seq. No.	54897
Seq. ID	zsg701128902.h1
Method	BLASTN
NCBI GI	g24478
BLAST score	282

E value	1.0e-157
Match length	298
% identity	99
NCBI Description	Human mRNA for alpha-1-microglobulin and HI-30

Seq. No.	54898
Seq. ID	zsg701128903.h1
Method	BLASTN
NCBI GI	g3043669
BLAST score	260
E value	1.0e-144
Match length	293
% identity	97
NCBI Description	Homo sapiens mRNA for KIAA0573 protein, partial cds

Seq. No.	54899
Seq. ID	zsg701128906.h1
Method	BLASTN
NCBI GI	g2335202
BLAST score	292
E value	1.0e-163
Match length	296
% identity	100
NCBI Description	Homo sapiens chromosome 11 from 11p15.5 region, complete sequence [Homo sapiens]

Seq. No.	54900
Seq. ID	zsg701128909.h1
Method	BLASTN
NCBI GI	g467308
BLAST score	182
E value	4.0e-98
Match length	198
% identity	98
NCBI Description	Human metallothionein-II gene (mt-II) and flanks

Seq. No.	54901
Seq. ID	zsg701128910.h1
Method	BLASTN
NCBI GI	g181962
BLAST score	191
E value	1.0e-103
Match length	195
% identity	99
NCBI Description	Human elongation factor EF-1-alpha gene, complete cds. >gi_2170857_dbj_E02629_E02629 DNA of human polypeptide chain elongation factor-1 alpha

Seq. No.	54902
Seq. ID	zsg701128919.h1
Method	BLASTN
NCBI GI	g4406629
BLAST score	139
E value	2.0e-72
Match length	143
% identity	99
NCBI Description	Homo sapiens clone 24955 mRNA sequence, partial cds

Seq. No.	54903
Seq. ID	zsg701128921.h1
Method	BLASTN
NCBI GI	g189265
BLAST score	294
E value	1.0e-165
Match length	294
% identity	100
NCBI Description	Human novel gene mRNA, complete cds

Seq. No.	54904
Seq. ID	zsg701128925.h1
Method	BLASTN
NCBI GI	g595279
BLAST score	175
E value	8.0e-94
Match length	295
% identity	90
NCBI Description	Rattus norvegicus Rap1B mRNA, complete cds

Seq. No.	54905
Seq. ID	zsg701128930.h1
Method	BLASTN
NCBI GI	g458553
BLAST score	266
E value	1.0e-148
Match length	278
% identity	99
NCBI Description	Human fibrinogen alpha chain gene, complete mRNAs

Seq. No.	54906
Seq. ID	zsg701128931.h1
Method	BLASTN
NCBI GI	g1294778
BLAST score	289
E value	1.0e-162
Match length	293
% identity	100
NCBI Description	Homo sapiens ERK3 protein kinase mRNA, complete cds

Seq. No.	54907
Seq. ID	zsg701128932.h1
Method	BLASTN
NCBI GI	g183677
BLAST score	271
E value	1.0e-151
Match length	291
% identity	99
NCBI Description	Human glutathione S-transferase (GST) a-subunit mRNA, complete cds

Seq. No.	54908
Seq. ID	zsg701128933.h1
Method	BLASTN
NCBI GI	g4507760
BLAST score	258

E value	1.0e-143
Match length	258
% identity	100
NCBI Description	Homo sapiens ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52) mRNA

Seq. No.	54909
Seq. ID	zsg701128934.h1
Method	BLASTN
NCBI GI	g180020
BLAST score	267
E value	1.0e-149
Match length	291
% identity	98
NCBI Description	Human monocyte antigen CD14 (CD14) mRNA, complete cds

Seq. No.	54910
Seq. ID	zsg701128935.h1
Method	BLASTN
NCBI GI	g179664
BLAST score	233
E value	1.0e-128
Match length	281
% identity	97
NCBI Description	Human complement component C3 mRNA, alpha and beta subunits, complete cds. >gi_4557384_ref_NM_000064.1_C3_ Homo sapiens complement component 3 (C3) mRNA

Seq. No.	54911
Seq. ID	zsg701128937.h1
Method	BLASTN
NCBI GI	g177828
BLAST score	217
E value	1.0e-119
Match length	275
% identity	99
NCBI Description	Human alpha-1-antitrypsin mRNA, complete cds

Seq. No.	54912
Seq. ID	zsg701128938.h1
Method	BLASTN
NCBI GI	g183891
BLAST score	285
E value	1.0e-159
Match length	289
% identity	100
NCBI Description	Human high density lipoprotein binding protein (HBP) mRNA, complete cds

Seq. No.	54913
Seq. ID	zsg701128940.h1
Method	BLASTN
NCBI GI	g4200326
BLAST score	285
E value	1.0e-159
Match length	292
% identity	100

NCBI Description	Human DNA sequence from clone 1119A7 on chromosome 22q12.2-12.3 thioredoxin, nuclear gene encoding mitochondrial protein, translation initiation factor EIF3-P66 subunit, EST, GSS, STS, CpG island, complete sequence [Hom

Seq. No.	54914
Seq. ID	zsg701128942.h1
Method	BLASTN
NCBI GI	g3851213
BLAST score	206
E value	1.0e-112
Match length	206
% identity	100
NCBI Description	Homo sapiens mRNA for NS1-binding protein (NS1-BP)

Seq. No.	54915
Seq. ID	zsg701128943.h1
Method	BLASTN
NCBI GI	g406289
BLAST score	230
E value	1.0e-127
Match length	242
% identity	99
NCBI Description	H.sapiens phosphatidylethanolamine binding protein mRNA >gi_4505620_ref_NM_002567.1_PBP_ Homo sapiens prostatic binding protein (PBP) mRNA

Seq. No.	54916
Seq. ID	zsg701128954.h1
Method	BLASTN
NCBI GI	g505101
BLAST score	263
E value	1.0e-146
Match length	283
% identity	99
NCBI Description	Human mRNA for KIAA0062 gene, partial cds

Seq. No.	54917
Seq. ID	zsg701128959.h1
Method	BLASTN
NCBI GI	g1458115
BLAST score	285
E value	1.0e-159
Match length	285
% identity	100
NCBI Description	Human nicotinic acetylcholine receptor alpha5 subunit precursor, mRNA, complete cds

Seq. No.	54918
Seq. ID	zsg701128960.h1
Method	BLASTN
NCBI GI	g337494
BLAST score	277
E value	1.0e-154
Match length	281
% identity	100

NCBI Description	Human ribosomal protein L7a (surf 3) large subunit mRNA, complete cds. >gi_4506660_ref_NM_000972.1_RPL7A_ Homo sapiens ribosomal protein L7a (RPL7A) mRNA

Seq. No.	54919
Seq. ID	zsg701128963.h1
Method	BLASTN
NCBI GI	g2723389
BLAST score	291
E value	1.0e-163
Match length	291
% identity	100
NCBI Description	Homo sapiens mRNA for SART-1, complete cds

Seq. No.	54920
Seq. ID	zsg701128966.h1
Method	BLASTN
NCBI GI	g3810672
BLAST score	195
E value	1.0e-106
Match length	195
% identity	100
NCBI Description	Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence [Homo sapiens]

Seq. No.	54921
Seq. ID	zsg701128971.h1
Method	BLASTN
NCBI GI	g1009165
BLAST score	175
E value	4.0e-94
Match length	179
% identity	99
NCBI Description	Homo sapiens phenylalanine hydroxylase (PAH) mutant Q20stop mRNA

Seq. No.	54922
Seq. ID	zsg701128972.h1
Method	BLASTN
NCBI GI	g36328
BLAST score	196
E value	1.0e-106
Match length	196
% identity	100
NCBI Description	H.sapiens mRNA for S-adenosylmethionine synthetase >gi_4557736_ref_NM_000429.1_MAT1A_ Homo sapiens methionine adenosyltransferase I, alpha (MAT1A) mRNA

Seq. No.	54923
Seq. ID	zsg701128974.h1
Method	BLASTX
NCBI GI	g4263748
BLAST score	151
E value	3.0e-10
Match length	64
% identity	48
NCBI Description	(AC004883) similar to KIAA0766; similar to PID:g3882253

[Homo sapiens]

Seq. No.	54924
Seq. ID	zsg701128975.h1
Method	BLASTN
NCBI GI	g3387880
BLAST score	122
E value	1.0e-62
Match length	122
% identity	100
NCBI Description	Homo sapiens clone 24706 mRNA sequence

Seq. No.	54925
Seq. ID	zsg701128976.h1
Method	BLASTN
NCBI GI	g189427
BLAST score	287
E value	1.0e-160
Match length	287
% identity	100
NCBI Description	Human protein phosphatase 2A regulatory subunit alpha-isotype (alpha-PR65) mRNA, complete cds

Seq. No.	54926
Seq. ID	zsg701128977.h1
Method	BLASTN
NCBI GI	g2780183
BLAST score	196
E value	1.0e-106
Match length	276
% identity	93
NCBI Description	Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS

Seq. No.	54927
Seq. ID	zsg701128978.h1
Method	BLASTN
NCBI GI	g4557830
BLAST score	272
E value	1.0e-152
Match length	284
% identity	99
NCBI Description	Homo sapiens pterin-4 alpha-carbinolamine dehydratase (PCBD) mRNA

Seq. No.	54928
Seq. ID	zsg701128979.h1
Method	BLASTN
NCBI GI	g219924
BLAST score	279
E value	1.0e-156
Match length	287
% identity	99
NCBI Description	Human mRNA for MGC-24, complete cds

Seq. No.	54929
Seq. ID	zsg701128980.h1

Method	BLASTN
NCBI GI	g1850083
BLAST score	284
E value	1.0e-159
Match length	288
% identity	100
NCBI Description	Homo sapiens mRNA for glia maturation factor, complete cds

Seq. No.	54930
Seq. ID	zsg701128982.h1
Method	BLASTN
NCBI GI	g4505370
BLAST score	237
E value	1.0e-131
Match length	249
% identity	99
NCBI Description	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 8 (23kD) (NADH-coenzyme Q reductase) (NDUFS8) mRNA, and translated products

Seq. No.	54931
Seq. ID	zsg701128983.h1
Method	BLASTN
NCBI GI	g439229
BLAST score	252
E value	1.0e-140
Match length	280
% identity	97
NCBI Description	Human mRNA for fructose-1,6-bisphosphatase, complete cds

Seq. No.	54932
Seq. ID	zsg701128984.h1
Method	BLASTN
NCBI GI	g3660662
BLAST score	246
E value	1.0e-136
Match length	246
% identity	100
NCBI Description	Homo sapiens D15F37 pseudogene, S3 allele, mRNA sequence

Seq. No.	54933
Seq. ID	zsg701128986.h1
Method	BLASTN
NCBI GI	g3687210
BLAST score	249
E value	1.0e-138
Match length	278
% identity	98
NCBI Description	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence [Homo sapiens]

Seq. No.	54934
Seq. ID	zsg701128988.h1
Method	BLASTN
NCBI GI	g297407
BLAST score	138
E value	5.0e-72

Match length	167
% identity	99
NCBI Description	H.sapiens p63 mRNA for transmembrane protein

Seq. No.	54935
Seq. ID	zsg701128989.h1
Method	BLASTN
NCBI GI	g4557320
BLAST score	250
E value	1.0e-138
Match length	283
% identity	96
NCBI Description	Homo sapiens apolipoprotein A-I (APOA1) mRNA

Seq. No.	54936
Seq. ID	zsg701128992.h1
Method	BLASTN
NCBI GI	g36572
BLAST score	155
E value	4.0e-82
Match length	186
% identity	99
NCBI Description	Human S-protein gene, complete cds

Seq. No.	54937
Seq. ID	zsg701128993.h1
Method	BLASTN
NCBI GI	g189225
BLAST score	167
E value	4.0e-89
Match length	273
% identity	98
NCBI Description	Human NK4 mRNA, complete cds

Seq. No.	54938
Seq. ID	zsg701129001.h1
Method	BLASTN
NCBI GI	g1418933
BLAST score	131
E value	7.0e-68
Match length	151
% identity	97
NCBI Description	H.sapiens mRNA for protein-tyrosine-phosphatase (tissue type: foreskin)

Seq. No.	54939
Seq. ID	zsg701129003.h1
Method	BLASTN
NCBI GI	g177808
BLAST score	155
E value	3.0e-82
Match length	155
% identity	100
NCBI Description	Human alpha-1-antichymotrypsin (AACT) mRNA, complete cds. >gi_4501842_ref_NM_001085.1_AACT_ Homo sapiens alpha-1-antichymotrypsin (AACT) mRNA

Seq. No.	54940
Seq. ID	zsg701129004.h1
Method	BLASTN
NCBI GI	g177932
BLAST score	197
E value	1.0e-107
Match length	209
% identity	99
NCBI Description	Human alpha-1-antichymotrypsin mRNA, 3' end

Seq. No.	54941
Seq. ID	zsg701129006.h1
Method	BLASTN
NCBI GI	g178051
BLAST score	220
E value	1.0e-121
Match length	220
% identity	100
NCBI Description	Human non-muscle alpha-actinin mRNA, complete cds. >gi_4501890_ref_NM_001102.1_ACTN1_ Homo sapiens actinin, alpha 1 (ACTN1) mRNA

Seq. No.	54942
Seq. ID	zsg701129008.h1
Method	BLASTN
NCBI GI	g182429
BLAST score	175
E value	4.0e-94
Match length	179
% identity	99
NCBI Description	Human fibrinogen beta-chain mRNA, partial cds

Seq. No.	54943
Seq. ID	zsg701129012.h1
Method	BLASTN
NCBI GI	g2511669
BLAST score	242
E value	1.0e-134
Match length	250
% identity	99
NCBI Description	H.sapiens mRNA for organic cation transporter, liver

Seq. No.	54944
Seq. ID	zsg701129013.h1
Method	BLASTN
NCBI GI	g4503714
BLAST score	156
E value	9.0e-83
Match length	164
% identity	99
NCBI Description	Homo sapiens fibrinogen, gamma polypeptide (FGG) mRNA

Seq. No.	54945
Seq. ID	zsg701129018.h1
Method	BLASTN
NCBI GI	g34353
BLAST score	130

E value	2.0e-67
Match length	134
% identity	99
NCBI Description	Human H2' mRNA coding for an asialoglycoprotein receptor

Seq. No.	54946
Seq. ID	zsg701129019.h1
Method	BLASTN
NCBI GI	g603230
BLAST score	102
E value	1.0e-50
Match length	117
% identity	97
NCBI Description	Human CDC16Hs mRNA, complete cds >gi_4502700_ref_NM_003903.1_CDC16_ Homo sapiens cell division cycle 16; anaphase promoting complex 6 (CDC16) mRNA

Seq. No.	54947
Seq. ID	zsg701129024.h1
Method	BLASTN
NCBI GI	g179881
BLAST score	131
E value	6.0e-68
Match length	150
% identity	97
NCBI Description	Human autoantigen calreticulin mRNA, complete cds

Seq. No.	54948
Seq. ID	zsg701129029.h1
Method	BLASTN
NCBI GI	g4165005
BLAST score	149
E value	1.0e-78
Match length	157
% identity	99
NCBI Description	Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence [Homo sapiens]

Seq. No.	54949
Seq. ID	zsg701129031.h1
Method	BLASTN
NCBI GI	g182291
BLAST score	163
E value	6.0e-87
Match length	163
% identity	100
NCBI Description	Human coagulation factor XII (Hageman) mRNA, 3' end

Seq. No.	54950
Seq. ID	zsg701129032.h1
Method	BLASTN
NCBI GI	g189059
BLAST score	191
E value	1.0e-103
Match length	248

% identity	95
NCBI Description	Human Na,K-ATPase beta subunit (ATP1B) gene, exons 3 through 6

Seq. No.	54951
Seq. ID	zsg701129033.h1
Method	BLASTN
NCBI GI	g177871
BLAST score	134
E value	1.0e-69
Match length	145
% identity	99
NCBI Description	Human alpha-2-macroglobulin mRNA, 3' end

Seq. No.	54952
Seq. ID	zsg701129035.h1
Method	BLASTN
NCBI GI	g179643
BLAST score	189
E value	1.0e-102
Match length	189
% identity	100
NCBI Description	Human complement C1r mRNA, complete cds

Seq. No.	54953
Seq. ID	zsg701129038.h1
Method	BLASTN
NCBI GI	g1029494
BLAST score	195
E value	1.0e-106
Match length	238
% identity	95
NCBI Description	H.sapiens CpG island DNA genomic Mse1 fragment, clone 33f2, forward read cpg33f2.ft1e

Seq. No.	54954
Seq. ID	zsg701129039.h1
Method	BLASTN
NCBI GI	g2257985
BLAST score	153
E value	5.0e-81
Match length	161
% identity	99
NCBI Description	Homo sapiens kruppel-related zinc finger protein hcKrox mRNA, complete cds

Seq. No.	54955
Seq. ID	zsg701129041.h1
Method	BLASTN
NCBI GI	g4454856
BLAST score	237
E value	1.0e-131
Match length	245
% identity	99
NCBI Description	Homo sapiens S6 kinase-related kinase mRNA, complete cds

Seq. No.	54956

Seq. ID	zsg701129043.h1
Method	BLASTN
NCBI GI	g31396
BLAST score	247
E value	1.0e-137
Match length	255
% identity	99
NCBI Description	Human mRNA for fibronectin (FN precursor)

Seq. No.	54957
Seq. ID	zsg701129048.h1
Method	BLASTN
NCBI GI	g3882170
BLAST score	219
E value	1.0e-120
Match length	231
% identity	99
NCBI Description	Homo sapiens mRNA for KIAA0725 protein, partial cds

Seq. No.	54958
Seq. ID	zsg701129050.h1
Method	BLASTN
NCBI GI	g1145798
BLAST score	217
E value	1.0e-119
Match length	224
% identity	99
NCBI Description	Human EBI3-associated protein p60 mRNA, complete cds

Seq. No.	54959
Seq. ID	zsg701129054.h1
Method	BLASTN
NCBI GI	g1162925
BLAST score	143
E value	5.0e-75
Match length	155
% identity	98
NCBI Description	Homo sapiens complement component 3 (C3) gene, exons 1-30

Seq. No.	54960
Seq. ID	zsg701129055.h1
Method	BLASTN
NCBI GI	g2280513
BLAST score	170
E value	5.0e-91
Match length	205
% identity	37
NCBI Description	Homo sapiens DNA for histidine-rich glycoprotein, complete cds

Seq. No.	54961
Seq. ID	zsg701129056.h1
Method	BLASTN
NCBI GI	g182429
BLAST score	201
E value	1.0e-109
Match length	212

% identity	99
NCBI Description	Human fibrinogen beta-chain mRNA, partial cds

Seq. No.	54962
Seq. ID	zsg701129060.h1
Method	BLASTN
NCBI GI	g179935
BLAST score	201
E value	1.0e-109
Match length	232
% identity	98
NCBI Description	Human carboxypeptidase N mRNA, 3' end

Seq. No.	54963
Seq. ID	zsg701129065.h1
Method	BLASTN
NCBI GI	g4505528
BLAST score	185
E value	1.0e-100
Match length	189
% identity	99
NCBI Description	Homo sapiens orosomucoid 2 (ORM2) mRNA

Seq. No.	54964
Seq. ID	zsg701129067.h1
Method	BLASTN
NCBI GI	g1263128
BLAST score	123
E value	3.0e-63
Match length	123
% identity	100
NCBI Description	H.sapiens mRNA for ribosomal protein S4

Seq. No.	54965
Seq. ID	zsg701129068.h1
Method	BLASTN
NCBI GI	g2358019
BLAST score	255
E value	1.0e-141
Match length	259
% identity	100
NCBI Description	Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence

Seq. No.	54966
Seq. ID	zsg701129073.h1
Method	BLASTN
NCBI GI	g28591
BLAST score	193
E value	1.0e-104
Match length	209
% identity	98
NCBI Description	H.sapiens mRNA for serum albumin

Seq. No.	54967
Seq. ID	zsg701129074.h1

Method	BLASTN
NCBI GI	g4503688
BLAST score	236
E value	1.0e-130
Match length	244
% identity	99
NCBI Description	Homo sapiens fibrinogen, A alpha polypeptide (FGA) mRNA

Seq. No.	54968
Seq. ID	zsg701129076.h1
Method	BLASTN
NCBI GI	g180947
BLAST score	135
E value	3.0e-70
Match length	188
% identity	94
NCBI Description	Human carboxylesterase mRNA, complete cds

Seq. No.	54969
Seq. ID	zsg701129077.h1
Method	BLASTN
NCBI GI	g3789715
BLAST score	115
E value	2.0e-58
Match length	139
% identity	96
NCBI Description	Homo sapiens chromosome 17, clone hRPK.62_F_10, complete sequence [Homo sapiens]

Seq. No.	54970
Seq. ID	zsg701129082.h1
Method	BLASTN
NCBI GI	g24437
BLAST score	172
E value	3.0e-92
Match length	217
% identity	95
NCBI Description	Human mRNA for alpha 1-antitrypsin carboxyterminal region (aa 268-394)

Seq. No.	54971
Seq. ID	zsg701129085.h1
Method	BLASTN
NCBI GI	g30223
BLAST score	201
E value	1.0e-109
Match length	209
% identity	99
NCBI Description	H.sapiens CRP mRNA for C-reactive protein

Seq. No.	54972
Seq. ID	zsg701129088.h1
Method	BLASTX
NCBI GI	g2494162
BLAST score	214
E value	9.0e-18
Match length	61

% identity	61
NCBI Description	HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR >gi_3879803_emb_CAA87414_ (Z47356) similar to DNAJ [Caenorhabditis elegans]

Seq. No.	54973
Seq. ID	zsg701129101.h1
Method	BLASTN
NCBI GI	g3483724
BLAST score	157
E value	4.0e-83
Match length	188
% identity	96
NCBI Description	Homo sapiens full length insert cDNA clone ZD69B11

Seq. No.	54974
Seq. ID	zsg701129108.h1
Method	BLASTN
NCBI GI	g163232
BLAST score	101
E value	1.0e-49
Match length	202
% identity	88
NCBI Description	Bovine interstitial retinol binding protein (IRBP) mRNA, 3' end

Seq. No.	54975
Seq. ID	zsg701129111.h1
Method	BLASTN
NCBI GI	g188621
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Human mononcyte/neutrophil elastase inhibitor mRNA sequence. >gi_2481183_gb_I63610_I63610 Sequence 12 from patent US

Seq. No.	54976
Seq. ID	zsg701129112.h1
Method	BLASTN
NCBI GI	g181359
BLAST score	152
E value	4.0e-80
Match length	228
% identity	92
NCBI Description	Human cytochrome P-450j mRNA, complete cds

Seq. No.	54977
Seq. ID	zsg701129113.h1
Method	BLASTN
NCBI GI	g4557332
BLAST score	267
E value	1.0e-149
Match length	279
% identity	99
NCBI Description	Homo sapiens arylsulfatase B (ARSB) mRNA

Seq. No.	54978
Seq. ID	zsg701129114.h1
Method	BLASTN
NCBI GI	g1654343
BLAST score	130
E value	4.0e-67
Match length	201
% identity	92
NCBI Description	Human guanine nucleotide exchange factor p115-RhoGEF mRNA, partial cds

Seq. No.	54979
Seq. ID	zsg701129124.h1
Method	BLASTN
NCBI GI	g190269
BLAST score	245
E value	1.0e-135
Match length	278
% identity	98
NCBI Description	Human pancreatic polypeptide gene, complete cds

Seq. No.	54980
Seq. ID	zsg701129125.h1
Method	BLASTN
NCBI GI	g4097194
BLAST score	275
E value	1.0e-153
Match length	275
% identity	100
NCBI Description	Human fumarase mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	54981
Seq. ID	zsg701129126.h1
Method	BLASTN
NCBI GI	g32063
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Human hepatoma mRNA for serine protease hepsin

Seq. No.	54982
Seq. ID	zsg701129129.h1
Method	BLASTN
NCBI GI	g4557322
BLAST score	63
E value	2.0e-27
Match length	63
% identity	100
NCBI Description	Homo sapiens apolipoprotein C-III (APOC3) mRNA

Seq. No.	54983
Seq. ID	zsg701129131.h1
Method	BLASTN
NCBI GI	g2795787

BLAST score	275
E value	1.0e-153
Match length	279
% identity	100
NCBI Description	Homo sapiens RNA adenosine deaminase (ADAR) gene, exon 15 and alternatively spliced products, complete cds

Seq. No.	54984
Seq. ID	zsg701129133.h1
Method	BLASTN
NCBI GI	g2623737
BLAST score	205
E value	1.0e-112
Match length	209
% identity	100
NCBI Description	Homo sapiens UDP-galactose-4-epimerase (GALE) mRNA, complete cds >gi_4503890_ref_NM_000403.1_GALE_ Homo sapiens galactose-4-epimerase, UDP- (GALE) mRNA

Seq. No.	54985
Seq. ID	zsg701129137.h1
Method	BLASTN
NCBI GI	g2351379
BLAST score	269
E value	1.0e-150
Match length	280
% identity	99
NCBI Description	Homo sapiens translation initiation factor eIF3 p40 subunit mRNA, complete cds >gi_4503514_ref_NM_003756.1_EIF3S3_ Homo sapiens eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD) (EIF3S3) mRNA

Seq. No.	54986
Seq. ID	zsg701129143.h1
Method	BLASTN
NCBI GI	g457563
BLAST score	271
E value	1.0e-151
Match length	275
% identity	100
NCBI Description	Human mRNA for BST-2, complete cds

Seq. No.	54987
Seq. ID	zsg701129149.h1
Method	BLASTN
NCBI GI	g2351377
BLAST score	262
E value	1.0e-146
Match length	282
% identity	98
NCBI Description	Homo sapiens translation initiation factor eIF3 p66 subunit mRNA, complete cds >gi_4503522_ref_NM_003753.1_EIF3S7_ Homo sapiens eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD) (EIF3S7) mRNA

Seq. No.	54988
Seq. ID	zsg701129150.h1

Method	BLASTN
NCBI GI	g3688073
BLAST score	257
E value	1.0e-143
Match length	265
% identity	100
NCBI Description	Homo sapiens chromosome 5, P1 clone 702A10 (LBNL H56), complete sequence [Homo sapiens]

Seq. No.	54989
Seq. ID	zsg701129151.h1
Method	BLASTN
NCBI GI	g4503628
BLAST score	175
E value	7.0e-94
Match length	261
% identity	92
NCBI Description	Homo sapiens coagulation factor XII (Hageman factor) (F12) mRNA

Seq. No.	54990
Seq. ID	zsg701129155.h1
Method	BLASTN
NCBI GI	g189952
BLAST score	214
E value	1.0e-117
Match length	277
% identity	92
NCBI Description	Human phospholipase A2 mRNA, complete cds. >gi_4507952_ref_NM_003406.1_YWHAZ_ Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA >gi_1825195_gb_I34404_I34404 Sequence 8 from patent US

Seq. No.	54991
Seq. ID	zsg701129156.h1
Method	BLASTN
NCBI GI	g184371
BLAST score	116
E value	1.0e-58
Match length	116
% identity	100
NCBI Description	Human hepsin mRNA, complete cds. >gi_4504480_ref_NM_002151.1_HPN_ Homo sapiens hepsin (transmembrane protease, serine 1) (HPN) mRNA

Seq. No.	54992
Seq. ID	zsg701129158.h1
Method	BLASTN
NCBI GI	g181228
BLAST score	80
E value	3.0e-37
Match length	80
% identity	100
NCBI Description	Human cytochrome b5 mRNA, 3' end

Seq. No.	54993

Seq. ID	zsg701129159.h1
Method	BLASTN
NCBI GI	g31091
BLAST score	273
E value	1.0e-152
Match length	273
% identity	100
NCBI Description	Human mRNA for elongation factor 1-alpha (clone CEF4)

Seq. No.	54994
Seq. ID	zsg701129160.h1
Method	BLASTN
NCBI GI	g432358
BLAST score	276
E value	1.0e-154
Match length	276
% identity	100
NCBI Description	Human mRNA for ribosomal protein, complete cds

Seq. No.	54995
Seq. ID	zsg701129162.h1
Method	BLASTN
NCBI GI	g4503714
BLAST score	272
E value	1.0e-152
Match length	276
% identity	100
NCBI Description	Homo sapiens fibrinogen, gamma polypeptide (FGG) mRNA

Seq. No.	54996
Seq. ID	zsg701129163.h1
Method	BLASTN
NCBI GI	g37995
BLAST score	267
E value	1.0e-149
Match length	275
% identity	99
NCBI Description	H.sapiens mRNA for xeroderma pigmentosum group C complementing factor (XP-C)

Seq. No.	54997
Seq. ID	zsg701129170.h1
Method	BLASTN
NCBI GI	g178397
BLAST score	240
E value	1.0e-132
Match length	273
% identity	96
NCBI Description	Human aldehyde dehydrogenase II (ALDH-2) mRNA, 3' end

Seq. No.	54998
Seq. ID	zsg701129174.h1
Method	BLASTN
NCBI GI	g1469196
BLAST score	273
E value	1.0e-152
Match length	273

% identity	100
NCBI Description	Human mRNA for KIAA0137 gene, complete cds

Seq. No.	54999
Seq. ID	zsg701129176.h1
Method	BLASTN
NCBI GI	g2588611
BLAST score	42
E value	2.0e-14
Match length	46
% identity	15
NCBI Description	Human BAC clone RG335O22 from 7q21-q22, complete sequence [Homo sapiens]

Seq. No.	55000
Seq. ID	zsg701129178.h1
Method	BLASTN
NCBI GI	g642794
BLAST score	271
E value	1.0e-151
Match length	271
% identity	100
NCBI Description	Human TFIID subunit TAFII55 (TAFII55) mRNA, complete cds

Seq. No.	55001
Seq. ID	zsg701129179.h1
Method	BLASTN
NCBI GI	g2887430
BLAST score	274
E value	1.0e-153
Match length	274
% identity	100
NCBI Description	Homo sapiens KIAA0428 mRNA, complete cds

Seq. No.	55002
Seq. ID	zsg701129182.h1
Method	BLASTN
NCBI GI	g187434
BLAST score	276
E value	1.0e-154
Match length	276
% identity	100
NCBI Description	Human monocyte chemotactic and activating factor (MCAF) mRNA, complete cds. >gi_641144_emb_A17786.1_A17786 MCP-1 mRNA

Seq. No.	55003
Seq. ID	zsg701129183.h1
Method	BLASTN
NCBI GI	g3851208
BLAST score	244
E value	1.0e-135
Match length	276
% identity	97
NCBI Description	Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence [Homo sapiens]

Seq. No.	55004
Seq. ID	zsg701129186.h1
Method	BLASTN
NCBI GI	g1561756
BLAST score	230
E value	1.0e-126
Match length	234
% identity	100
NCBI Description	Human ubiquitin conjugating enzyme 9 (hUBC9) mRNA, complete cds

Seq. No.	55005
Seq. ID	zsg701129190.h1
Method	BLASTN
NCBI GI	g31749
BLAST score	250
E value	1.0e-138
Match length	270
% identity	60
NCBI Description	Human mRNA for haptoglobin alpha(2FS)-beta precursor

Seq. No.	55006
Seq. ID	zsg701129191.h1
Method	BLASTN
NCBI GI	g1890049
BLAST score	258
E value	1.0e-143
Match length	270
% identity	99
NCBI Description	Homo sapiens mRNA for cysteine protease, complete cds

Seq. No.	55007
Seq. ID	zsg701129195.h1
Method	BLASTN
NCBI GI	g31786
BLAST score	207
E value	1.0e-113
Match length	207
% identity	100
NCBI Description	Human glucagon gene

Seq. No.	55008
Seq. ID	zsg701129208.h1
Method	BLASTN
NCBI GI	g559712
BLAST score	260
E value	1.0e-144
Match length	260
% identity	100
NCBI Description	Human mRNA for KIAA0073 gene, partial cds

Seq. No.	55009
Seq. ID	zsg701129211.h1
Method	BLASTN
NCBI GI	g177801
BLAST score	251
E value	1.0e-139

Match length	258
% identity	100
NCBI Description	Human interferon-inducible protein 9-27 mRNA, complete cds

Seq. No.	55010
Seq. ID	zsg701129212.h1
Method	BLASTN
NCBI GI	g182406
BLAST score	244
E value	1.0e-135
Match length	244
% identity	100
NCBI Description	Homo sapiens fibrinogen alpha subunit and fibrinogen alpha subunit precursor, genes, complete cds

Seq. No.	55011
Seq. ID	zsg701129215.h1
Method	BLASTN
NCBI GI	g434844
BLAST score	260
E value	1.0e-144
Match length	260
% identity	100
NCBI Description	H.sapiens DAP-1 mRNA

Seq. No.	55012
Seq. ID	zsg701129219.h1
Method	BLASTN
NCBI GI	g531170
BLAST score	253
E value	1.0e-140
Match length	260
% identity	100
NCBI Description	Human Csa-19 mRNA, complete cds

Seq. No.	55013
Seq. ID	zsg701129223.h1
Method	BLASTN
NCBI GI	g416016
BLAST score	259
E value	1.0e-144
Match length	259
% identity	100
NCBI Description	H.sapiens PMI1 mRNA for phosphomannose isomerase >gi_4505234_ref_NM_002435.1_MPI_ Homo sapiens mannose phosphate isomerase (MPI) mRNA

Seq. No.	55014
Seq. ID	zsg701129224.h1
Method	BLASTN
NCBI GI	g30212
BLAST score	228
E value	1.0e-125
Match length	253
% identity	97
NCBI Description	H.sapiens mRNA for C-reactive protein

Seq. No.	55015
Seq. ID	zsg701129226.h1
Method	BLASTN
NCBI GI	g3287673
BLAST score	98
E value	6.0e-48
Match length	262
% identity	100
NCBI Description	Homo sapiens chromosome 19, cosmid F23149, complete sequence [Homo sapiens]

Seq. No.	55016
Seq. ID	zsg701129227.h1
Method	BLASTN
NCBI GI	g31912
BLAST score	241
E value	1.0e-133
Match length	259
% identity	98
NCBI Description	Human mRNA for coupling protein G(s) alpha-subunit (alpha-S1) (stimulatory regulatory component Gs of adenylyl cyclase)

Seq. No.	55017
Seq. ID	zsg701129233.h1
Method	BLASTN
NCBI GI	g32531
BLAST score	254
E value	1.0e-141
Match length	254
% identity	100
NCBI Description	Human Hums3 mRNA for 40S ribosomal protein s3 >gi_4506720_ref_NM_001005.1_RPS3_ Homo sapiens ribosomal protein S3 (RPS3) mRNA

Seq. No.	55018
Seq. ID	zsg701129239.h1
Method	BLASTN
NCBI GI	g177865
BLAST score	258
E value	1.0e-143
Match length	258
% identity	100
NCBI Description	Human tumor necrosis factor alpha inducible protein A20 mRNA, complete cds

Seq. No.	55019
Seq. ID	zsg701129240.h1
Method	BLASTN
NCBI GI	g179912
BLAST score	245
E value	1.0e-135
Match length	257
% identity	99
NCBI Description	Human protein tyrosine phosphatase mRNA, complete cds. >gi_4506292_ref_NM_002829.1_PTPN3_ Homo sapiens protein tyrosine phosphatase, non-receptor type 3 (PTPN3) mRNA

Seq. No.	55020
Seq. ID	zsg701129241.h1
Method	BLASTN
NCBI GI	g179757
BLAST score	259
E value	1.0e-144
Match length	259
% identity	100
NCBI Description	Human N-type calcium channel alpha-1 subunit mRNA, complete cds. >gi_4502522_ref_NM_000718.1_CACNA1B_ Homo sapiens calcium channel, voltage-dependent, L type, alpha 1B subunit (CACNA1B) mRNA

Seq. No.	55021
Seq. ID	zsg701129242.h1
Method	BLASTN
NCBI GI	g598241
BLAST score	198
E value	1.0e-107
Match length	198
% identity	100
NCBI Description	Homo sapiens spliced UHG RNA

Seq. No.	55022
Seq. ID	zsg701129243.h1
Method	BLASTN
NCBI GI	g28589
BLAST score	213
E value	1.0e-116
Match length	239
% identity	98
NCBI Description	Human messenger RNA for serum albumin (HSA)

Seq. No.	55023
Seq. ID	zsg701129246.h1
Method	BLASTN
NCBI GI	g3169112
BLAST score	153
E value	9.0e-81
Match length	247
% identity	100
NCBI Description	Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and

Seq. No.	55024
Seq. ID	zsg701129251.h1
Method	BLASTN
NCBI GI	g338029
BLAST score	244
E value	1.0e-135
Match length	256
% identity	99
NCBI Description	Human serine dehydratase mRNA, complete cds

Seq. No.	55025
Seq. ID	zsg701129254.h1
Method	BLASTN
NCBI GI	g993045
BLAST score	223
E value	1.0e-122
Match length	231
% identity	100
NCBI Description	Human tryptophan oxygenase (TDO) mRNA, complete cds

Seq. No.	55026
Seq. ID	zsg701129256.h1
Method	BLASTN
NCBI GI	g178728
BLAST score	249
E value	1.0e-138
Match length	257
% identity	99
NCBI Description	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29

Seq. No.	55027
Seq. ID	zsg701129257.h1
Method	BLASTN
NCBI GI	g3483859
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	Homo sapiens full length insert cDNA clone ZE03C06

Seq. No.	55028
Seq. ID	zsg701129260.h1
Method	BLASTN
NCBI GI	g2642452
BLAST score	201
E value	1.0e-109
Match length	221
% identity	98
NCBI Description	Human Xp22 PAC RPCI1-258N20, complete sequence [Homo sapiens]

Seq. No.	55029
Seq. ID	zsg701129263.h1
Method	BLASTN
NCBI GI	g4502098
BLAST score	254
E value	1.0e-141
Match length	254
% identity	100
NCBI Description	Homo sapiens adenine nucleotide translocator 2 (fibroblast) (ANT2), nuclear gene encoding mitochondrial protein, mRNA

Seq. No.	55030
Seq. ID	zsg701129265.h1
Method	BLASTN
NCBI GI	g182425
BLAST score	257

E value	1.0e-143
Match length	257
% identity	100
NCBI Description	Human fibrinogen A-alpha-chain mRNA, complete cds

Seq. No.	55031
Seq. ID	zsg701129269.h1
Method	BLASTN
NCBI GI	g498147
BLAST score	258
E value	1.0e-143
Match length	258
% identity	100
NCBI Description	Human mRNA for XP-C repair complementing protein (p58/HHR23B), complete cds >gi_4506386_ref_NM_002874.1_RAD23B_ Homo sapiens RAD23 (S. cerevisiae) homolog B (RAD23B) mRNA

Seq. No.	55032
Seq. ID	zsg701129275.h1
Method	BLASTN
NCBI GI	g35564
BLAST score	248
E value	1.0e-137
Match length	255
% identity	100
NCBI Description	Human mRNA for purine nucleoside phosphorylase (PNP; EC 2.4.2.1) >gi_1408345_gb_G28530_G28530 human STS SHGC-31518. >gi_4557800_ref_NM_000270.1_NP_ Homo sapiens nucleoside phosphorylase (NP) mRNA

Seq. No.	55033
Seq. ID	zsg701129279.h1
Method	BLASTN
NCBI GI	g1945270
BLAST score	260
E value	1.0e-144
Match length	260
% identity	100
NCBI Description	H.sapiens mRNA for protein phosphatase 6 >gi_4506028_ref_NM_002721.1_PPP6C_ Homo sapiens protein phosphatase 6, catalytic subunit (PPP6C) mRNA

Seq. No.	55034
Seq. ID	zsg701129282.h1
Method	BLASTN
NCBI GI	g665587
BLAST score	256
E value	1.0e-142
Match length	256
% identity	100
NCBI Description	Human mRNA for calmodulin, complete cds

Seq. No.	55035
Seq. ID	zsg701129283.h1
Method	BLASTN
NCBI GI	g4324406

BLAST score	214
E value	1.0e-117
Match length	214
% identity	100
NCBI Description	Gallus gallus peptide elongation factor 1-beta mRNA, complete cds

Seq. No.	55036
Seq. ID	zsg701129284.h1
Method	BLASTN
NCBI GI	g35219
BLAST score	219
E value	1.0e-120
Match length	243
% identity	97
NCBI Description	Human mRNA for p68 protein

Seq. No.	55037
Seq. ID	zsg701129286.h1
Method	BLASTN
NCBI GI	g1063607
BLAST score	258
E value	1.0e-143
Match length	258
% identity	100
NCBI Description	Human nicotinamide N-methyltransferase (NNMT) gene, exons 1 and 2

Seq. No.	55038
Seq. ID	zsg701129287.h1
Method	BLASTN
NCBI GI	g37579
BLAST score	134
E value	1.0e-69
Match length	141
% identity	99
NCBI Description	Human mRNA for mitochondrial ubiquinone-binding protein (QP-C) >gi_190815_gb_M22348_HUMQPC Human mitochondrial ubiquinone-binding protein mRNA, complete cds

Seq. No.	55039
Seq. ID	zsg701129289.h1
Method	BLASTN
NCBI GI	g1204117
BLAST score	199
E value	1.0e-108
Match length	255
% identity	95
NCBI Description	H.sapiens serine hydroxymethyltransferase pseudogene

Seq. No.	55040
Seq. ID	zsg701129290.h1
Method	BLASTX
NCBI GI	g2135070
BLAST score	223
E value	1.0e-18
Match length	84

% identity	52
NCBI Description	enoyl-CoA hydratase (EC 4.2.1.17) / AU-specific RNA-binding protein - human >gi_780241_emb_CAA56260_ (X79888) AU-binding protein/Enoyl-CoA hydratase [Homo sapiens] >gi_4502327_ref_NP_001689.1_pAUH_ AU RNA-binding protein/enoyl-Coenzyme A hydratase

Seq. No.	55041
Seq. ID	zsg701129292.h1
Method	BLASTN
NCBI GI	g3660677
BLAST score	247
E value	1.0e-137
Match length	255
% identity	99
NCBI Description	Oryctolagus cuniculus heterogeneous nuclear ribonucleoprotein C (hnRNPC) mRNA, complete cds

Seq. No.	55042
Seq. ID	zsg701129293.h1
Method	BLASTN
NCBI GI	g3776070
BLAST score	237
E value	1.0e-131
Match length	253
% identity	98
NCBI Description	Homo sapiens mRNA for histone deacetylase-like protein (JM21)

Seq. No.	55043
Seq. ID	zsg701129296.h1
Method	BLASTN
NCBI GI	g178868
BLAST score	252
E value	1.0e-140
Match length	256
% identity	100
NCBI Description	Human acute phase serum amyloid A protein (SAA2.2) gene, exons 1 through 4

Seq. No.	55044
Seq. ID	zsg701129314.h1
Method	BLASTN
NCBI GI	g3242784
BLAST score	45
E value	2.0e-16
Match length	61
% identity	93
NCBI Description	Arabidopsis thaliana respiratory burst oxidase protein C (RbohC) gene, complete cds

Seq. No.	55045
Seq. ID	zsg701129319.h1
Method	BLASTX
NCBI GI	g4538624
BLAST score	263
E value	2.0e-23

Match length	74
% identity	37
NCBI Description	(AJ133502) hypothetical protein [Nicotiana tabacum]

Seq. No.	55046
Seq. ID	zsg701129349.h1
Method	BLASTX
NCBI GI	g542157
BLAST score	380
E value	5.0e-37
Match length	85
% identity	82
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	55047
Seq. ID	zsg701129401.h1
Method	BLASTX
NCBI GI	g2833389
BLAST score	398
E value	5.0e-39
Match length	97
% identity	79
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III) >gi_1200154_emb_CAA65065_ (X95759) glycogen (starch) synthase [Solanum tuberosum]

Seq. No.	55048
Seq. ID	zsg701129405.h1
Method	BLASTX
NCBI GI	g4455331
BLAST score	233
E value	1.0e-19
Match length	91
% identity	12
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	55049
Seq. ID	zsg701129425.h1
Method	BLASTX
NCBI GI	g1359905
BLAST score	161
E value	2.0e-11
Match length	71
% identity	49
NCBI Description	(X85138) homologous to glucosyltransferases [Lycopersicon esculentum]

Seq. No.	55050
Seq. ID	zsg701129435.h1
Method	BLASTX
NCBI GI	g2598603
BLAST score	147
E value	2.0e-10
Match length	39
% identity	87
NCBI Description	(AJ002315) shaggy-like kinase 59 [Nicotiana tabacum]

Seq. No.	55051
Seq. ID	zsg701129453.h1
Method	BLASTX
NCBI GI	g3860245
BLAST score	147
E value	1.0e-09
Match length	90
% identity	42
NCBI Description	(AC005824) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	55052
Seq. ID	zsg701129486.h1
Method	BLASTX
NCBI GI	g4455334
BLAST score	227
E value	3.0e-19
Match length	72
% identity	64
NCBI Description	(AL035525) myosin-like protein [Arabidopsis thaliana]

Seq. No.	55053
Seq. ID	zsg701129510.h1
Method	BLASTN
NCBI GI	g170089
BLAST score	223
E value	1.0e-122
Match length	279
% identity	95
NCBI Description	G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No.	55054
Seq. ID	zsg701129512.h1
Method	BLASTN
NCBI GI	g2204063
BLAST score	64
E value	1.0e-27
Match length	215
% identity	82
NCBI Description	Pisum sativum mRNA for F1 ATPase, complete cds

Seq. No.	55055
Seq. ID	zsg701129513.h1
Method	BLASTN
NCBI GI	g169899
BLAST score	204
E value	1.0e-111
Match length	276
% identity	93
NCBI Description	G.max 31 kDa protein mRNA, 3' end

Seq. No.	55056
Seq. ID	zsg701129514.h1
Method	BLASTX
NCBI GI	g4559339
BLAST score	321
E value	5.0e-30

Match length	93
% identity	72
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	55057
Seq. ID	zsg701129526.h1
Method	BLASTX
NCBI GI	g3738327
BLAST score	162
E value	1.0e-11
Match length	59
% identity	56
NCBI Description	(AC005170) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	55058
Seq. ID	zsg701129532.h1
Method	BLASTX
NCBI GI	g3123515
BLAST score	265
E value	2.0e-23
Match length	77
% identity	64
NCBI Description	(Y08761) Mago Nashi-like protein [Euphorbia lagascae]

Seq. No.	55059
Seq. ID	zsg701129548.h1
Method	BLASTX
NCBI GI	g1495802
BLAST score	310
E value	9.0e-29
Match length	91
% identity	60
NCBI Description	(X96405) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	55060
Seq. ID	zsg701129550.h1
Method	BLASTX
NCBI GI	g4510406
BLAST score	277
E value	6.0e-25
Match length	88
% identity	66
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	55061
Seq. ID	zsg701129567.h1
Method	BLASTN
NCBI GI	g3522932
BLAST score	108
E value	7.0e-54
Match length	212
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	55062
Seq. ID	zsg701129573.h1
Method	BLASTX
NCBI GI	g4455336
BLAST score	388
E value	6.0e-38
Match length	90
% identity	72
NCBI Description	(AL035525) pectinesterase-like protein [Arabidopsis thaliana]

Seq. No.	55063
Seq. ID	zsg701129635.h1
Method	BLASTX
NCBI GI	g1946367
BLAST score	252
E value	6.0e-22
Match length	70
% identity	67
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	55064
Seq. ID	zsg701129650.h1
Method	BLASTX
NCBI GI	g1732511
BLAST score	141
E value	3.0e-16
Match length	88
% identity	61
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	55065
Seq. ID	zsg701129720.h1
Method	BLASTN
NCBI GI	g2160155
BLAST score	67
E value	2.0e-29
Match length	151
% identity	86
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	55066
Seq. ID	zsg701129735.h1
Method	BLASTX
NCBI GI	g4544431
BLAST score	220
E value	3.0e-18
Match length	82
% identity	60
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55067
Seq. ID	zsg701129778.h1
Method	BLASTX
NCBI GI	g4580394

BLAST score	152
E value	3.0e-10
Match length	55
% identity	45
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	55068
Seq. ID	zsg701129793.h1
Method	BLASTN
NCBI GI	g18644
BLAST score	194
E value	1.0e-105
Match length	247
% identity	95
NCBI Description	Soybean mRNA for HMG-1 like protein

Seq. No.	55069
Seq. ID	zsg701129813.h1
Method	BLASTX
NCBI GI	g3859659
BLAST score	251
E value	8.0e-22
Match length	73
% identity	74
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	55070
Seq. ID	zsg701129902.h1
Method	BLASTX
NCBI GI	g2642502
BLAST score	229
E value	3.0e-19
Match length	74
% identity	55
NCBI Description	(AF030694) CG3 [Plasmodium falciparum]

Seq. No.	55071
Seq. ID	zsg701129945.h1
Method	BLASTX
NCBI GI	g3540199
BLAST score	266
E value	1.0e-23
Match length	68
% identity	69
NCBI Description	(AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No.	55072
Seq. ID	zsg701129951.h1
Method	BLASTX
NCBI GI	g2959767
BLAST score	264
E value	2.0e-23
Match length	70
% identity	73

NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	55073
Seq. ID	zsg701129972.h1
Method	BLASTN
NCBI GI	g1218003
BLAST score	62
E value	1.0e-26
Match length	138
% identity	86
NCBI Description	Glycine max dynamin-like protein SDL5A mRNA, complete cds

Seq. No.	55074
Seq. ID	zsg701130012.h1
Method	BLASTN
NCBI GI	g1220521
BLAST score	40
E value	3.0e-13
Match length	73
% identity	97
NCBI Description	Glycine max TATA-box binding protein (STBP1) mRNA, complete cds

Seq. No.	55075
Seq. ID	zsg701130036.h1
Method	BLASTN
NCBI GI	g18449
BLAST score	39
E value	1.0e-12
Match length	51
% identity	94
NCBI Description	F.ananassa 26s rRNA gene

Seq. No.	55076
Seq. ID	zsg701130053.h1
Method	BLASTX
NCBI GI	g2829903
BLAST score	161
E value	2.0e-11
Match length	31
% identity	94
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	55077
Seq. ID	zsg701130065.h1
Method	BLASTN
NCBI GI	g21895
BLAST score	52
E value	2.0e-20
Match length	71
% identity	100
NCBI Description	T.aestivum (clone pTAU2.3) U2 snRNA

Seq. No.	55078
Seq. ID	zsg701130139.h1

Method	BLASTN
NCBI GI	g3452136
BLAST score	211
E value	1.0e-115
Match length	255
% identity	96
NCBI Description	Glycine max mRNA for glucose-6-phosphate-dehydrogenase, partial

Seq. No.	55079
Seq. ID	zsg701130161.h1
Method	BLASTX
NCBI GI	g120680
BLAST score	184
E value	3.0e-14
Match length	45
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66010_pir__DEBHG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - barley >gi_18978_emb_CAA42901_ (X60343) glyceraldehyde 3-phosphate dehydrogenase [Hordeum vulgare]

Seq. No.	55080
Seq. ID	zsg701130219.h1
Method	BLASTX
NCBI GI	g3927836
BLAST score	316
E value	2.0e-29
Match length	76
% identity	82
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	55081
Seq. ID	zsg701130251.h1
Method	BLASTN
NCBI GI	g170089
BLAST score	37
E value	2.0e-11
Match length	41
% identity	98
NCBI Description	G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No.	55082
Seq. ID	zsg701130280.h1
Method	BLASTN
NCBI GI	g3264762
BLAST score	78
E value	5.0e-36
Match length	178
% identity	86
NCBI Description	Prunus armeniaca 40S ribosomal protein S4 (RPS4) mRNA, complete cds

Seq. No.	55083
Seq. ID	zsg701130290.h1
Method	BLASTX

NCBI GI	g3915826
BLAST score	381
E value	4.0e-37
Match length	87
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	55084
Seq. ID	zsg701130305.h1
Method	BLASTX
NCBI GI	g2252867
BLAST score	258
E value	1.0e-22
Match length	84
% identity	64
NCBI Description	(AF013294) contains region of similarity to beta transducin family [Arabidopsis thaliana]

Seq. No.	55085
Seq. ID	zsg701130306.h1
Method	BLASTN
NCBI GI	g1675195
BLAST score	93
E value	5.0e-45
Match length	153
% identity	90
NCBI Description	Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, complete cds

Seq. No.	55086
Seq. ID	zsg701130310.h1
Method	BLASTX
NCBI GI	g1888357
BLAST score	336
E value	7.0e-32
Match length	85
% identity	74
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	55087
Seq. ID	zsg701130315.h1
Method	BLASTX
NCBI GI	g1568637
BLAST score	242
E value	4.0e-24
Match length	77
% identity	81
NCBI Description	(U69554) 6a-hydroxymaackiain methyltransferase [Pisum sativum]

Seq. No.	55088
Seq. ID	zsg701130328.h1
Method	BLASTX
NCBI GI	g4127662
BLAST score	163

E value	1.0e-11
Match length	55
% identity	55
NCBI Description	(Y11176) fructosidase [Cichorium intybus]

Seq. No.	55089
Seq. ID	zsg701130361.h1
Method	BLASTX
NCBI GI	g3915020
BLAST score	165
E value	8.0e-12
Match length	66
% identity	61
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE) >gi_1022365_emb_CAA91217_ (Z56278) sucrose phosphate synthase [Vicia faba]

Seq. No.	55090
Seq. ID	zsg701130375.h1
Method	BLASTX
NCBI GI	g4107099
BLAST score	304
E value	1.0e-28
Match length	78
% identity	77
NCBI Description	(AB015141) AHP1 [Arabidopsis thaliana] >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No.	55091
Seq. ID	zsg701130393.h1
Method	BLASTX
NCBI GI	g4539335
BLAST score	186
E value	2.0e-14
Match length	81
% identity	44
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	55092
Seq. ID	zsg701130443.h1
Method	BLASTX
NCBI GI	g3367576
BLAST score	141
E value	6.0e-09
Match length	58
% identity	48
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	55093
Seq. ID	zsg701130468.h1
Method	BLASTN
NCBI GI	g3982595
BLAST score	144
E value	2.0e-75
Match length	270
% identity	89

NCBI Description	Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.	55094
Seq. ID	zsg701130481.h1
Method	BLASTN
NCBI GI	g255576
BLAST score	105
E value	4.0e-52
Match length	124
% identity	98
NCBI Description	small auxin up RNA gene cluster: orf 6B [Glycine max=soybeans, cv. Wayne, Genomic, 665 nt]

Seq. No.	55095
Seq. ID	zvj700605114.h2
Method	BLASTN
NCBI GI	g1150683
BLAST score	47
E value	2.0e-17
Match length	171
% identity	85
NCBI Description	V.radiata atpB, rbcL and trnK genes

Seq. No.	55096
Seq. ID	zvj700605194.h2
Method	BLASTX
NCBI GI	g2832618
BLAST score	163
E value	2.0e-11
Match length	42
% identity	69
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	55097
Seq. ID	zvp700764138.h1
Method	BLASTN
NCBI GI	g170007
BLAST score	205
E value	1.0e-111
Match length	281
% identity	95
NCBI Description	Soybean 18 kD late embryogenesis abundant (Lea) protein mRNA, complete cds

Seq. No.	55098
Seq. ID	zvp700764144.h1
Method	BLASTX
NCBI GI	g1526422
BLAST score	176
E value	6.0e-13
Match length	52
% identity	69
NCBI Description	(D64139) LEA protein in group 5 [Arabidopsis thaliana]

Seq. No.	55099
Seq. ID	zvp700764212.h1
Method	BLASTN

NCBI GI	g3273242
BLAST score	66
E value	1.0e-28
Match length	122
% identity	89
NCBI Description	Oryza sativa mRNA for NLS receptor, complete cds

Seq. No.	55100
Seq. ID	zvp700764247.h1
Method	BLASTN
NCBI GI	g18749
BLAST score	220
E value	1.0e-120
Match length	241
% identity	99
NCBI Description	G.max mRNA for seed maturation polypeptide

Seq. No.	55101
Seq. ID	zvp700764284.h1
Method	BLASTX
NCBI GI	g1946371
BLAST score	296
E value	2.0e-27
Match length	63
% identity	84
NCBI Description	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]

Seq. No.	55102
Seq. ID	zzp700829515.h1
Method	BLASTX
NCBI GI	g431162
BLAST score	188
E value	1.0e-14
Match length	74
% identity	59
NCBI Description	(D21822) ORF [Lilium longiflorum]

Seq. No.	55103
Seq. ID	zzp700829607.h1
Method	BLASTX
NCBI GI	g2905893
BLAST score	269
E value	4.0e-24
Match length	77
% identity	65
NCBI Description	(U66424) fimbrin-like protein [Arabidopsis thaliana]

Seq. No.	55104
Seq. ID	zzp700829617.h1
Method	BLASTX
NCBI GI	g2497543
BLAST score	155
E value	1.0e-10
Match length	54
% identity	61
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379

pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	55105
Seq. ID	zzp700829625.h1
Method	BLASTN
NCBI GI	g3142328
BLAST score	110
E value	4.0e-55
Match length	133
% identity	96
NCBI Description	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq. No.	55106
Seq. ID	zzp700829706.h1
Method	BLASTX
NCBI GI	g3687240
BLAST score	308
E value	1.0e-28
Match length	78
% identity	40
NCBI Description	(AC005169) extensin-like protein [Arabidopsis thaliana]

Seq. No.	55107
Seq. ID	zzp700829744.h1
Method	BLASTX
NCBI GI	g2983755
BLAST score	304
E value	3.0e-28
Match length	76
% identity	74
NCBI Description	(AE000735) ATP-dependent Clp protease proteolytic subunit [Aquifex aeolicus]

Seq. No.	55108
Seq. ID	zzp700829816.h1
Method	BLASTX
NCBI GI	g3413513
BLAST score	263
E value	2.0e-23
Match length	79
% identity	63
NCBI Description	(AJ000266) glucose-6-phosphate isomerase [Spinacia oleracea]

Seq. No.	55109
Seq. ID	zzp700829836.h1
Method	BLASTX
NCBI GI	g485512
BLAST score	197
E value	1.0e-15
Match length	70
% identity	69
NCBI Description	salt-associated protein csaA - sweet orange

Seq. No.	55110
Seq. ID	zzp700829908.h1
Method	BLASTX
NCBI GI	g4467125
BLAST score	137
E value	1.0e-08
Match length	39
% identity	72
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	55111
Seq. ID	zzp700829916.h1
Method	BLASTX
NCBI GI	g3402712
BLAST score	136
E value	1.0e-08
Match length	43
% identity	67
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55112
Seq. ID	zzp700829926.h1
Method	BLASTN
NCBI GI	g166915
BLAST score	71
E value	6.0e-32
Match length	79
% identity	97
NCBI Description	Arabidopsis thaliana alpha-4 tubulin (TUA4) gene, complete cds

Seq. No.	55113
Seq. ID	zzp700829932.h1
Method	BLASTX
NCBI GI	g3367788
BLAST score	184
E value	3.0e-14
Match length	60
% identity	58
NCBI Description	(AL031154) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	55114
Seq. ID	zzp700829978.h1
Method	BLASTN
NCBI GI	g169090
BLAST score	71
E value	6.0e-32
Match length	159
% identity	87
NCBI Description	Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA, complete cds

Seq. No.	55115
Seq. ID	zzp700830084.h1
Method	BLASTN
NCBI GI	g1619904
BLAST score	76

E value	4.0e-35
Match length	95
% identity	96
NCBI Description	Glycine max thiol protease isoform A mRNA, partial cds

Seq. No.	55116
Seq. ID	zzp700830094.h1
Method	BLASTX
NCBI GI	g1531758
BLAST score	298
E value	2.0e-27
Match length	63
% identity	86
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	55117
Seq. ID	zzp700830101.h1
Method	BLASTN
NCBI GI	g4454587
BLAST score	32
E value	7.0e-09
Match length	52
% identity	90
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	55118
Seq. ID	zzp700830123.h1
Method	BLASTN
NCBI GI	g3790450
BLAST score	87
E value	2.0e-41
Match length	183
% identity	87
NCBI Description	Chlorarachnion CCMP621 beta-tubulin-2 (btub-2) gene, partial cds

Seq. No.	55119
Seq. ID	zzp700830238.h1
Method	BLASTN
NCBI GI	g1183936
BLAST score	57
E value	2.0e-23
Match length	183
% identity	84
NCBI Description	P.sativum 5S rRNA gene

Seq. No.	55120
Seq. ID	zzp700830333.h1
Method	BLASTX
NCBI GI	g3142289
BLAST score	132
E value	1.0e-16
Match length	71
% identity	65
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase

gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	55121
Seq. ID	zzp700830413.h1
Method	BLASTX
NCBI GI	g1706082
BLAST score	145
E value	2.0e-09
Match length	73
% identity	47
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	55122
Seq. ID	zzp700830517.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	222
E value	1.0e-122
Match length	245
% identity	98
NCBI Description	G.max ADR6 mRNA

Seq. No.	55123
Seq. ID	zzp700830542.h1
Method	BLASTN
NCBI GI	g2058281
BLAST score	45
E value	2.0e-16
Match length	100
% identity	87
NCBI Description	A.thaliana mRNA for AtRanBP1a protein

Seq. No.	55124
Seq. ID	zzp700830550.h1
Method	BLASTN
NCBI GI	g18729
BLAST score	61
E value	6.0e-26
Match length	153
% identity	85
NCBI Description	Soybean (Glycine max) 18S ribosomal RNA

Seq. No.	55125
Seq. ID	zzp700830551.h1
Method	BLASTX
NCBI GI	g3522956
BLAST score	141
E value	6.0e-19
Match length	74
% identity	59
NCBI Description	(AC004411) putative pectinacetylesterase precursor

[Arabidopsis thaliana]

Seq. No.	55126
Seq. ID	zzp700830594.h1
Method	BLASTX
NCBI GI	g2660670
BLAST score	122
E value	2.0e-13
Match length	63
% identity	86
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	55127
Seq. ID	zzp700830652.h1
Method	BLASTX
NCBI GI	g1532167
BLAST score	194
E value	2.0e-15
Match length	51
% identity	65
NCBI Description	(U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis thaliana]

Seq. No.	55128
Seq. ID	zzp700830681.h1
Method	BLASTX
NCBI GI	g4468990
BLAST score	233
E value	5.0e-20
Match length	64
% identity	66
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	55129
Seq. ID	zzp700830683.h1
Method	BLASTX
NCBI GI	g1402918
BLAST score	279
E value	2.0e-25
Match length	69
% identity	75
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	55130
Seq. ID	zzp700830760.h1
Method	BLASTN
NCBI GI	g3021374
BLAST score	211
E value	1.0e-115
Match length	247
% identity	96

NCBI Description	Glycine max mRNA for profilin, PRO1

Seq. No.	55131
Seq. ID	zzp700830793.h1
Method	BLASTX
NCBI GI	g2129559
BLAST score	229
E value	2.0e-19
Match length	50
% identity	84
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	55132
Seq. ID	zzp700830820.h1
Method	BLASTX
NCBI GI	g1495366
BLAST score	158
E value	3.0e-11
Match length	64
% identity	45
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	55133
Seq. ID	zzp700830829.h1
Method	BLASTX
NCBI GI	g4490737
BLAST score	176
E value	4.0e-13
Match length	60
% identity	57
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	55134
Seq. ID	zzp700830845.h1
Method	BLASTX
NCBI GI	g130188
BLAST score	321
E value	4.0e-30
Match length	79
% identity	73
NCBI Description	PHYTOCHROME A >gi_81937_pir__S06856 phytochrome - garden pea >gi_169132 (M37217) phytochrome [Pisum sativum] >gi_295830_emb_CAA32242_ (X14077) phytochrome apoprotein [Pisum sativum] >gi_226757_prf__1604466A phytochrome [Pisum sativum]

Seq. No.	55135
Seq. ID	zzp700830872.h1
Method	BLASTX
NCBI GI	g2213581
BLAST score	217
E value	5.0e-18

Match length 43
% identity 95
NCBI Description (AC000348) T7N9.1 [Arabidopsis thaliana]

Seq. No. 55136
Seq. ID zzp700830873.h1
Method BLASTN
NCBI GI g169360
BLAST score 110
E value 4.0e-55
Match length 195
% identity 90
NCBI Description P.vulgaris PVPK-1 protein, complete cds

Seq. No. 55137
Seq. ID zzp700830890.h1
Method BLASTX
NCBI GI g3763921
BLAST score 95
E value 3.0e-09
Match length 41
% identity 83
NCBI Description (AC004450) putative pirin protein [Arabidopsis thaliana]

Seq. No. 55138
Seq. ID zzp700830996.h1
Method BLASTN
NCBI GI g170071
BLAST score 202
E value 1.0e-110
Match length 246
% identity 96
NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds

Seq. No. 55139
Seq. ID zzp700831011.h1
Method BLASTN
NCBI GI g777757
BLAST score 112
E value 3.0e-56
Match length 156
% identity 26
NCBI Description Saccharum hybrid (clone SCUBI561) polyubiquitin mRNA, complete cds

Seq. No. 55140
Seq. ID zzp700831023.h1
Method BLASTX
NCBI GI g4544436
BLAST score 143
E value 3.0e-09
Match length 82
% identity 44
NCBI Description (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase, 3' partial [Arabidopsis thaliana]

Seq. No. 55141

Seq. ID	zzp700831038.h1
Method	BLASTX
NCBI GI	g729092
BLAST score	400
E value	2.0e-39
Match length	82
% identity	90
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) >gi_477484_pir__A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana >gi_304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	55142
Seq. ID	zzp700831054.h1
Method	BLASTX
NCBI GI	g4455206
BLAST score	165
E value	7.0e-12
Match length	41
% identity	71
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	55143
Seq. ID	zzp700831056.h1
Method	BLASTX
NCBI GI	g4490730
BLAST score	188
E value	1.0e-14
Match length	81
% identity	54
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	55144
Seq. ID	zzp700831059.h1
Method	BLASTN
NCBI GI	g3021372
BLAST score	73
E value	4.0e-33
Match length	80
% identity	97
NCBI Description	Glycine max mRNA for profilin, PRO2

Seq. No.	55145
Seq. ID	zzp700831075.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	217
E value	1.0e-119
Match length	233
% identity	98
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	55146
Seq. ID	zzp700831106.h1
Method	BLASTX
NCBI GI	g421955

BLAST score 233
E value 7.0e-20
Match length 75
% identity 55
NCBI Description hypothetical protein 4 - potato transposon Tst1 >gi_21434_emb_CAA36616_ (X52387) ORF4 [Solanum tuberosum]

Seq. No. 55147
Seq. ID zzp700831115.h1
Method BLASTX
NCBI GI g1495366
BLAST score 246
E value 2.0e-21
Match length 64
% identity 67
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 55148
Seq. ID zzp700831167.h1
Method BLASTX
NCBI GI g3702327
BLAST score 139
E value 6.0e-09
Match length 38
% identity 71
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 55149
Seq. ID zzp700831184.h1
Method BLASTX
NCBI GI g3193316
BLAST score 162
E value 1.0e-11
Match length 42
% identity 71
NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 55150
Seq. ID zzp700831185.h1
Method BLASTX
NCBI GI g3402758
BLAST score 342
E value 1.0e-32
Match length 75
% identity 87
NCBI Description (AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No. 55151
Seq. ID zzp700831273.h1
Method BLASTX
NCBI GI g3874271
BLAST score 181
E value 6.0e-14
Match length 51
% identity 67

NCBI Description	(Z81467) predicted using Genefinder; Similarity to Drosophila UDP-glucose:glycoprotein glucosyltransferase (TR:Q09332); cDNA EST yk250b10.3 comes from this gene; cDNA EST yk250b10.5 comes from this gene [Caenorhabditis elegans] >gi_3876437_emb_CAB04207_ (Z81516) predicted using Genefinder; Similarity to Drosophila UDP-glucose:glycoprotein glucosyltransferase (TR:Q09332); cDNA EST yk250b10.3 comes from this gene; cDNA EST yk250b10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	55152
Seq. ID	zzp700831281.h1
Method	BLASTN
NCBI GI	g4512690
BLAST score	74
E value	1.0e-33
Match length	182
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	55153
Seq. ID	zzp700831343.h1
Method	BLASTX
NCBI GI	g4455155
BLAST score	188
E value	1.0e-14
Match length	59
% identity	64
NCBI Description	(AL022023) EF-1 alpha - like protein (fragment) [Arabidopsis thaliana]

Seq. No.	55154
Seq. ID	zzp700831404.h1
Method	BLASTX
NCBI GI	g584825
BLAST score	151
E value	3.0e-10
Match length	29
% identity	93
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	55155
Seq. ID	zzp700831452.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	235
E value	1.0e-130
Match length	235
% identity	100
NCBI Description	G.max ADR6 mRNA

Seq. No.	55156
Seq. ID	zzp700831454.h1
Method	BLASTX

NCBI GI g2842493
BLAST score 174
E value 6.0e-13
Match length 42
% identity 76
NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 55157
Seq. ID zzp700831485.h1
Method BLASTX
NCBI GI g4567225
BLAST score 215
E value 8.0e-18
Match length 57
% identity 68
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 55158
Seq. ID zzp700831486.h1
Method BLASTX
NCBI GI g4544411
BLAST score 216
E value 6.0e-18
Match length 73
% identity 15
NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 55159
Seq. ID zzp700831503.h1
Method BLASTX
NCBI GI g4580515
BLAST score 260
E value 6.0e-23
Match length 84
% identity 55
NCBI Description (AF036301) scarecrow-like 3 [Arabidopsis thaliana]

Seq. No. 55160
Seq. ID zzp700831536.h1
Method BLASTX
NCBI GI g2662310
BLAST score 98
E value 7.0e-09
Match length 56
% identity 59
NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 55161
Seq. ID zzp700831579.h1
Method BLASTX
NCBI GI g2880057
BLAST score 220
E value 2.0e-18
Match length 79
% identity 61
NCBI Description (AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]

Seq. No.	55162
Seq. ID	zzp700831614.h1
Method	BLASTX
NCBI GI	g4263509
BLAST score	143
E value	3.0e-09
Match length	41
% identity	61
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55163
Seq. ID	zzp700831620.h1
Method	BLASTN
NCBI GI	g2149954
BLAST score	102
E value	2.0e-50
Match length	217
% identity	87
NCBI Description	Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA, complete cds

Seq. No.	55164
Seq. ID	zzp700831630.h1
Method	BLASTX
NCBI GI	g4512698
BLAST score	234
E value	2.0e-40
Match length	86
% identity	86
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55165
Seq. ID	zzp700831693.h1
Method	BLASTX
NCBI GI	g322752
BLAST score	101
E value	3.0e-09
Match length	68
% identity	45
NCBI Description	auxin-independent growth promoter - Nicotiana tabacum >gi_559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]

Seq. No.	55166
Seq. ID	zzp700831735.h1
Method	BLASTX
NCBI GI	g3941460
BLAST score	168
E value	3.0e-12
Match length	51
% identity	69
NCBI Description	(AF062884) putative transcription factor [Arabidopsis thaliana]

Seq. No.	55167
Seq. ID	zzp700831790.h1
Method	BLASTN

NCBI GI	g2317899
BLAST score	178
E value	1.0e-95
Match length	214
% identity	96
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	55168
Seq. ID	zzp700831812.h1
Method	BLASTX
NCBI GI	g3337352
BLAST score	354
E value	6.0e-34
Match length	89
% identity	75
NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	55169
Seq. ID	zzp700831838.h1
Method	BLASTX
NCBI GI	g3080420
BLAST score	170
E value	2.0e-12
Match length	48
% identity	62
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	55170
Seq. ID	zzp700831852.h1
Method	BLASTX
NCBI GI	g1351791
BLAST score	257
E value	1.0e-22
Match length	84
% identity	58
NCBI Description	HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION >gi_83249_pir__S19487 hypothetical protein YCR072c - yeast (Saccharomyces cerevisiae) >gi_1907211_emb_CAA42270_ (X59720) YCR072c, len:515 [Saccharomyces cerevisiae]

Seq. No.	55171
Seq. ID	zzp700831857.h1
Method	BLASTX
NCBI GI	g3033398
BLAST score	359
E value	1.0e-34
Match length	87
% identity	80
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	55172
Seq. ID	zzp700831858.h1
Method	BLASTN

NCBI GI	g1019945
BLAST score	39
E value	1.0e-12
Match length	123
% identity	83
NCBI Description	Gossypium hirsutum ascorbate peroxidase mRNA, complete cds

Seq. No.	55173
Seq. ID	zzp700831934.h1
Method	BLASTX
NCBI GI	g2911344
BLAST score	182
E value	8.0e-14
Match length	85
% identity	46
NCBI Description	(AF032442) putative E1-E2 ATPase [Homo sapiens]

Seq. No.	55174
Seq. ID	zzp700831940.h1
Method	BLASTN
NCBI GI	g20892
BLAST score	87
E value	2.0e-41
Match length	151
% identity	90
NCBI Description	Pea U2 snRNA (clone pPSU2.1)

Seq. No.	55175
Seq. ID	zzp700831955.h1
Method	BLASTN
NCBI GI	g791097
BLAST score	89
E value	1.0e-42
Match length	97
% identity	98
NCBI Description	P.vulgaris plsB mRNA

Seq. No.	55176
Seq. ID	zzp700831969.h1
Method	BLASTX
NCBI GI	g1931655
BLAST score	207
E value	3.0e-17
Match length	68
% identity	74
NCBI Description	(U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No.	55177
Seq. ID	zzp700831991.h1
Method	BLASTX
NCBI GI	g4469025
BLAST score	171
E value	1.0e-12
Match length	39
% identity	74
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	55178
Seq. ID	zzp700832057.h1
Method	BLASTX
NCBI GI	g2347188
BLAST score	263
E value	2.0e-23
Match length	68
% identity	65
NCBI Description	(AC002338) laccase isolog [Arabidopsis thaliana] >gi_3150401 (AC004165) putative laccase [Arabidopsis thaliana]

Seq. No.	55179
Seq. ID	zzp700832074.h1
Method	BLASTN
NCBI GI	g4455168
BLAST score	42
E value	1.0e-14
Match length	62
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	55180
Seq. ID	zzp700832180.h1
Method	BLASTX
NCBI GI	g4104972
BLAST score	176
E value	3.0e-13
Match length	71
% identity	62
NCBI Description	(AF043108) spermidine synthase 1 [Pisum sativum]

Seq. No.	55181
Seq. ID	zzp700832207.h1
Method	BLASTX
NCBI GI	g3548801
BLAST score	143
E value	3.0e-09
Match length	52
% identity	52
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	55182
Seq. ID	zzp700832220.h1
Method	BLASTN
NCBI GI	g603218
BLAST score	55
E value	2.0e-22
Match length	75
% identity	93
NCBI Description	Medicago sativa glucose-6-phosphate dehydrogenase mRNA, complete cds

Seq. No.	55183

Seq. ID	zzp700832221.h1
Method	BLASTX
NCBI GI	g2618699
BLAST score	153
E value	2.0e-10
Match length	65
% identity	45
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	55184
Seq. ID	zzp700832256.h1
Method	BLASTX
NCBI GI	g4371293
BLAST score	174
E value	4.0e-13
Match length	79
% identity	16
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55185
Seq. ID	zzp700832290.h1
Method	BLASTX
NCBI GI	g2702268
BLAST score	222
E value	1.0e-18
Match length	62
% identity	76
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	55186
Seq. ID	zzp700832291.h1
Method	BLASTX
NCBI GI	g4371296
BLAST score	138
E value	9.0e-09
Match length	44
% identity	61
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	55187
Seq. ID	zzp700832294.h1
Method	BLASTX
NCBI GI	g1354849
BLAST score	177
E value	2.0e-13
Match length	54
% identity	63
NCBI Description	(U57350) epoxide hydrolase [Nicotiana tabacum]

Seq. No.	55188
Seq. ID	zzp700832334.h1
Method	BLASTN
NCBI GI	g555615
BLAST score	76
E value	7.0e-35
Match length	215

% identity	85
NCBI Description	Glycine max Mandarin cytokinin induced message (cim1) mRNA, complete cds

Seq. No.	55189
Seq. ID	zzp700832383.h1
Method	BLASTN
NCBI GI	g1808591
BLAST score	49
E value	8.0e-19
Match length	100
% identity	88
NCBI Description	C.arietinum mRNA for SAM-synthetase

Seq. No.	55190
Seq. ID	zzp700832462.h1
Method	BLASTX
NCBI GI	g2833311
BLAST score	171
E value	2.0e-12
Match length	46
% identity	63
NCBI Description	HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III >gi_630728_pir__S43605 R07E5.13 protein (clone R07E5) - Caenorhabditis elegans >gi_3878946_emb_CAA83622_ (Z32683) R07E5.13 [Caenorhabditis elegans]

Seq. No.	55191
Seq. ID	zzp700832484.h1
Method	BLASTX
NCBI GI	g2642432
BLAST score	241
E value	6.0e-21
Match length	63
% identity	65
NCBI Description	(AC002391) putative elicitor response element binding protein (WRKY3) [Arabidopsis thaliana]

Seq. No.	55192
Seq. ID	zzp700832525.h1
Method	BLASTX
NCBI GI	g1335862
BLAST score	389
E value	3.0e-38
Match length	78
% identity	95
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	55193
Seq. ID	zzp700832551.h1
Method	BLASTX
NCBI GI	g2982444
BLAST score	181
E value	9.0e-14
Match length	72
% identity	56
NCBI Description	(AL022224) CLV1 receptor kinase like protein [Arabidopsis

thaliana]

Seq. No.	55194
Seq. ID	zzp700832567.h1
Method	BLASTX
NCBI GI	g882341
BLAST score	216
E value	7.0e-18
Match length	65
% identity	60
NCBI Description	(U24702) LRP1 [Arabidopsis thaliana]

Seq. No.	55195
Seq. ID	zzp700832586.h1
Method	BLASTN
NCBI GI	g1183936
BLAST score	72
E value	2.0e-32
Match length	174
% identity	86
NCBI Description	P.sativum 5S rRNA gene

Seq. No.	55196
Seq. ID	zzp700832613.h1
Method	BLASTX
NCBI GI	g3169883
BLAST score	144
E value	2.0e-09
Match length	80
% identity	39
NCBI Description	(AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No.	55197
Seq. ID	zzp700832616.h1
Method	BLASTX
NCBI GI	g3647355
BLAST score	263
E value	3.0e-23
Match length	79
% identity	63
NCBI Description	(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA

Seq. No.	55198
Seq. ID	zzp700832756.h1
Method	BLASTX
NCBI GI	g2828293
BLAST score	235
E value	4.0e-20
Match length	73
% identity	66
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	55199
Seq. ID	zzp700832885.h1
Method	BLASTX
NCBI GI	g1086250
BLAST score	144
E value	2.0e-11
Match length	70
% identity	56
NCBI Description	SUC1-sucrose proton symporter - Plantago major >gi_667047_emb_CAA59113_ (X84379) SUC1-sucrose proton symporter [Plantago major]

Seq. No.	55200
Seq. ID	zzp700832909.h1
Method	BLASTN
NCBI GI	g4097879
BLAST score	72
E value	2.0e-32
Match length	195
% identity	92
NCBI Description	Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No.	55201
Seq. ID	zzp700832944.h1
Method	BLASTX
NCBI GI	g2979543
BLAST score	124
E value	2.0e-09
Match length	46
% identity	74
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55202
Seq. ID	zzp700832991.h1
Method	BLASTX
NCBI GI	g2760537
BLAST score	132
E value	4.0e-09
Match length	65
% identity	49
NCBI Description	(Y16088) cytosolic form of cyclophilin [Lupinus luteus]

Seq. No.	55203
Seq. ID	zzp700833003.h1
Method	BLASTX
NCBI GI	g2160175
BLAST score	254
E value	3.0e-22
Match length	81
% identity	54
NCBI Description	(AC000132) Strong similarity to Dianthus cysteine proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No.	55204
Seq. ID	zzp700833011.h1

Method	BLASTX
NCBI GI	g2651308
BLAST score	135
E value	3.0e-13
Match length	77
% identity	60
NCBI Description	(AC002336) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	55205
Seq. ID	zzp700833023.h1
Method	BLASTX
NCBI GI	g2245139
BLAST score	151
E value	6.0e-11
Match length	49
% identity	80
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55206
Seq. ID	zzp700833051.h1
Method	BLASTX
NCBI GI	g3818624
BLAST score	173
E value	2.0e-20
Match length	81
% identity	67
NCBI Description	(AF095912) actin related protein 2; ARP2 [Arabidopsis thaliana]

Seq. No.	55207
Seq. ID	zzp700833122.h1
Method	BLASTX
NCBI GI	g2618687
BLAST score	222
E value	2.0e-18
Match length	87
% identity	57
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55208
Seq. ID	zzp700833139.h1
Method	BLASTX
NCBI GI	g3738339
BLAST score	351
E value	9.0e-34
Match length	76
% identity	91
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	55209
Seq. ID	zzp700833148.h1
Method	BLASTX
NCBI GI	g2244990
BLAST score	284
E value	8.0e-26
Match length	82

% identity	79
NCBI Description	(Z97340) similarity to LIM homeobox protein - Caenorhabditis [Arabidopsis thaliana]

Seq. No.	55210
Seq. ID	zzp700833173.h1
Method	BLASTX
NCBI GI	g4406780
BLAST score	191
E value	6.0e-15
Match length	41
% identity	83
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	55211
Seq. ID	zzp700833179.h1
Method	BLASTN
NCBI GI	g2351070
BLAST score	44
E value	1.0e-15
Match length	76
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	55212
Seq. ID	zzp700833193.h1
Method	BLASTX
NCBI GI	g2498490
BLAST score	217
E value	6.0e-18
Match length	70
% identity	57
NCBI Description	VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6_ murine mammary tumor integration site 6 (oncogene homolog)

Seq. No.	55213
Seq. ID	zzp700833212.h1
Method	BLASTX
NCBI GI	g3242787
BLAST score	164
E value	9.0e-12
Match length	43
% identity	77
NCBI Description	(AF055356) respiratory burst oxidase protein E [Arabidopsis thaliana]

Seq. No.	55214
Seq. ID	zzp700833222.h1
Method	BLASTX
NCBI GI	g4336205

BLAST score	266
E value	1.0e-23
Match length	57
% identity	79
NCBI Description	(AF077372) cytochrome b5 reductase [Zea mays]

Seq. No.	55215
Seq. ID	zzp700833227.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	66
E value	7.0e-29
Match length	158
% identity	85
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	55216
Seq. ID	zzp700833236.h1
Method	BLASTX
NCBI GI	g3063710
BLAST score	333
E value	2.0e-31
Match length	84
% identity	71
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	55217
Seq. ID	zzp700833258.h1
Method	BLASTX
NCBI GI	g2959781
BLAST score	201
E value	5.0e-16
Match length	49
% identity	71
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	55218
Seq. ID	zzp700833291.h1
Method	BLASTX
NCBI GI	g2842493
BLAST score	106
E value	4.0e-12
Match length	53
% identity	68
NCBI Description	(AL021749) predicted protein [Arabidopsis thaliana]

Seq. No.	55219
Seq. ID	zzp700833339.h1
Method	BLASTN
NCBI GI	g529093
BLAST score	43
E value	4.0e-15
Match length	103
% identity	89
NCBI Description	Rice mRNA for proteasome C2 subunit, complete cds

Seq. No.	55220
Seq. ID	zzp700833371.h1
Method	BLASTX
NCBI GI	g2662469
BLAST score	278
E value	4.0e-25
Match length	57
% identity	91
NCBI Description	(AF034217) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	55221
Seq. ID	zzp700833387.h1
Method	BLASTX
NCBI GI	g3193284
BLAST score	153
E value	1.0e-10
Match length	65
% identity	46
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	55222
Seq. ID	zzp700833388.h1
Method	BLASTN
NCBI GI	g3869075
BLAST score	38
E value	2.0e-12
Match length	86
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	55223
Seq. ID	zzp700833447.h1
Method	BLASTX
NCBI GI	g2565011
BLAST score	160
E value	2.0e-11
Match length	73
% identity	45
NCBI Description	(AC002983) putative MuDR-A-like transposon protein [Arabidopsis thaliana]

Seq. No.	55224
Seq. ID	zzp700833473.h1
Method	BLASTX
NCBI GI	g2316016
BLAST score	189
E value	1.0e-14
Match length	80
% identity	47
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	55225
Seq. ID	zzp700833570.h1
Method	BLASTX
NCBI GI	g2129516

BLAST score	217
E value	6.0e-18
Match length	80
% identity	51
NCBI Description	1-aminocyclopropane-1-carboxylate oxidase homolog (clone 2A6) - Arabidopsis thaliana >gi_599622_emb_CAA58151_ (X83096) 2A6 [Arabidopsis thaliana] >gi_2809261 (AC002560) F21B7.30 [Arabidopsis thaliana]

Seq. No.	55226
Seq. ID	zzp700833572.h1
Method	BLASTX
NCBI GI	g1703082
BLAST score	159
E value	3.0e-11
Match length	37
% identity	81
NCBI Description	PROBABLE ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi_1326262 (U58727) coded for by C. elegans cDNA yk133b7.5; coded for by C. elegans cDNA yk133b7.3; coded for by C. elegans cDNA CEESE58F; strong similarity to ATP citrate lyase and the alpha chain of succinyl-coa synthases [Caenorhabditis elegans]

Seq. No.	55227
Seq. ID	zzp700833578.h1
Method	BLASTX
NCBI GI	g4510421
BLAST score	223
E value	7.0e-19
Match length	66
% identity	68
NCBI Description	(AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	55228
Seq. ID	zzp700833609.h1
Method	BLASTX
NCBI GI	g3036812
BLAST score	196
E value	1.0e-15
Match length	48
% identity	77
NCBI Description	(AL022373) ATM-like protein [Arabidopsis thaliana]

Seq. No.	55229
Seq. ID	zzp700833624.h1
Method	BLASTX
NCBI GI	g3176660
BLAST score	160
E value	2.0e-11
Match length	40
% identity	72
NCBI Description	(AC004393) Similar to ERECTA receptor protein kinase gb_U47029 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	55230
Seq. ID	zzp700833627.h1

Method	BLASTX
NCBI GI	g3426041
BLAST score	184
E value	3.0e-14
Match length	48
% identity	65
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	55231
Seq. ID	zzp700833708.h1
Method	BLASTX
NCBI GI	g2739002
BLAST score	155
E value	1.0e-10
Match length	80
% identity	42
NCBI Description	(AF022460) CYP83D1p [Glycine max]

Seq. No.	55232
Seq. ID	zzp700833746.h1
Method	BLASTX
NCBI GI	g548856
BLAST score	185
E value	3.0e-14
Match length	59
% identity	64
NCBI Description	40S RIBOSOMAL PROTEIN S3 >gi_422496_pir__S35620 ribosomal protein S3 - fruit fly (Drosophila melanogaster) >gi_290275 (L13690) ribosomal protein S3/AP endonuclease DNA repair protein [Drosophila melanogaster]

Seq. No.	55233
Seq. ID	zzp700833778.h1
Method	BLASTX
NCBI GI	g1419090
BLAST score	157
E value	6.0e-11
Match length	47
% identity	66
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	55234
Seq. ID	zzp700833806.h1
Method	BLASTX
NCBI GI	g3128228
BLAST score	223
E value	1.0e-18
Match length	68
% identity	59
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	55235
Seq. ID	zzp700833842.h1
Method	BLASTX

NCBI GI g4406781
BLAST score 247
E value 2.0e-21
Match length 78
% identity 64
NCBI Description (AC006532) putative Na+/H+ antiporter [Arabidopsis thaliana]

Seq. No. 55236
Seq. ID zzp700833843.h1
Method BLASTX
NCBI GI g559713
BLAST score 117
E value 2.0e-12
Match length 73
% identity 47
NCBI Description (D38552) The ha1539 protein is related to cyclophilin. [Homo sapiens]

Seq. No. 55237
Seq. ID zzp700833867.h1
Method BLASTN
NCBI GI g2317899
BLAST score 88
E value 3.0e-42
Match length 136
% identity 91
NCBI Description Glycine max Sali3-2 mRNA, complete cds

Seq. No. 55238
Seq. ID zzp700833880.h1
Method BLASTX
NCBI GI g3831457
BLAST score 181
E value 8.0e-14
Match length 77
% identity 47
NCBI Description (AC005700) putative ion channel protein [Arabidopsis thaliana]

Seq. No. 55239
Seq. ID zzp700834009.h1
Method BLASTX
NCBI GI g4210712
BLAST score 158
E value 5.0e-11
Match length 73
% identity 48
NCBI Description (AJ006870) purple acid phosphatase [Ipomoea batatas]

Seq. No. 55240
Seq. ID zzp700834011.h1
Method BLASTX
NCBI GI g629757
BLAST score 206
E value 1.0e-16
Match length 53

% identity	72
NCBI Description	cynarase - cardoon

Seq. No.	55241
Seq. ID	zzp700834014.h1
Method	BLASTX
NCBI GI	g3785995
BLAST score	340
E value	2.0e-32
Match length	82
% identity	79
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	55242
Seq. ID	zzp700834083.h1
Method	BLASTX
NCBI GI	g1773014
BLAST score	298
E value	2.0e-27
Match length	78
% identity	74
NCBI Description	(Y10338) chloride channel Stclc1 [Solanum tuberosum]

Seq. No.	55243
Seq. ID	zzp700834088.h1
Method	BLASTX
NCBI GI	g2570203
BLAST score	272
E value	2.0e-24
Match length	75
% identity	68
NCBI Description	(U59235) unknown [Synechococcus PCC7942]

Seq. No.	55244
Seq. ID	zzp700834092.h1
Method	BLASTN
NCBI GI	g1237081
BLAST score	73
E value	4.0e-33
Match length	101
% identity	93
NCBI Description	P.sativum mRNA for ADP-glucose pyrophosphorylase (agpS2)

Seq. No.	55245
Seq. ID	zzp700834167.h1
Method	BLASTX
NCBI GI	g4559342
BLAST score	373
E value	3.0e-36
Match length	80
% identity	84
NCBI Description	(AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No.	55246
Seq. ID	zzp700834171.h1
Method	BLASTX

NCBI GI	g4049353
BLAST score	239
E value	1.0e-20
Match length	80
% identity	51
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	55247
Seq. ID	zzp700834192.h1
Method	BLASTX
NCBI GI	g2129953
BLAST score	195
E value	2.0e-15
Match length	47
% identity	72
NCBI Description	laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542) diphenol oxidase [Nicotiana tabacum]

Seq. No.	55248
Seq. ID	zzp700834194.h1
Method	BLASTX
NCBI GI	g2961085
BLAST score	320
E value	4.0e-30
Match length	73
% identity	79
NCBI Description	(AF037228) transcription factor [Arabidopsis thaliana]

Seq. No.	55249
Seq. ID	zzp700834220.h1
Method	BLASTX
NCBI GI	g3559816
BLAST score	343
E value	1.0e-32
Match length	82
% identity	78
NCBI Description	(Y15782) transketolase 2 [Capsicum annuum]

Seq. No.	55250
Seq. ID	zzp700834245.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	260
E value	1.0e-144
Match length	260
% identity	100
NCBI Description	G.max ADR6 mRNA

Seq. No.	55251
Seq. ID	zzp700834257.h1
Method	BLASTN
NCBI GI	g1370200
BLAST score	60
E value	3.0e-25
Match length	92
% identity	91
NCBI Description	L.japonicus mRNA for small GTP-binding protein, RAC2

Seq. No.	55252
Seq. ID	zzp700834262.h1
Method	BLASTN
NCBI GI	g3318610
BLAST score	79
E value	1.0e-36
Match length	143
% identity	100
NCBI Description	Glycine max mRNA for mitochondrial phosphate transporter, complete cds

Seq. No.	55253
Seq. ID	zzp700834294.h1
Method	BLASTN
NCBI GI	g1142620
BLAST score	94
E value	1.0e-45
Match length	142
% identity	92
NCBI Description	Phaseolus vulgaris phaseolin G-box binding protein PG2 (PG2) mRNA, partial cds

Seq. No.	55254
Seq. ID	zzp700834305.h1
Method	BLASTX
NCBI GI	g4406825
BLAST score	241
E value	8.0e-21
Match length	67
% identity	69
NCBI Description	(AC006201) putative ATM-like protein, 3' partial [Arabidopsis thaliana]

Seq. No.	55255
Seq. ID	zzp700834321.h1
Method	BLASTX
NCBI GI	g2660670
BLAST score	149
E value	2.0e-13
Match length	87
% identity	47
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	55256
Seq. ID	zzp700834406.h1
Method	BLASTN
NCBI GI	g534971
BLAST score	64
E value	4.0e-28
Match length	100
% identity	91
NCBI Description	V.faba (var. minor) mRNA for alpha 1,4-glucan phosphorylase L isoform

Seq. No.	55257

Seq. ID	zzp700834409.h1
Method	BLASTX
NCBI GI	g2347188
BLAST score	156
E value	6.0e-11
Match length	43
% identity	67
NCBI Description	(AC002338) laccase isolog [Arabidopsis thaliana] >gi_3150401 (AC004165) putative laccase [Arabidopsis thaliana]

Seq. No.	55258
Seq. ID	zzp700834432.h1
Method	BLASTX
NCBI GI	g1706082
BLAST score	225
E value	5.0e-19
Match length	55
% identity	71
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	55259
Seq. ID	zzp700834445.h1
Method	BLASTX
NCBI GI	g1706082
BLAST score	143
E value	2.0e-09
Match length	33
% identity	76
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	55260
Seq. ID	zzp700834457.h1
Method	BLASTN
NCBI GI	g975887
BLAST score	55
E value	9.0e-23
Match length	99
% identity	89
NCBI Description	Mesembryanthemum crystallinum myo-inositol-1-phosphate synthase mRNA, complete cds

Seq. No.	55261
Seq. ID	zzp700834461.h1
Method	BLASTX

NCBI GI	g2501056
BLAST score	171
E value	1.0e-12
Match length	33
% identity	91
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No.	55262
Seq. ID	zzp700834464.h1
Method	BLASTX
NCBI GI	g1706082
BLAST score	143
E value	2.0e-09
Match length	33
% identity	76
NCBI Description	SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3) >gi_629787_pir__S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley >gi_619350_bbs_153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] >gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3 [Hordeum vulgare]

Seq. No.	55263
Seq. ID	zzp700834507.h1
Method	BLASTX
NCBI GI	g4323240
BLAST score	260
E value	6.0e-23
Match length	75
% identity	63
NCBI Description	(AF098972) phosphatidylinositol 3-kinase TOR1 [Filobasidiella neoformans]

Seq. No.	55264
Seq. ID	zzp700834538.h1
Method	BLASTX
NCBI GI	g4572671
BLAST score	276
E value	7.0e-25
Match length	80
% identity	65
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]

Seq. No.	55265
Seq. ID	zzp700834555.h1
Method	BLASTX
NCBI GI	g3885339
BLAST score	155
E value	1.0e-10
Match length	79
% identity	39
NCBI Description	(AC005623) putative bzip protein [Arabidopsis thaliana]

Seq. No.	55266
Seq. ID	zzp700834575.h1
Method	BLASTN
NCBI GI	g667048
BLAST score	57
E value	2.0e-23
Match length	97
% identity	90
NCBI Description	P.vulgaris mRNA for protein phosphatase 1 (PP1)

Seq. No.	55267
Seq. ID	zzp700834621.h1
Method	BLASTX
NCBI GI	g1931641
BLAST score	219
E value	3.0e-18
Match length	71
% identity	63
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]

Seq. No.	55268
Seq. ID	zzp700834626.h1
Method	BLASTX
NCBI GI	g2842482
BLAST score	301
E value	7.0e-28
Match length	81
% identity	72
NCBI Description	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	55269
Seq. ID	zzp700834646.h1
Method	BLASTX
NCBI GI	g2224911
BLAST score	169
E value	1.0e-12
Match length	54
% identity	76
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	55270
Seq. ID	zzp700834647.h1
Method	BLASTX
NCBI GI	g4115534
BLAST score	239
E value	1.0e-20
Match length	79
% identity	58
NCBI Description	(AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No.	55271
Seq. ID	zzp700834672.h1
Method	BLASTN

NCBI GI	g1663536
BLAST score	46
E value	6.0e-17
Match length	46
% identity	100
NCBI Description	Glycine max clone RLG1 disease resistance protein homolog gene, partial cds

Seq. No.	55272
Seq. ID	zzp700834727.h1
Method	BLASTX
NCBI GI	g3687225
BLAST score	295
E value	4.0e-27
Match length	81
% identity	65
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55273
Seq. ID	zzp700834735.h1
Method	BLASTX
NCBI GI	g4191744
BLAST score	181
E value	1.0e-13
Match length	41
% identity	88
NCBI Description	(L81172) importin alpha homolog [Arabidopsis thaliana]

Seq. No.	55274
Seq. ID	zzp700834821.h1
Method	BLASTN
NCBI GI	g609224
BLAST score	57
E value	2.0e-23
Match length	137
% identity	86
NCBI Description	P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete cds

Seq. No.	55275
Seq. ID	zzp700834861.h1
Method	BLASTN
NCBI GI	g1143318
BLAST score	52
E value	1.0e-20
Match length	52
% identity	100
NCBI Description	Glycine max biotin carboxyl carrier protein precursor (accB-1) mRNA, complete cds

Seq. No.	55276
Seq. ID	zzp700834907.h1
Method	BLASTN
NCBI GI	g2317899
BLAST score	58
E value	4.0e-24

Match length	58
% identity	100
NCBI Description	Glycine max Sali3-2 mRNA, complete cds

Seq. No.	55277
Seq. ID	zzp700834955.h1
Method	BLASTX
NCBI GI	g3335351
BLAST score	221
E value	2.0e-18
Match length	60
% identity	13
NCBI Description	(AC004512) Similar to ERECTA receptor protein kinase gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072 come from this gene. [Arabidopsis thaliana]

Seq. No.	55278
Seq. ID	zzp700834965.h1
Method	BLASTN
NCBI GI	g829118
BLAST score	105
E value	4.0e-52
Match length	205
% identity	88
NCBI Description	P.vulgaris gene for cyclophilin

Seq. No.	55279
Seq. ID	zzp700834981.h1
Method	BLASTX
NCBI GI	g2244970
BLAST score	144
E value	2.0e-09
Match length	53
% identity	53
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	55280
Seq. ID	zzp700835043.h1
Method	BLASTX
NCBI GI	g4056478
BLAST score	308
E value	1.0e-28
Match length	87
% identity	76
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	55281
Seq. ID	zzp700835104.h1
Method	BLASTX
NCBI GI	g3785980
BLAST score	231
E value	1.0e-19
Match length	84
% identity	50
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55282
Seq. ID	zzp700835130.h1
Method	BLASTN
NCBI GI	g3510337
BLAST score	40
E value	2.0e-13
Match length	80
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	55283
Seq. ID	zzp700835134.h1
Method	BLASTX
NCBI GI	g3935178
BLAST score	178
E value	2.0e-15
Match length	62
% identity	61
NCBI Description	(AC004557) F17L21.21 [Arabidopsis thaliana]

Seq. No.	55284
Seq. ID	zzp700835168.h1
Method	BLASTX
NCBI GI	g4204294
BLAST score	271
E value	3.0e-24
Match length	71
% identity	73
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	55285
Seq. ID	zzp700835209.h1
Method	BLASTX
NCBI GI	g1655637
BLAST score	277
E value	6.0e-25
Match length	60
% identity	78
NCBI Description	(Z54179) orf [Mus musculus]

Seq. No.	55286
Seq. ID	zzp700835226.h1
Method	BLASTX
NCBI GI	g3892058
BLAST score	183
E value	6.0e-14
Match length	43
% identity	72
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No.	55287
Seq. ID	zzp700835230.h1
Method	BLASTX

NCBI GI	g2289003
BLAST score	269
E value	5.0e-24
Match length	75
% identity	69
NCBI Description	(AC002335) membrane transporter D1 isolog [Arabidopsis thaliana]

Seq. No.	55288
Seq. ID	zzp700835242.h1
Method	BLASTX
NCBI GI	g1843628
BLAST score	192
E value	5.0e-15
Match length	46
% identity	49
NCBI Description	(U88061) SNF5 homolog BSH [Arabidopsis thaliana]

Seq. No.	55289
Seq. ID	zzp700835273.h1
Method	BLASTX
NCBI GI	g3033397
BLAST score	142
E value	3.0e-09
Match length	27
% identity	93
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	55290
Seq. ID	zzp700835380.h1
Method	BLASTN
NCBI GI	g20412
BLAST score	81
E value	7.0e-38
Match length	161
% identity	88
NCBI Description	P.amygdalus mRNA for alpha-tubulin

Seq. No.	55291
Seq. ID	zzp700835422.h1
Method	BLASTN
NCBI GI	g2765818
BLAST score	37
E value	1.0e-11
Match length	49
% identity	94
NCBI Description	O.sativa OsMlo-h1 gene

Seq. No.	55292
Seq. ID	zzp700835433.h1
Method	BLASTN
NCBI GI	g938299
BLAST score	33
E value	3.0e-09
Match length	61
% identity	89
NCBI Description	V.ungiculata mRNA for unknown protein (A3 gene)

Seq. No.	55293
Seq. ID	zzp700835469.h1
Method	BLASTX
NCBI GI	g4100325
BLAST score	121
E value	6.0e-09
Match length	45
% identity	69
NCBI Description	(U96736) SL-TPS/P [Selaginella lepidophylla]

Seq. No.	55294
Seq. ID	zzp700835470.h1
Method	BLASTX
NCBI GI	g3953603
BLAST score	172
E value	1.0e-12
Match length	46
% identity	83
NCBI Description	(AB008490) response regulator 7 [Arabidopsis thaliana]

Seq. No.	55295
Seq. ID	zzp700835505.h1
Method	BLASTX
NCBI GI	g4538961
BLAST score	299
E value	1.0e-27
Match length	81
% identity	67
NCBI Description	(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis thaliana]

Seq. No.	55296
Seq. ID	zzp700835508.h1
Method	BLASTX
NCBI GI	g3687234
BLAST score	172
E value	1.0e-12
Match length	64
% identity	55
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	55297
Seq. ID	zzp700835527.h1
Method	BLASTX
NCBI GI	g3242715
BLAST score	204
E value	1.0e-16
Match length	76
% identity	58
NCBI Description	(AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55298
Seq. ID	zzp700835540.h1
Method	BLASTX
NCBI GI	g3953458

BLAST score	273
E value	2.0e-24
Match length	55
% identity	89
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	55299
Seq. ID	zzp700835563.h1
Method	BLASTX
NCBI GI	g4454019
BLAST score	197
E value	1.0e-15
Match length	70
% identity	51
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	55300
Seq. ID	zzp700835564.h1
Method	BLASTX
NCBI GI	g1514643
BLAST score	263
E value	2.0e-23
Match length	74
% identity	66
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	55301
Seq. ID	zzp700835610.h1
Method	BLASTX
NCBI GI	g862650
BLAST score	126
E value	3.0e-15
Match length	74
% identity	64
NCBI Description	(U20193) MADS-box protein AGL12 [Arabidopsis thaliana]

Seq. No.	55302
Seq. ID	zzp700835613.h1
Method	BLASTX
NCBI GI	g4544445
BLAST score	290
E value	3.0e-28
Match length	77
% identity	83
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No.	55303
Seq. ID	zzp700835631.h1
Method	BLASTN
NCBI GI	g296444
BLAST score	239
E value	1.0e-132
Match length	253
% identity	99
NCBI Description	G.max ADR6 mRNA

Seq. No.	55304
Seq. ID	zzp700835637.h1
Method	BLASTX
NCBI GI	g4455177
BLAST score	154
E value	5.0e-14
Match length	82
% identity	55
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	55305
Seq. ID	zzp700835682.h1
Method	BLASTX
NCBI GI	g3252854
BLAST score	186
E value	5.0e-17
Match length	53
% identity	94
NCBI Description	(AF020424) glutamate decarboxylase isozyme 2 [Nicotiana tabacum]

Seq. No.	55306
Seq. ID	zzp700835731.h1
Method	BLASTX
NCBI GI	g2244876
BLAST score	231
E value	4.0e-29
Match length	72
% identity	92
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55307
Seq. ID	zzp700835734.h1
Method	BLASTX
NCBI GI	g2191136
BLAST score	119
E value	6.0e-14
Match length	87
% identity	59
NCBI Description	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]

Seq. No.	55308
Seq. ID	zzp700835739.h1
Method	BLASTN
NCBI GI	g16508
BLAST score	63
E value	5.0e-27
Match length	131
% identity	87
NCBI Description	A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No.	55309

Seq. ID	zzp700835786.h1
Method	BLASTX
NCBI GI	g2894612
BLAST score	159
E value	4.0e-11
Match length	46
% identity	65
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	55310
Seq. ID	zzp700835878.h1
Method	BLASTX
NCBI GI	g3941480
BLAST score	200
E value	1.0e-21
Match length	58
% identity	78
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	55311
Seq. ID	zzp700835927.h1
Method	BLASTX
NCBI GI	g2335100
BLAST score	385
E value	1.0e-37
Match length	84
% identity	83
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	55312
Seq. ID	zzp700835935.h1
Method	BLASTX
NCBI GI	g4185499
BLAST score	253
E value	4.0e-22
Match length	86
% identity	53
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	55313
Seq. ID	zzp700835937.h1
Method	BLASTX
NCBI GI	g1786115
BLAST score	189
E value	1.0e-14
Match length	75
% identity	52
NCBI Description	(U85250) phosphoinositide-specific phospholipase C [Vigna unguiculata]

Seq. No.	55314
Seq. ID	zzp700835938.h1
Method	BLASTX

NCBI GI	g4567250
BLAST score	184
E value	5.0e-14
Match length	65
% identity	51
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	55315
Seq. ID	zzp700835977.h1
Method	BLASTN
NCBI GI	g515691
BLAST score	176
E value	2.0e-94
Match length	176
% identity	100
NCBI Description	Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds

Seq. No.	55316
Seq. ID	zzp700835992.h1
Method	BLASTX
NCBI GI	g3096947
BLAST score	322
E value	3.0e-30
Match length	82
% identity	72
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	55317
Seq. ID	zzp700836085.h1
Method	BLASTX
NCBI GI	g3687243
BLAST score	199
E value	5.0e-16
Match length	46
% identity	83
NCBI Description	(AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	55318
Seq. ID	zzp700836106.h1
Method	BLASTX
NCBI GI	g2842482
BLAST score	148
E value	8.0e-10
Match length	38
% identity	76
NCBI Description	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	55319
Seq. ID	zzp700836217.h1
Method	BLASTX
NCBI GI	g3135269
BLAST score	188
E value	1.0e-14
Match length	74

% identity	53
NCBI Description	(AC003058) unknown protein [Arabidopsis thaliana]

Seq. No.	55320
Seq. ID	zzp700836220.h1
Method	BLASTX
NCBI GI	g4467148
BLAST score	228
E value	4.0e-19
Match length	88
% identity	68
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	55321
Seq. ID	zzp700836233.h1
Method	BLASTX
NCBI GI	g1084393
BLAST score	205
E value	2.0e-16
Match length	52
% identity	71
NCBI Description	peroxidase (EC 1.11.1.7) precursor - parsley >gi_559235 (L36981) anionic peroxidase [Petroselinum crispum]

Seq. No.	55322
Seq. ID	zzp700836244.h1
Method	BLASTX
NCBI GI	g2911059
BLAST score	329
E value	5.0e-31
Match length	86
% identity	73
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	55323
Seq. ID	zzp700836253.h1
Method	BLASTN
NCBI GI	g4519188
BLAST score	34
E value	6.0e-10
Match length	50
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	55324
Seq. ID	07-V4L-01-Q1-E1-B11

Seq. No.	55325
Seq. ID	10-V4R-02-Q1-E1-C9

Seq. No.	55326
Seq. ID	11-V4L-01-Q1-E1-C11

Seq. No.	55327
Seq. ID	14-V4R-02-Q1-E1-D9

Seq. No. 55328
Seq. ID 15-V4L-01-Q1-E1-D11

Seq. No. 55329
Seq. ID 17-V4L-01-Q1-E1-E9

Seq. No. 55330
Seq. ID 18-V4R-02-Q1-E1-E9

Seq. No. 55331
Seq. ID 19-V4L-01-Q1-E1-E11

Seq. No. 55332
Seq. ID 26-V4R-02-Q1-E1-G9

Seq. No. 55333
Seq. ID 28-V4R-02-Q1-E1-G11

Seq. No. 55334
Seq. ID 2DA-01-Q1-B1-A10

Seq. No. 55335
Seq. ID 2DA-01-Q1-B1-A12

Seq. No. 55336
Seq. ID 2DA-01-Q1-B1-A3

Seq. No. 55337
Seq. ID 2DA-01-Q1-B1-B1

Seq. No. 55338
Seq. ID 2DA-01-Q1-B1-B4

Seq. No. 55339
Seq. ID 2DA-01-Q1-B1-C9

Seq. No. 55340
Seq. ID 2DA-01-Q1-B1-E12

Seq. No. 55341
Seq. ID 2DA-01-Q1-B1-E2

Seq. No. 55342
Seq. ID 2DA-01-Q1-B1-F8

Seq. No. 55343
Seq. ID 2DA-01-Q1-B1-G10

Seq. No. 55344
Seq. ID 2DA-01-Q1-B1-G7

Seq. No. 55345
Seq. ID 2DA-01-Q1-B1-H1

Seq. No. 55346
Seq. ID 2DA-01-Q1-B1-H12

Seq. No.	55347
Seq. ID	2DA-01-Q1-B1-H2
Seq. No.	55348
Seq. ID	2DA-02-Q1-B1-B10
Seq. No.	55349
Seq. ID	2DA-02-Q1-B1-B5
Seq. No.	55350
Seq. ID	2DA-02-Q1-B1-D3
Seq. No.	55351
Seq. ID	2DA-02-Q1-B1-E2
Seq. No.	55352
Seq. ID	2DA-02-Q1-B1-G11
Seq. No.	55353
Seq. ID	2DA-02-Q1-B1-G7
Seq. No.	55354
Seq. ID	2DA-02-Q1-B1-H1
Seq. No.	55355
Seq. ID	2DA-02-Q1-B1-H9
Seq. No.	55356
Seq. ID	2DC-01-Q1-B1-A5
Seq. No.	55357
Seq. ID	2DC-01-Q1-B1-B11
Seq. No.	55358
Seq. ID	2DC-01-Q1-B1-B2
Seq. No.	55359
Seq. ID	2DC-01-Q1-B1-B4
Seq. No.	55360
Seq. ID	2DC-01-Q1-B1-C12
Seq. No.	55361
Seq. ID	2DC-01-Q1-B1-D9
Seq. No.	55362
Seq. ID	2DC-01-Q1-B1-E2
Seq. No.	55363
Seq. ID	2DC-01-Q1-B1-F12
Seq. No.	55364
Seq. ID	2DC-01-Q1-B1-H10
Seq. No.	55365
Seq. ID	2DC-01-Q1-B1-H2

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Seq. No. 55366
Seq. ID 2DC-01-Q1-B1-H6

Seq. No. 55367
Seq. ID 2DC-01-Q1-E1-A6

Seq. No. 55368
Seq. ID 2DC-01-Q1-E1-B3

Seq. No. 55369
Seq. ID 2DC-01-Q1-E1-D10

Seq. No. 55370
Seq. ID 2DC-01-Q1-E1-F3

Seq. No. 55371
Seq. ID 2DC-01-Q1-E1-G7

Seq. No. 55372
Seq. ID 2DC-01-Q1-E1-H1

Seq. No. 55373
Seq. ID 2DC-01-Q1-E1-H10

Seq. No. 55374
Seq. ID 2DC-01-Q1-E1-H2

Seq. No. 55375
Seq. ID 2DC-02-Q1-B1-A1

Seq. No. 55376
Seq. ID 2DC-02-Q1-B1-A4

Seq. No. 55377
Seq. ID 2DC-02-Q1-B1-A8

Seq. No. 55378
Seq. ID 2DC-02-Q1-B1-B10

Seq. No. 55379
Seq. ID 2DC-02-Q1-B1-C1

Seq. No. 55380
Seq. ID 2DC-02-Q1-B1-C11

Seq. No. 55381
Seq. ID 2DC-02-Q1-B1-D8

Seq. No. 55382
Seq. ID 2DC-02-Q1-B1-E9

Seq. No. 55383
Seq. ID 2DC-02-Q1-B1-G5

Seq. No. 55384
Seq. ID 2DC-02-Q1-B1-G9

Seq. No. 55385
Seq. ID 2DC-02-Q1-B1-H10

Seq. No. 55386
Seq. ID 2DC-02-Q1-B1-H4

Seq. No. 55387
Seq. ID 2DC-02-Q1-B1-H5

Seq. No. 55388
Seq. ID 2DC-02-Q1-B1-H6

Seq. No. 55389
Seq. ID 2DC-02-Q1-B1-H8

Seq. No. 55390
Seq. ID 30-V4R-02-Q1-E1-H9

Seq. No. 55391
Seq. ID 31-V4L-01-Q1-E1-H11

Seq. No. 55392
Seq. ID 40-V4R-02-Q1-E1-B12

Seq. No. 55393
Seq. ID 46-V4R-02-Q1-E1-D10

Seq. No. 55394
Seq. ID 47-V4L-01-Q1-E1-D12

Seq. No. 55395
Seq. ID 48-V4R-02-Q1-E1-D12

Seq. No. 55396
Seq. ID 50-V4R-02-Q1-E1-E10

Seq. No. 55397
Seq. ID 51-V4L-01-Q1-E1-E12

Seq. No. 55398
Seq. ID 52-V4R-02-Q1-E1-E12

Seq. No. 55399
Seq. ID 53-V4L-01-Q1-E1-F10

Seq. No. 55400
Seq. ID 55-V4L-01-Q1-E1-F12

Seq. No. 55401
Seq. ID 58-V4R-02-Q1-E1-G10

Seq. No. 55402
Seq. ID 63-V4L-01-Q1-E1-H12

Seq. No. 55403
Seq. ID 6HA-01-Q1-B1-A11

Seq. No. 55404
Seq. ID 6HA-01-Q1-B1-A2

Seq. No. 55405
Seq. ID 6HA-01-Q1-B1-B4

Seq. No. 55406
Seq. ID 6HA-01-Q1-B1-C2

Seq. No. 55407
Seq. ID 6HA-01-Q1-B1-C8

Seq. No. 55408
Seq. ID 6HA-01-Q1-B1-D10

Seq. No. 55409
Seq. ID 6HA-01-Q1-B1-F1

Seq. No. 55410
Seq. ID 6HA-01-Q1-B1-F10

Seq. No. 55411
Seq. ID 6HA-01-Q1-B1-F12

Seq. No. 55412
Seq. ID 6HA-01-Q1-B1-H4

Seq. No. 55413
Seq. ID 6HA-01-Q1-B1-H6

Seq. No. 55414
Seq. ID 6HA-01-Q1-B1-H9

Seq. No. 55415
Seq. ID 6HA-01-Q1-E1-A10

Seq. No. 55416
Seq. ID 6HA-01-Q1-E1-A12

Seq. No. 55417
Seq. ID 6HA-01-Q1-E1-A3

Seq. No. 55418
Seq. ID 6HA-01-Q1-E1-A5

Seq. No. 55419
Seq. ID 6HA-01-Q1-E1-B3

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Seq. ID LIB3087-004-Q1-K1-E8

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